

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
16 January 2003 (16.01.2003)

PCT

(10) International Publication Number
WO 03/003906 A2

(51) International Patent Classification⁷: **A61B**

(21) International Application Number: PCT/US02/21338

(22) International Filing Date: 3 July 2002 (03.07.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/302,814	3 July 2001 (03.07.2001)	US
60/310,099	3 August 2001 (03.08.2001)	US
60/343,705	8 November 2001 (08.11.2001)	US
60/350,666	13 November 2001 (13.11.2001)	US
60/372,246	12 April 2002 (12.04.2002)	US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(71) Applicant: **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

(72) Inventors: **MACK, David, H.**; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **AZIZ, Natasha**; 411 California Avenue, Palo Alto, CA 94306 (US).

(74) Agents: **PARENT, Annette, S.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).

(54) Title: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.



WO 03/003906 A2

CROSS-REFERENCES TO RELATED APPLICATIONS

10 FIELD OF THE INVENTION

BACKGROUND OF THE INVENTION

Bladder cancer rarely occurs in people younger than 40 years of age, being primarily a disease of older men. Nonetheless, bladder cancer is a significant cause of illness and death in the United States. The risk of bladder cancer increases steeply with age, with over half of all bladder cancer deaths occurring after age 70. In white men older than 65, the annual disease rate of bladder cancer is approximately 2 cases per 1,000 persons; this contrasts with a rate of 0.1 cases per 1,000 persons younger than 65.

Within the United States, bladder cancer rates are higher among people who reside in northern versus southern states, and is higher for people who live in urban versus rural areas. Although this difference suggests that environmental as well as genetic factors may contribute to the development and progression of the disease, other studies confirm that certain genes play a role in bladder cancer. For example, expression of the tumor suppressor gene p53 has been associated with an adverse prognosis for patients with invasive bladder cancer. A retrospective study of 243 patients treated by radical cystectomy found that the presence of nuclear p53 was an independent predictor for recurrence among patients with mid to late stage tumors. Esrig, et al (1994) N.E.J. Med. 331:1259-64.

Urinary bladder cancers represent a spectrum of diseases that can be grouped into three general categories: superficial, invasive, and metastatic. The prognosis for treatment is highly dependent on the stage at which the tumor is first diagnosed. A unique aspect of bladder cancer treatment is that repeated surgical biopsy is an integral part of routine patient management. This has permitted the conduct of molecular genetic studies of tumors from specific stages of the disease. The results of these studies suggest that bladder cancers develop and progress along at least two discrete pathways, which may account for differences in invasiveness and metastatic potential. Incorporating molecular genetic factors into the current paradigm for diagnosis and treatment will optimize the probability of cure and allow the quality of life for bladder cancer patients to be maintained.

Early detection and treatment can prevent reoccurrence and progression of the disease to an incurable stage. Thus, the identification of novel diagnostic markers and therapeutic targets will improve the current treatment of bladder cancer patients. While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences in disease states. The elucidation of a role for novel proteins and compounds in disease states for identification of diagnostic markers and therapeutic targets is essential for improving the current treatment of bladder cancer patients. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of bladder cancer. Additionally, provided herein are molecular targets for therapeutic intervention in bladder cancer and other related bladder diseases. Further provided are

methods that can be used to screen candidate bioactive agents for the ability to modulate bladder cancer.

SUMMARY OF THE INVENTION

5 The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in bladder cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate bladder cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

10 In one aspect, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

15 In one embodiment, the present invention provides a method of determining the level of a bladder cancer associated transcript in a cell from a patient.

 In one embodiment, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

20 In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-13.

 In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

 In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

25 In one embodiment, the polynucleotide is immobilized on a solid surface.

 In one embodiment, the patient is undergoing a therapeutic regimen to treat bladder cancer. In another embodiment, the patient is suspected of having metastatic bladder cancer.

 In one embodiment, the patient is a human.

 In one embodiment, the bladder cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of bladder cancer, the method comprising the steps of: (i) providing
5 a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a bladder cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic bladder cancer. In a further
10 embodiment, the patient has a drug resistant form of bladder cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the bladder cancer-associated transcript to a level of the bladder cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

15 Additionally, provided herein is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1A-
20 13.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded
25 by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, the antibody is conjugated to an effector component, e.g., a
30 fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to bladder cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1A-13.

In another aspect, the present invention provides a method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a bladder cancer-associated cell to treat bladder cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having bladder cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence

as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

5 In one embodiment, the control is a mammal with bladder cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

 In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time
10 periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

 In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 are individually compared to their respective levels in a control cell sample or mammal. In a
15 preferred embodiment the plurality of polynucleotides is from three to ten.

 In another aspect, the present invention provides a method for treating a mammal having bladder cancer comprising administering a compound identified by the assay described herein.

 In another aspect, the present invention provides a pharmaceutical composition for
20 treating a mammal having bladder cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

 In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a bladder cancer. In one embodiment, a gene is selected from Tables 1A-13. The method further includes
25 adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

 In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary
30 when present, and wherein the comparison can occur after addition or removal of the drug

candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the
5 bladder cancer modulatory protein, or an animal lacking the bladder cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1A-13, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three
10 nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with bladder cancer is provided. The method comprises determining the expression of a gene of Tables 1A-13 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected
15 individual. A difference in the expression indicates that the first individual has a disorder associated with bladder cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in bladder cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering
20 with the binding of a bladder cancer modulating protein (bladder cancer modulatory protein) or a fragment thereof and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a bladder cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. The method
25 further includes determining the binding of said bladder cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits bladder cancer.

Also provided herein are methods of eliciting an immune response in an individual.
30 In one embodiment a method provided herein comprises administering to an individual a

composition comprising a bladder cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a bladder cancer modulating protein, preferably encoded by a nucleic acid of Tables 1A-13 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a bladder cancer modulating protein, preferably selected from the nucleic acids of Tables 1A-13, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a bladder cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

In another aspect of the invention, a method of treating an individual for bladder cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a bladder cancer modulating protein. In another embodiment, the method comprises administering to a patient having bladder cancer an antibody to a bladder cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for bladder disease (BD), e.g., cancer, including metastatic bladder cancer, as well as methods for screening for compositions which modulate bladder diseases. Also provided are methods and compositions for treating bladder disease. Various related conditions where these markers may be useful also, include, e.g., carcinoma in situ, various stages of papillary carcinomas; and such conditions in different stages, layers, structural portions, etc.

Recent advances in molecular medicine, generally, have increased the interest in tumor-specific cell surface antigens that could serve as diagnostic or prognostic markers, or as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in other, e.g., normal, adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, as a physiological consequence of such expression would be limited. Examples of such antigens in cancers other than bladder cancer include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer.

Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; and Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Definitions

The term "bladder cancer protein" or "bladder cancer polynucleotide" or "bladder cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1A-13; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-13 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of at least

about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A
5 "bladder cancer polypeptide" and a "bladder cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" bladder cancer protein or nucleic acid refers to a bladder cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type bladder cancer
10 polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of splicing, including alternative splicing, or post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid, e.g., that contains nucleic acids or polypeptides of a bladder cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g.,
15 humans, or rodents, e.g., mice and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, urine, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most
20 preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, or mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g.,
25 isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same
30 or have a specified percentage of amino acid residues or nucleotides that are the same (e.g.,

about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, substitutions, naturally occurring variants, e.g., polymorphic or allelic, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison computer algorithm, test and reference sequences, subsequence coordinates, and sequence algorithm program parameters are typically designated. Default or alternative program parameters can be selected. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, by, e.g., the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-448, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred algorithms suitable for determining percent sequence identity and sequence
5 similarity include the BLAST and BLAST 2.0 algorithms. See Altschul, et al. (1977) Nuc.
Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and
BLAST 2.0 are used, with the parameters described herein, to determine percent sequence
identity for the nucleic acids and proteins of the invention. Software for performing BLAST
analyses is publicly available through the National Center for Biotechnology Information
10 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring
sequence pairs (HSPs) by identifying short words of length W in the query sequence, which
either match or satisfy some positive-valued threshold score T when aligned with a word of
the same length in a database sequence. T is referred to as the neighborhood word score
threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for
15 initiating searches to find longer HSPs containing them. The word hits are extended in both
directions along each sequence for as far as the cumulative alignment score can be increased.
Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M
(reward score for a pair of matching residues; always > 0) and N (penalty score for
mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to
20 calculate the cumulative score. Extension of the word hits in each direction are halted when:
the cumulative alignment score falls off by the quantity X from its maximum achieved value;
the cumulative score goes to zero or below, due to the accumulation of one or more negative-
scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm
parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN
25 program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation
(E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the
BLASTP program uses as defaults a wordlength of 3, expectation (E) of 10, and the
BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA
89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of
30 both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between
5 two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

10 An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another
15 indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an
20 expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

25 The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a
30 preparation is substantially purified. In particular, an isolated nucleic acid is separated from

some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments typically denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95%
5 pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which
10 at least one amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and a non-naturally occurring amino acid polymer.

The term "amino acid" embraces naturally occurring or synthetic amino acids, amino acid analogs, and amino acid mimetics. Naturally occurring amino acids are those encoded
15 by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs include compounds that share a basic chemical structure with a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, or an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have
20 modified R groups (e.g., norleucine) or modified peptide backbones, but share some basic chemical structure with a naturally occurring amino acid. Amino acid mimetics include chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by their commonly known three letter symbols
25 or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to amino acid or nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to
30 those nucleic acids which encode identical or essentially identical amino acid sequences, or

where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at
5 each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Each nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each
10 codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

15 As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution
20 tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another include: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L),
25 Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman.

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. See, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the
30 Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The

Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, which are portions of a polypeptide that often form a compact unit of the polypeptide, and are typically about 25-500 amino acids long. Typical domains are made of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. In some cases, nucleic acid analogs are included that may have alternate backbones, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149); phosphorothioate (Mag, et al. (1991), Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048); phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-322); O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207. Other analog nucleic acids include those with positively charged backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (U.S. Patent Nos. 5,386,023; 5,637,684; 5,602,240; 5,216,141; and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426;

Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2-3 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 5 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx; and non-ribose backbones (see U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6-7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also contemplated. See Jenkins and Turner (1995) Chem. Soc. Rev. 24:169-176. Several nucleic acid analogs are described in 10 Rawls (page 35, June 2, 1997) C&E News. Modifications of the ribose-phosphate backbone may be made, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

15 Particularly preferred are peptide nucleic acids (PNA) which include peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. The PNA backbone typically exhibits improved hybridization kinetics, exhibiting larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. 20 DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. And due to their non-ionic nature, hybridization of the polymers is relatively insensitive to salt concentration. In addition, PNAs are not as easily degraded by cellular enzymes, and can be more stable.

25 The nucleic acids may be single stranded or double stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, 30 including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine, hypoxanthine,

isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures.

5 Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Direct or indirect methods are contemplated. For example, useful labels include ³²P, fluorescent
10 dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the bladder cancer nucleic acids, proteins, and antibodies. Methods are well known for conjugating the antibody to the label,
15 including those methods described by Hunter, et al. (1962) Nature 144:945-946; David, et al. (1974) Biochemistry 13:1014-021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or
20 noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to a target, e.g., an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds; fluorescent compounds; an enzyme or substrate; tags such as epitope tags; a toxin; activatable moieties; a chemotherapeutic agent; a lipase; an antibiotic; a radioisotope emitting "hard", e.g., beta radiation; or an attracting moiety.

25 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding
30 partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which streptavidin linked label may bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced

recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

5 The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a
10 coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid
15 sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is
20 active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

25 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

- 5 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview
10 of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Techniques in Biochemistry and Molecular Biology; vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which
15 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g.,
20 about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least about two times background, preferably about 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC,
25 and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-

65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least about twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a bladder cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the bladder cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease bladder cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cell viability, cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a bladder cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects.

Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the bladder cancer protein;

5 measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation or metabolism. Determination of the functional effect of a compound on bladder cancer can also be performed using bladder cancer assays, such as, in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or

10 serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. Functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for bladder

15 cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of bladder cancer polynucleotide and

20 polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of bladder cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of bladder cancer proteins, e.g., antagonists. Antisense nucleic acids

25 may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate bladder cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of bladder cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small

30 chemical molecules and the like. Such assays for inhibitors and activators include, e.g.,

expressing the bladder cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of bladder cancer can also be identified by incubating bladder cancer cells with the test compound and determining increases or decreases in the expression of 1 or more bladder cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more bladder cancer proteins, such as bladder cancer proteins encoded by the sequences set out in Tables 1A-13.

Samples or assays comprising bladder cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably about 50%, more preferably about 25-0%. Activation of a bladder cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably about 150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably about 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 of Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.

Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using

recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of bladder cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal bladder or other

tissue) may be distinguished from cancerous or metastatic cancerous tissue of the bladder, or bladder cancer tissue or metastatic bladder cancerous tissue can be compared with tissue samples of bladder and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different bladder cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in bladder cancer versus non-bladder cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate bladder cancer, and thus tumor growth or recurrence, in a particular patient; or does chemotherapy or radiation therapy induce expression of particular targets. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of bladder cancer in the tissue or origin of a primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the bladder cancer expression profile. This may be done by making biochips comprising sets of important bladder cancer genes, which can then be used in these screens. These methods can also be applied on the protein basis; that is, protein expression levels of the bladder cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the bladder cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or inhibitory nucleic acids, or the bladder cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in bladder disease or cancer relative to normal tissues and/or non-malignant bladder tissue, herein termed "bladder cancer sequences." As outlined below, bladder cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in bladder cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the bladder cancer sequences are from humans; however,

as will be appreciated by those in the art, bladder cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other bladder cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Bladder cancer sequences from other organisms may be obtained using the techniques outlined below.

Bladder cancer sequences can include both nucleic acid and amino acid sequences. Bladder cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications. Biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the bladder cancer sequences can be generated.

A bladder cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying bladder cancer-associated sequences, the bladder cancer screen typically includes comparing genes identified in different tissues, e.g., normal, non-malignant, or cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing bladder cancer samples with metastatic cancer samples from other cancers, such as lung, bladder, gastrointestinal cancers, ovarian, etc. Samples of different stages of bladder cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal bladder, but also including, and not limited to lung, heart, brain, liver, bladder, kidney,

muscle, colon, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the bladder cancer screen that are expressed in a significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, e.g., not be expressed on critical organs.

In a preferred embodiment, bladder cancer sequences are those that are up-regulated in bladder cancer; that is, the expression of these genes is higher in the bladder cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and sequences of accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, bladder cancer sequences are those that are down-regulated in the bladder cancer; that is, the expression of these genes is lower in bladder cancer tissue as compared to non-cancerous tissue (see, e.g., Tables 1A-13). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in bladder cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with bladder cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference,

Coronado, CA. Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, 5 saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic 10 database of the invention can be maintained on an electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent that similar databases can be assembled for 15 assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing bladder cancer, e.g., the identification of bladder cancer-associated sequences described herein, provide an abundance of information, which can be correlated 20 with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

25 An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing 30 information in a format that allows a collection of partial-length DNA sequences to be

catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity
5 between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis
10 described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as
15 the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler
20 (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Oxford Univ. Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to
25 Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g.,

with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for bladder cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention
5 in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at
10 least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem,
15 ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result
20 obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data
25 file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of
30 the query target and results are output via an I/O device. For example, a central processor

can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of bladder cancer-associated proteins

Bladder cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the bladder cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In

addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the bladder cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases

and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain
5 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors
10 include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved
15 motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example,
20 growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or
25 may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Bladder cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful
30 in imaging modalities. Antibodies may be used to label such readily accessible proteins in

situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods.

- 5 Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

- In another embodiment, the bladder cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted
- 10 proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a
- 15 duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Bladder cancer proteins that are secreted or released proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum,
- 20 or urine tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of bladder cancer nucleic acids

- As described above, bladder cancer sequence is initially identified by substantial
- 25 nucleic acid and/or amino acid sequence homology or linkage to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The bladder cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-13, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the bladder cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a bladder cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire bladder cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant bladder cancer nucleic acid can be further-used as a probe to identify and isolate other bladder cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant bladder cancer nucleic acids and proteins.

The bladder cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the bladder cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense/inhibition applications. Alternatively, the bladder cancer nucleic acids that include coding regions of bladder cancer proteins can be put into expression vectors for the expression of bladder cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to bladder cancer nucleic acids (both the nucleic acid sequences outlined in the tables and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the bladder cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that

hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

10 A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole
15 genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or
20 separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of
25 the biotinylated probe to the streptavidin. By "covalent binding" and grammatical
30

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being

particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of bladder cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a bladder cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of bladder cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification. See, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com.

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1080; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, and linker adapter PCR, etc.

Expression of bladder cancer proteins from nucleic acids

In a preferred embodiment, bladder cancer nucleic acids, e.g., encoding bladder cancer proteins, are used to make a variety of expression vectors to express bladder cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the bladder cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a

promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; two sequences may be operably linked if they are physically linked on a single polynucleotide. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the bladder cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are useful in the present invention.

In addition, an expression vector may comprise additional elements. The expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and replication. For integrating expression vectors, the expression vector may contain at least one sequence homologous to the host cell genome, and preferably two homologous sequences

which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known (e.g., Fernandez and Hoeffler, *supra*).

- 5 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

 The bladder cancer proteins of the present invention may be produced by culturing a host cell transformed with an expression vector under the appropriate conditions to induce or
10 cause expression of the bladder cancer protein. Conditions appropriate for bladder cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will typically require optimizing the growth and proliferation of the host cell, while the use of an
15 inducible promoter typically requires identifying the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and harvest time selection can be crucial for product yield.

 Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, insect, and
20 animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

 In a preferred embodiment, the bladder cancer proteins are expressed in mammalian
25 cells. Mammalian expression systems include retroviral and adenoviral systems. Retroviral vector systems are described in PCT/US97/01019 and PCT/US97/01048. Of particular use are promoters from mammalian viral genes, since viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the
30 CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription

termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

5 Methods of introducing exogenous nucleic acid into mammalian and other hosts are well known, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

10 In another embodiment, bladder cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. Synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. A bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. Often an efficient
15 ribosome binding site is desirable. The expression vector may include a signal peptide sequence that provides for secretion of the bladder cancer protein. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may include a selectable marker gene to allow for the selection of bacterial
20 strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs, e.g., ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline, or biosynthetic genes, e.g., those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus*
25 *cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using, e.g., calcium chloride treatment, electroporation, and other methods.

 Bladder cancer proteins can also be produced in insect cells. See, e.g., Miller, et al. (1997) Baculovirus Expression Vectors: A Laboratory Manual Oxford Books; ISBN: 0716770172; and Makrides (1999) Prot. Expr. Purif. 17:183-202.

30

Bladder cancer protein may be produced in yeast cells. Yeast expression systems exist with expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. See, e.g., Jones, et al. (eds. 5 1993) The Molecular and Cellular Biology of the Yeast Saccharomyces: Gene Expression CSH Press; ISBN: 0879693657.

The bladder cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the bladder cancer protein may be fused to a carrier protein to form an 10 immunogen. Alternatively, the bladder cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the bladder cancer protein is a bladder cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression or purification purposes.

The bladder cancer protein is typically purified or isolated after expression. Bladder 15 cancer proteins may be isolated or purified in a variety of ways, depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, reverse-phase HPLC chromatography, and chromatofocusing. The bladder cancer protein may be purified using a standard anti-bladder cancer protein antibody 20 affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see, e.g., Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the bladder cancer protein. In some instances no purification will be necessary, which may depend on the intended use.

25 Once expressed and purified, if necessary, the bladder cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of bladder cancer proteins

In one embodiment, the bladder cancer proteins are derivative or variant bladder cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative bladder cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most residues within the bladder cancer peptide.

Certain embodiments of bladder cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the bladder cancer protein, using cassette or PCR, mutagenesis, or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant bladder cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are often characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the bladder cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. To optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed bladder cancer variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is performed using assays of bladder cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be

tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combinations thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the bladder cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the bladder cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the bladder cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. Substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic acid or aspartic acid; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Covalent modifications of bladder cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a bladder cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a bladder cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for crosslinking bladder

cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-bladder cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginy residues to the corresponding glutamic and aspartic residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (pp. 79-86, Creighton (1984) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the bladder cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence bladder cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence bladder cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express bladder cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to bladder cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence bladder cancer polypeptide (for O-linked glycosylation sites). The bladder cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the bladder cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the bladder cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

Such methods are described in the art, e.g., in WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the bladder cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art. See, e.g., Hakimuddin, et al. (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of bladder cancer comprises linking the bladder cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Bladder cancer polypeptides of the present invention may also be modified to form chimeric molecules comprising a bladder cancer polypeptide fused to a heterologous polypeptide or amino acid sequence. In one embodiment, a chimeric molecule comprises a fusion of a bladder cancer polypeptide with an epitope tag. The epitope tag is generally placed at the amino-or carboxyl-terminus of the bladder cancer polypeptide. The presence of such epitope-tagged forms of a bladder cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the bladder cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a bladder cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616);

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other bladder cancer proteins of the bladder cancer family, and bladder cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related bladder cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the bladder cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis (1990) PCR Protocols, supra.

Antibodies to bladder cancer proteins

In a preferred embodiment, when the bladder cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the bladder cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller bladder cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known (see, e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a

nucleic acid of the tables or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor.

- 5 Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected as appropriate.

- The antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1A-13 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (pp. 59-103, Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 10
15
20
25

- In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two
- 30

epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1A-13 or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to bladder cancer protein are capable of reducing or eliminating a biological function of a bladder cancer protein, as is described below. That is, the addition of anti-bladder cancer protein antibodies (either polyclonal or preferably monoclonal) to bladder cancer tissue (or cells containing bladder cancer) may reduce or eliminate the bladder cancer. Generally, at least about 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred, and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the bladder cancer proteins are humanized antibodies (e.g., Xenex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin. See Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596. Humanization can be performed, e.g., following the method of Winter and co-workers (see Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or of human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of bladder cancer with an antibody raised against bladder cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient), which may be used to target a label or toxin. Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As

appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

5 In a preferred embodiment the bladder cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted bladder cancer protein.

10 In another preferred embodiment, the bladder cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the bladder cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane bladder cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-
15 competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the bladder cancer protein. The antibody is also an antagonist of the bladder cancer protein. Further, the antibody prevents activation of the transmembrane bladder cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the bladder cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or
20 sensitize the cell to cytotoxic agents, including, but not limited to $\text{TNF-}\alpha$, $\text{TNF-}\beta$, IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, bladder cancer is
25 treated by administering to a patient antibodies directed against the transmembrane bladder cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

 In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be a number of molecules, including labelling moieties such as
30 radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the

therapeutic moiety is a small molecule that modulates the activity of the bladder cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the bladder cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with bladder cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to bladder cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with bladder cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against bladder cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane bladder cancer proteins not only serves to increase the local concentration of therapeutic moiety in the bladder cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the bladder cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the bladder cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The bladder cancer antibodies of the invention specifically bind to bladder cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_D of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of bladder cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the bladder cancer phenotype. Expression levels of genes in normal tissue (e.g., not experiencing bladder cancer) and in bladder cancer tissue (and in some cases, for varying severities of bladder cancer that relate to prognosis, as outlined below), or in non-malignant disease, are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus bladder cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR,

northern analysis and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from about 300-1000% being especially preferred.

5 Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the bladder cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass
10 spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to bladder cancer genes, e.g., those identified as being important in a bladder cancer or disease phenotype, can be evaluated in a bladder cancer diagnostic test.

 In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.
15 Similarly, these assays may be performed on an individual basis as well.

 In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

20 In a preferred embodiment nucleic acids encoding the bladder cancer protein are detected. Although DNA or RNA encoding the bladder cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a bladder cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to,
25 oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
30 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid

probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a bladder cancer protein is detected by binding the digoxigenin with an anti-digoxigenin
5 secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells
10 containing bladder cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, bladder cancer proteins, including intracellular, transmembrane or secreted proteins, find use as diagnostic or prognostic markers of bladder cancer, or to assist in selecting therapy based on expression profile and archival data. Detection of these proteins in putative bladder cancer tissue allows for detection or diagnosis of bladder cancer. In one embodiment, antibodies are used to detect bladder cancer proteins.
20 A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the bladder cancer protein is detected, e.g., by immunoblotting with antibodies raised against the bladder cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the bladder cancer protein find use in in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) "Antibodies in Cell Biology" Methods in Cell Biology (vol. 37). In this method cells are contacted with from one to many antibodies to the bladder cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment
30 the antibody is detected by incubating with a secondary antibody that contains a detectable

label. In another method the primary antibody to the bladder cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of bladder cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing bladder cancer from blood, serum, plasma, stool, urine, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of bladder cancer proteins. Antibodies can be used to detect a bladder cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous bladder cancer protein.

In a preferred embodiment, in situ hybridization of labeled bladder cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including bladder cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to bladder cancer, clinical, pathological, or other information, e.g., in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, bladder cancer probes may

be attached to biochips for the detection and quantification of bladder cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR methods may provide more sensitive and accurate quantification.

5 Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression
10 profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids,
15 modified proteins and cells containing the native or modified bladder cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the bladder cancer phenotype or an identified physiological function of a bladder cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred
20 embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein
25 level. That is, having identified a particular gene as up regulated in bladder cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the bladder cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing bladder cancer, with changes of at least
30 about 10%, preferably about 50%, more preferably about 100-300%, and in some

embodiments about 300-1000% or greater. Thus, if a gene exhibits about 4-fold increase in bladder cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, about 10-fold decrease in bladder cancer tissue compared to normal tissue often provides a target value of about 10-fold increase in expression to be induced by the test
5 compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the bladder cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of
10 expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as
15 outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the
20 expression of one or more bladder cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1A-13. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate bladder cancer, modulate bladder cancer proteins, bind to a bladder cancer protein, or interfere with the binding of a bladder cancer protein and an antibody or other
25 binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the bladder cancer phenotype or the expression of a bladder cancer sequence,
30 e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter

expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a bladder cancer phenotype, e.g., to a normal tissue or non-malignant fingerprint. In another embodiment, a modulator induced a bladder cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than about 100 and less than about 2,500 daltons. Preferred small molecules are less than about 2000, or less than about 1500 or less than about 1000 or less than about 500 D.

Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl, or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups.

Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a bladder cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a bladder cancer polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88); peptoids (PCT Publication No WO 91/19735); encoded peptides (PCT Publication WO 93/20242); random bio-oligomers (PCT Publication WO 92/00091); benzodiazepines (U.S. Pat. No. 5,288,514); diversomers such as hydantoins, benzodiazepines, and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913); vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-6570); nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218); analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-2662); oligocarbamates (Cho, et al. (1993) Science 261:1303-1305); and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Strategene, Corp.); peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083); antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287);

carbohydrate libraries (Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853); and small organic molecule libraries (see, e.g., benzodiazepines, Baum (p. 33, Jan 18, 1993) C&E News); isoprenoid (U.S. Patent No. 5,569,588); thiazolidinones and metathiazanones (U.S. Patent No. 5,549,974); pyrrolidines (U.S. Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (U.S. Patent No. 5,506,337); benzodiazepines (U.S. Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; and 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of bladder cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in

arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid substitutions. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the

length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of bladder cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag

or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the bladder cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a bladder cancer expression pattern leading to a normal expression pattern, or to modulate a single bladder cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated bladder cancer tissue reveals genes that are not expressed in normal tissue or bladder cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for bladder cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated bladder cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of bladder cancer cells, that have an associated bladder cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or

retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some
5 period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., bladder cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the bladder cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on
10 bladder cancer activity. By defining such a signature for the bladder cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual
15 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins" or a "bladder cancer modulatory protein". The bladder cancer modulatory protein may be a
20 fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables 1A-13. Preferably, the bladder cancer modulatory protein is a fragment. In a preferred embodiment, the bladder cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are naturally occurring allelic variants of a protein
25 encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the bladder cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has

an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the bladder cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the bladder cancer protein is conjugated to

5 BSA.

Measurements of bladder cancer polypeptide activity, or of bladder cancer or the bladder cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the bladder cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of bladder cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian bladder cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a bladder cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the bladder cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the bladder cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the bladder cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein,

30

CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual
5 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins." The bladder cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown
10 herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate
15 differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products,
20 and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the bladder cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a bladder cancer protein and a candidate compound, and determining the binding of the compound to the bladder cancer protein. Preferred embodiments utilize the human bladder cancer protein,
25 although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative bladder cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the bladder cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated
30 sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the bladder cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the bladder cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the bladder cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the bladder cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also
5 useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., a bladder cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the
10 binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically
15 between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding
20 to the bladder cancer protein and thus is capable of binding to, and potentially modulating, the activity of the bladder cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate
25 that the test compound is bound to the bladder cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the bladder
30 cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the bladder cancer proteins. In this embodiment, the methods comprise combining a bladder cancer protein and a competitor in a first sample. A second sample comprises a test compound, a bladder cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the bladder cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the bladder cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native bladder cancer protein, but cannot bind to modified bladder cancer proteins. The structure of the bladder cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a bladder cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a bladder cancer protein. The methods

comprise adding a test compound, as defined above, to a cell comprising bladder cancer proteins. Many different cell types may be transfected to contain a recombinant nucleic acid that encodes a bladder cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

5 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, and pharmacological agents including, e.g., chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In one example, the determinations are determined at different stages of the cell cycle process.

10 In this way, compounds that modulate bladder cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the bladder cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

 In one embodiment, a method of inhibiting bladder cancer cell division is provided.

15 The method comprises administration of a bladder cancer inhibitor. In another embodiment, a method of inhibiting bladder cancer is provided. The method comprises administration of a bladder cancer inhibitor. In a further embodiment, methods of treating cells or individuals with bladder cancer are provided. The method comprises administration of a bladder cancer inhibitor. In one embodiment, a bladder cancer inhibitor is an antibody as discussed above.

20 In another embodiment, the bladder cancer inhibitor is an antisense molecule.

 A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

 Normal cells require a solid substrate to attach and grow. When the cells are

25 transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify

30 modulators of bladder cancer sequences, which when expressed in host cells, inhibit

abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a bladder cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; Freshney (1994), *supra*). This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. See also, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer, Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate bladder cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1984), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (2000), supra.

Tumor growth in vivo

Effects of bladder cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the bladder cancer gene is disrupted or in which a bladder cancer gene is inserted. Knock-out

transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous bladder cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous bladder cancer gene with a mutated version of the bladder cancer gene, or by mutating the endogenous bladder cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be made. See Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a bladder cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of bladder cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a bladder cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a bladder cancer protein mRNA, or a subsequence thereof.

- 5 Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-
10 sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the bladder cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means,
15 or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-
20 sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for bladder cancer molecules. A preferred antisense molecule is for a bladder cancer sequences in Tables 1A-13, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at
25 least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific
30 manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999)

Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g.,
5 treatment of or validation of relevance to disease

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of bladder cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have
10 been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes.

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.
15 5,254,678. Methods of preparing them are well known. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of bladder cancer may be introduced into a cell containing
20 the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its
25 corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of bladder cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be
30 used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating bladder cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-bladder cancer antibody that reduces or eliminates the biological activity of an endogenous bladder cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a bladder cancer protein. This may be accomplished in many ways. In a preferred embodiment, e.g., when the bladder cancer sequence is down-regulated in bladder cancer, such state may be reversed by increasing the amount of bladder cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous bladder cancer gene or administering a gene encoding the bladder cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the bladder cancer sequence is up-regulated in bladder cancer, the activity of the endogenous bladder cancer gene is decreased, e.g., by the administration of a bladder cancer antisense nucleic acid.

In one embodiment, the bladder cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to bladder cancer proteins. Similarly, the bladder cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify bladder cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a bladder cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The bladder cancer antibodies may be coupled to standard affinity chromatography columns and used to purify bladder cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the bladder cancer protein.

Methods of identifying variant bladder cancer-associated sequences

Without being bound by theory, expression of various bladder cancer sequences is correlated with bladder cancer. Accordingly, disorders based on mutant or variant bladder cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant bladder cancer genes, e.g., determining all or part of the sequence of at least one endogenous bladder cancer genes in a cell. This may be accomplished using many sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the bladder cancer genotype of an individual, e.g.,

5 determining all or part of the sequence of at least one bladder cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced bladder cancer gene to a known bladder cancer gene, e.g., a wild-type gene.

10 The sequence of all or part of the bladder cancer gene can then be compared to the sequence of a known bladder cancer gene to determine if differences exist. This can be done using many known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the bladder cancer gene of the patient and the known bladder cancer gene correlates with a disease state or a propensity for a disease
15 state, as outlined herein.

In a preferred embodiment, the bladder cancer genes are used as probes to determine the number of copies of the bladder cancer gene in the genome.

In another preferred embodiment, the bladder cancer genes are used as probes to determine the chromosomal localization of the bladder cancer genes. Information such as
20 chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the bladder cancer gene locus.

Administration of pharmaceutical and vaccine compositions

25 In one embodiment, a therapeutically effective dose of a bladder cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug
30 Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker,

ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharma. Assn.; and Pickar (1999) Dosage Calculations Thomson. As is known in the art, adjustments for bladder cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. USSN 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in bladder cancer and is hereby expressly incorporated by reference.

10 A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the bladder cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the bladder cancer proteins and modulators may be directly applied as a solution or spray.

20 The pharmaceutical compositions of the present invention comprise a bladder cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that bladder cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a bladder cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary

widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics McGraw-Hill.

5 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1-10 mg per patient per day. Dosages from about 0.1-100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
10 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman: The Pharmacological Basis of Therapeutics, supra.

 The compositions containing modulators of bladder cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications,
15 compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered
20 depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition
25 and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies
30 may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present bladder cancer protein-modulating compounds can be administered alone or in combination with additional bladder cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides
5 comprising nucleic acid sequences set forth in Tables 1A-13, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of bladder cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

10 The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other methods for introducing cloned genomic DNA,
15 cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Vol. 1-3) CSH Press.

20 In a preferred embodiment, bladder cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, bladder cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the bladder cancer coding regions) can be administered in a gene therapy application. These bladder cancer genes can include antisense applications, either as gene therapy (e.g., for
25 incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Bladder cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (Vitiello, et al. (1995) J. Clin. Invest. 95:341-349);
30 peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres

(Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681); peptide compositions contained in immune stimulating complexes (ISCOMS) (Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243); multiple antigen peptide systems (MAPs) (Tam
5 (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32); peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-547; Kieny, et al. (1986) AIDS
10 Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J.
15 Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies,
20 also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc., Needham, MA, may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or
25 Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated
30 tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A.

Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA
5 encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et al. (1990) Science 247:1465-1468 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery,
10 cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of
15 vaccinia virus, e.g., as a vector to express nucleotide sequences that encode bladder cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are
20 described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

25 Methods for the use of genes as DNA vaccines are well known, and include placing a bladder cancer gene or portion of a bladder cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a bladder cancer patient. The bladder cancer gene used for DNA vaccines can encode full-length bladder cancer proteins, but more preferably encodes portions of the bladder cancer proteins including peptides
30 derived from the bladder cancer protein. In one embodiment, a patient is immunized with a

DNA vaccine comprising a plurality of nucleotide sequences derived from a bladder cancer gene. For example, bladder cancer-associated genes or sequence encoding subfragments of a bladder cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the bladder cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment bladder cancer genes find use in generating animal models of bladder cancer. When the bladder cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the bladder cancer gene will also diminish or repress expression of the gene. Animal models of bladder cancer find use in screening for modulators of a bladder cancer-associated sequence or modulators of bladder cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the bladder cancer protein. When desired, tissue-specific expression or knockout of the bladder cancer protein may be necessary.

It is also possible that the bladder cancer protein is overexpressed in bladder cancer. As such, transgenic animals can be generated that overexpress the bladder cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of bladder cancer and are additionally useful in screening for modulators to treat bladder cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include one or more of the following: assay reagents, buffers, bladder cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense or inhibitory

5 polynucleotides, ribozymes, dominant negative bladder cancer polypeptides or polynucleotides, small molecules inhibitors of bladder cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g.,
10 protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such
15 media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of bladder cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a bladder cancer-associated polypeptide or polynucleotide, control positive or negative
20 samples, reaction tubes, and instructions for testing bladder cancer-associated activity. Optionally, the kit contains biologically active bladder cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on
25 correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described
 5 (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE DESCRIPTIONS

Table 1A shows about 3413 that exhibit increased or decreased expression in bladder cancer
 10 samples. See USSN 60/302,814.

Table 2A shows about 485 genes overexpressed in bladder tumors relative to normal tissues as analyzed using the Affymetrix/Eos Hu03 GeneChip array. See USSN 60/343,705.

15 Table 3A shows about 414 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as small molecule, antibody, DNA vaccine targets for the therapy of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the
 20 relative level of mRNA expression.

Table 4A shows about 129 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as diagnostics of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for
 25 each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A shows about 149 genes upregulated in bladder cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
 30 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A shows about 199 genes upregulated in bladder cancer relative to normal bladder
 35 tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

40 Table 7A shows about 63 genes downregulated in bladder tumors relative to normal bladder. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip

array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Table 8A shows about 1440 genes upregulated in Ta or T1 bladder tumors from patients who later presented with muscle-invasive bladder tumors (stage T2-T4). Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

10 Table 9A shows about 1200 genes upregulated in Ta or T1 tumors of patients who later presented with either more Ta tumors or no tumors at all. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Table 10A shows about 65 genes upregulated in non-invasive exophytic Ta bladder tumors relative to T2-T4 muscle-invasive tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

20 Table 11A shows about 106 genes upregulated in muscle-invasive T2-T4 bladder tumors relative to non-invasive exophytic Ta bladder tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

25 Table 12A shows the Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 13. Seq ID No. is used to link Table 12A to table 13.

30 Tables 1B-12B show the accession numbers for those Pkey's lacking UnigeneID's for tables 1A-12A, respectively. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Tables 1C-12C show genomic positioning for Pkey's lacking Unigene ID's and accession numbers for tables 1A-12A, respectively. For each predicted exon, is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

40 **TABLE 1A:**

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	please refer to original application
R2:	please refer to original application
Target Type:	downregulate stage if target is downregulated in bladder tumors relative to normal bladder or

early stage if target is an earl stage (Ta) bladder tumor marker or
late stage if target is a late stage (T2-T4) bladder tumor marker or
T2-T4 grade 3 papilloma marker or T2-T4 grade 3 solid tumor marker or Upregulate stage

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	Target Type
5	400440	XB3957	Hs.83870	nebulin	0.17	2.05	downregulate stage
	400888				0.24	1.97	downregulate stage
	401566				0.19	4.05	downregulate stage
	401669				0.2	2.05	downregulate stage
10	401691				0.04	10.13	downregulate stage
	401905				0.3	1.87	downregulate stage
	402076				0.06	6.51	downregulate stage
	402110				0.43	2.35	downregulate stage
15	402271	NM_002197	Hs.154721	aconitase 1, soluble	0.21	2.16	downregulate stage
	403362				0.18	4.44	downregulate stage
	403687				0.32	1.91	downregulate stage
	403959				0.14	2.27	downregulate stage
20	404015				0.2	2.48	downregulate stage
	404059				0.36	1.84	downregulate stage
	404152				0.32	1.85	downregulate stage
	404498				0.14	2.18	downregulate stage
	404819	U58196	Hs.296281	Interleukin enhancer binding factor 1	0.19	5.25	downregulate stage
	405001				0.16	2.92	downregulate stage
	405349				0.18	3.8	downregulate stage
	405390				0.3	2.64	downregulate stage
25	405735				0.13	2.44	downregulate stage
	405968				0.26	1.85	downregulate stage
	406017				0.32	2.28	downregulate stage
	406305				0.42	1.93	downregulate stage
30	406320	BE261320	Hs.297096	transcriptional adaptor 3 (ADA3, yeast h	0.37	2.01	downregulate stage
	406704				0.3	2.84	downregulate stage
	406706				0.14	7.4	downregulate stage
	406707				0.05	12.51	downregulate stage
	407013	U35637	Hs.172004	gbtHuman nebulin mRNA, partial cds	0.14	2.17	downregulate stage
35	407245				0.02	15.21	downregulate stage
	407330				0.42	1.87	downregulate stage
	407571				0.38	2.13	downregulate stage
	407682	AL035858	Hs.3807	FXD domain-containing ion transport reg	0.34	2.56	downregulate stage
	407815				0.31	2.44	downregulate stage
	407834				0.15	2.98	downregulate stage
	407891				0.15	3.33	downregulate stage
40	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp56401262 (f	0.12	8.05	downregulate stage
	407938				0.08	8.77	downregulate stage
	407965				0.26	2.29	downregulate stage
	408009				0.49	1.91	downregulate stage
45	408139	AA451966	Hs.43005	RAB9-like protein	0.41	1.88	downregulate stage
	408221				0.04	24.1	downregulate stage
	408374				0.35	2.85	downregulate stage
	408493				0.09	9.04	downregulate stage
50	408508	AI805109	Hs.135736	KIAA1580 protein	0.45	2.2	downregulate stage
	408614				0.13	5.48	downregulate stage
	408652				0.33	2.5	downregulate stage
	408753				0.05	6.94	downregulate stage
	408896	AI610447	Hs.48778	niban protein	0.39	2.01	downregulate stage
55	409277				0.18	2.75	downregulate stage
	410023				0.07	2.7	downregulate stage
	410036				0.09	5.23	downregulate stage
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	0.24	2.34	downregulate stage
	410168				0.39	2.17	downregulate stage
	410243				0.11	2.82	downregulate stage
60	410339				0.15	2.16	downregulate stage
	410677	NM_003278	Hs.65424	telranectin (plasminogen-binding protein	0.32	2.65	downregulate stage
	410868				0.2	2.74	downregulate stage
	411048				0.2	1.92	downregulate stage
	411067				0.11	3.41	downregulate stage
65	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	0.17	5.8	downregulate stage
	411644				0.06	13.8	downregulate stage
	411741				0.36	2.5	downregulate stage
	412047				0.18	3.57	downregulate stage
70	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	0.32	1.89	downregulate stage
	412389				0.38	2.6	downregulate stage
	412442				0.12	3.67	downregulate stage
	412519				0.24	1.86	downregulate stage
	412622	AW564708	Hs.171959	troponin T1, skeletal, slow	0.06	5.45	downregulate stage
75	412649				0.29	2.95	downregulate stage
	412659				0.18	2.06	downregulate stage
	412758				0.3	2.23	downregulate stage

	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	0.11	2.71	downregulate stage
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, S	0.44	2.03	downregulate stage
	413074	A1871368	Hs.8417	ESTs	0.47	1.91	downregulate stage
5	413272	AA127923	Hs.293256	ESTs	0.09	4.44	downregulate stage
	413276	Z24725	Hs.75260	mitogen inducible 2	0.23	2.48	downregulate stage
	413508	BE145364		gb3L0-HT0198-151099-125-e05 HT0198 Homo	0.31	2.53	downregulate stage
	413624	BE177019	Hs.75445	SPARC-like 1 (masi9, hevin)	0.33	2.17	downregulate stage
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	0.33	2.63	downregulate stage
10	414063	H26904	Hs.75736	apoptoprotein D	0.42	1.85	downregulate stage
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	0.16	2.22	downregulate stage
	414280	AI568801	Hs.71721	ESTs	0.02	10	downregulate stage
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	0.13	4.14	downregulate stage
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	0.33	2.14	downregulate stage
	414712	N88858	Hs.77039	ribosomal protein S3A	0.4	2.5	downregulate stage
15	414903	AA451700	Hs.85835	Homo sapiens cDNA: FLJ22841 fis, clone K	0.3	3.3	downregulate stage
	415165	AW887604	Hs.78065	complement component 7	0.04	3.41	downregulate stage
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	0.2	3.29	downregulate stage
	415447	Z97171	Hs.78454	myoclin, trabecular meshwork inducible	0.15	6.55	downregulate stage
	415672	N53097	Hs.193579	ESTs	0.28	3.55	downregulate stage
20	415934	NM_000928	Hs.992	phospholipase A2, group 1B (pancreas)	0.34	2.64	downregulate stage
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	0.3	1.98	downregulate stage
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	0.41	1.95	downregulate stage
	416585	X54162	Hs.79386	leiomodlin 1 (smooth muscle)	0.02	49.3	downregulate stage
	416854	H40164	Hs.80296	Purkinje cell protein 4	0.02	7.55	downregulate stage
25	416941	BE000150	Hs.48778	niban protein	0.27	2.16	downregulate stage
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	0.29	2.43	downregulate stage
	417011	F08212	Hs.234898	ESTs	0.41	2.06	downregulate stage
	417298	AW665639	Hs.37958	ESTs	0.27	3.7	downregulate stage
30	417501	AL041219	Hs.82222	sama domain, immunoglobulin domain (Ig),	0.39	2.08	downregulate stage
	417553	L09190	Hs.82276	trichohyalin	0.29	2.59	downregulate stage
	417987	AA210872	Hs.50133	ESTs	0.22	2.09	downregulate stage
	418297	R91254		ghyp94e12a1 Soares fetal liver spleen	0.28	1.9	downregulate stage
	418332	R34976	Hs.78293	ESTs	0.2	3.9	downregulate stage
35	418391	NM_003281	Hs.84673	tropontin 1, skeletal, slow	0.35	2.02	downregulate stage
	418409	AA219332	Hs.120869	ESTs, Weakly similar to AF092922 1 retin	0.21	3.8	downregulate stage
	418421	R58620	Hs.85050	phospholamban	0.2	2.08	downregulate stage
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.05	21.55	downregulate stage
	418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	0.42	1.95	downregulate stage
40	418787	AW286134	Hs.86999	ESTs	0.48	1.87	downregulate stage
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	0.26	2.43	downregulate stage
	418947	W52990	Hs.22860	ESTs	0.13	7.18	downregulate stage
	419037	R39895	Hs.7864	ESTs	0.27	2	downregulate stage
	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp5861524 (f	0.19	5.25	downregulate stage
45	419535	AW139550	Hs.115173	ESTs	0.31	2.59	downregulate stage
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	0.28	2.38	downregulate stage
	419685	W76083	Hs.173077	ESTs	0.4	2.21	downregulate stage
	419703	AI793257	Hs.128151	ESTs	0.09	3.52	downregulate stage
	419942	U25138	Hs.83841	potassium large conductance calcium-acti	0.28	2.96	downregulate stage
50	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.3	2.09	downregulate stage
	420195	N44348	Hs.300794	ESTs	0.22	2.79	downregulate stage
	420261	AW206093	Hs.748	fibroblast growth factor receptor 1 (fms	0.35	1.98	downregulate stage
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.29	3.5	downregulate stage
	421296	NM_002666	Hs.103253	perilipin	0.36	2.11	downregulate stage
55	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDN	0.13	4.3	downregulate stage
	421763	AW163500	Hs.108080	cysteine and glycine-rich protein 1	0.26	3.49	downregulate stage
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	0.14	5	downregulate stage
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	0.2	2.29	downregulate stage
	422287	F16365	Hs.114345	cytochrome c oxidase subunit VIIa polype	0.27	2.58	downregulate stage
60	422320	AI745249	Hs.23650	ESTs, Weakly similar to AAB47496 NG5 (H.	0.24	2.95	downregulate stage
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	0.23	3.57	downregulate stage
	422639	AI929377	Hs.173724	creatine kinase, brain	0.39	1.97	downregulate stage
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	0.37	2.29	downregulate stage
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to	0.37	2.47	downregulate stage
	423889	AL035447	Hs.134594	hypothetical protein LOC57158	0.24	2.43	downregulate stage
65	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	0.27	2.28	downregulate stage
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	0.3	2.59	downregulate stage
	424479	AF064238	Hs.149098	smoothelin	0.26	3.29	downregulate stage
	424580	AA446539	Hs.35092	ESTs	0.15	2.57	downregulate stage
70	424846	AU077324	Hs.1832	neuropeptide Y	0.4	2.04	downregulate stage
	424938	AW102607	Hs.245233	ESTs	0.29	2.16	downregulate stage
	424982	U94777	Hs.154084	phosphorylase, glycogen; muscle (McArdle	0.42	1.89	downregulate stage
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.14	1.86	downregulate stage
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	0.03	13.25	downregulate stage
	425622	AW360847	Hs.16578	ESTs	0.3	2.19	downregulate stage
75	425751	T19239	Hs.1940	crystallin, alpha B	0.47	1.92	downregulate stage
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	0.45	1.85	downregulate stage
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	0.19	2.85	downregulate stage

	425932	M81650	Hs.1968	semenogelin I	0.02	16.3	downregulate stage
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	0.27	2.52	downregulate stage
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	0.1	10.3	downregulate stage
5	426752	X69490	Hs.172004	titin	0.03	31.3	downregulate stage
	426809	BE313114	Hs.29706	ESTs	0.34	2.95	downregulate stage
	427078	AI676062	Hs.111902	ESTs	0.22	2.11	downregulate stage
	427136	AL117415	Hs.173716	Homo sapiens mRNA; cDNA DKFZp434K0521 (f	0.37	2.33	downregulate stage
	427164	AB037721	Hs.173871	KJAA1300 protein	0.12	5.47	downregulate stage
10	427185	AA398930	Hs.186674	ESTs	0.22	4.65	downregulate stage
	427373	AB007972	Hs.177533	Homo sapiens mRNA; cDNA DKFZp586N0318 (f	0.22	3.18	downregulate stage
	427393	AB029018	Hs.177635	KJAA1095 protein	0.27	2.13	downregulate stage
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	0.05	4	downregulate stage
	427676	AA394062	Hs.180266	tropomyosin 2 (beta)	0.45	1.87	downregulate stage
15	427888	AA417088	Hs.137598	ESTs	0.36	2.04	downregulate stage
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapi	0.32	2.39	downregulate stage
	428087	AA100573	Hs.182421	tropoin C2, fast	0.17	4.37	downregulate stage
	428138	AA773842	Hs.293799	ESTs	0.45	2.2	downregulate stage
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.23	3.36	downregulate stage
20	428329	AA426091	Hs.98453	ESTs	0.21	2.09	downregulate stage
	428409	AW117207	Hs.98523	ESTs	0.1	7.63	downregulate stage
	428411	AW291464	Hs.10338	ESTs	0.32	1.98	downregulate stage
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	0.08	2.99	downregulate stage
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL	0.11	2.07	downregulate stage
25	428899	AA744610	Hs.194431	palladin	0.42	1.84	downregulate stage
	429350	AI754634	Hs.131987	ESTs	0.06	4.73	downregulate stage
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	0.18	2.31	downregulate stage
	429545	AI824164	Hs.17667	lymphocyte antigen 6 complex, locus E	0.31	2.07	downregulate stage
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	0.33	2.18	downregulate stage
30	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	0.36	2.17	downregulate stage
	429930	AI580809	Hs.99569	ESTs	0.18	5.6	downregulate stage
	429956	AI374651	Hs.22542	ESTs	0.22	4.45	downregulate stage
	430013	AA463833	Hs.151275	ESTs	0.21	3.03	downregulate stage
	430271	T06199	Hs.237506	heat shock cognate 40	0.47	1.85	downregulate stage
35	430310	U60115	Hs.239069	four and a half LIM domains 1	0.18	3.44	downregulate stage
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	0.38	2.26	downregulate stage
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	0.16	2.52	downregulate stage
	430712	AW044647	Hs.196284	ESTs	0.29	1.94	downregulate stage
40	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.14	4.48	downregulate stage
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.35	1.87	downregulate stage
	432247	AA531287	Hs.105805	ESTs	0.21	3.99	downregulate stage
	432689	AB018320	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.11	1.98	downregulate stage
	432792	AA448114	Hs.278950	protocadherin beta 1	0.22	2.93	downregulate stage
	433142	AL120697	Hs.110640	ESTs	0.21	2.18	downregulate stage
45	433633	AI880516	Hs.84630	ESTs	0.34	2.67	downregulate stage
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	0.35	2.27	downregulate stage
	433826	AA609938	Hs.144492	ESTs	0.24	1.91	downregulate stage
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	0.07	3.46	downregulate stage
50	434160	BE551196	Hs.114275	ESTs	0.5	2	downregulate stage
	434352	AF129505	Hs.86492	small muscle protein, X-linked	0.34	2.13	downregulate stage
	434361	AF129755	Hs.117772	ESTs	0.03	31.3	downregulate stage
	435731	AA699581	Hs.186811	ESTs	0.31	3.25	downregulate stage
	435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.21	3.73	downregulate stage
55	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	0.35	2.25	downregulate stage
	436359	Z63806		gb:HL.sapiens mRNA for axonemal dynein he	0.24	3.28	downregulate stage
	436638	AI271945	Hs.134984	ESTs	0.36	1.87	downregulate stage
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	0.14	6.95	downregulate stage
	437176	AW176909	Hs.42346	calcineurin-binding protein calcisarcin-1	0.32	2.19	downregulate stage
60	437233	D81448	Hs.153951	ARP1 (actin-related protein 1, yeast) ho	0.27	2.38	downregulate stage
	438619	AB032773	Hs.6341	TUJ1B1-TY protein	0.19	2.69	downregulate stage
	438666	AW014493	Hs.128727	ESTs	0.16	1.98	downregulate stage
	439231	AW581935	Hs.141480	ESTs	0.1	3.9	downregulate stage
	439973	AI733308	Hs.124663	ESTs	0.16	6.2	downregulate stage
65	440172	AA868584	Hs.126154	ESTs	0.24	2.34	downregulate stage
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.11	3.02	downregulate stage
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	0.19	2.95	downregulate stage
	440700	AW952281	Hs.296184	ESTs, Highly similar to GB01_HUMAN GUANI	0.13	2.69	downregulate stage
	440737	AI375167	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	0.5	2	downregulate stage
70	441805	AA285136	Hs.7974	neuronal specific transcription factor D	0.07	13.55	downregulate stage
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.38	1.86	downregulate stage
	442109	BE218975	Hs.212395	ESTs	0.24	2.86	downregulate stage
75	442985	AI025984	Hs.55467	ESTs	0.19	2	downregulate stage
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.09	3.66	downregulate stage
	443164	AI038503	Hs.55780	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.2	1.86	downregulate stage
	443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-1	0.11	2.79	downregulate stage
	443604	C03577	Hs.5515	myosin regulatory light chain 2, smooth	0.24	3.41	downregulate stage
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	0.28	3.6	downregulate stage
	443932	AW888222	Hs.9973	tensin	0.32	2.57	downregulate stage

	444195	AB002351	Hs.10587	KIAA0353 protein	0.19	4.04	downregulate stage
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	0.38	2.04	downregulate stage
	444684	AW044070	Hs.147037	ESTs	0.36	2.25	downregulate stage
5	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	0.29	2.19	downregulate stage
	444938	AW470690	Hs.148814	ESTs	0.43	2.3	downregulate stage
	445230	U97018	Hs.12451	echinoderm microtubule-associated protel	0.13	2.64	downregulate stage
	445235	AI564022	Hs.138207	ESTs	0.13	2.4	downregulate stage
	445621	AI733818	Hs.145549	ESTs	0.25	1.91	downregulate stage
10	445687	W80382	Hs.149297	ESTs	0.2	3.5	downregulate stage
	445850	AI262049	Hs.145560	ESTs	0.53	1.9	downregulate stage
	446406	AI553681	Hs.25248	ESTs	0.07	3.25	downregulate stage
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.33	1.9	downregulate stage
	447595	AW379130	Hs.18953	phosphodiesterase 9A	0.28	1.85	downregulate stage
	447918	AI129320	Hs.16930	ESTs	0.29	2.46	downregulate stage
15	448076	AJ133123	Hs.20196	adenylate cyclase 9	0.2	2.27	downregulate stage
	448283	AJ340462	Hs.182979	ribosomal protein L12	0.53	1.9	downregulate stage
	448303	BE622468	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.39	1.84	downregulate stage
	448425	AI500359	Hs.233401	ESTs	0.16	1.97	downregulate stage
20	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	0.12	5.43	downregulate stage
	448555	AI536697	Hs.159863	ESTs	0.32	2.86	downregulate stage
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	0.17	2.66	downregulate stage
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	0.24	1.86	downregulate stage
	449226	AB002365	Hs.23311	KIAA0367 protein	0.1	4.96	downregulate stage
25	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	0.14	2.53	downregulate stage
	449422	AA001373	Hs.59821	ESTs	0.43	2.3	downregulate stage
	449690	AA002140	Hs.33024	ESTs	0.5	2	downregulate stage
	449874	AA135688	Hs.10083	ESTs	0.33	2.7	downregulate stage
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	0.11	5.57	downregulate stage
30	450300	AL041440	Hs.58210	ESTs	0.41	2.13	downregulate stage
	450578	AI971773	Hs.232268	ESTs	0.44	2.25	downregulate stage
	450810	BE207588	Hs.25511	transforming growth factor beta 1 induce	0.51	1.86	downregulate stage
	450831	R37974	Hs.25255	ESTs	0.23	1.96	downregulate stage
	451331	AK002039	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	0.37	2.18	downregulate stage
35	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.1	9.36	downregulate stage
	451782	AF233588	Hs.27018	Ris	0.35	2.43	downregulate stage
	451948	AW452473	Hs.211125	ESTs	0.43	1.88	downregulate stage
	452422	AA521416	Hs.22701	ESTs	0.41	1.85	downregulate stage
	452463	R36452	Hs.300817	ESTs	0.09	4.05	downregulate stage
40	452776	AA194540	Hs.13522	ESTs	0.36	2.16	downregulate stage
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	0.06	4.7	downregulate stage
	453064	R40334	Hs.301395	Homo sapiens cDNA: FLJ21204 fis, clone C	0.07	4.47	downregulate stage
	453351	AI625721	Hs.61814	Homo sapiens cDNA: FLJ22750 fis, clone K	0.33	3.05	downregulate stage
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	0.03	7.14	downregulate stage
45	453359	AA448787	Hs.24872	ESTs, Weakly similar toortic carboxype	0.4	1.92	downregulate stage
	453464	AI884911	Hs.32989	receptor (calcionin) activity modifying	0.24	3.29	downregulate stage
	453500	AI478427	Hs.43125	ESTs	0.02	11.41	downregulate stage
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	0.39	2.04	downregulate stage
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	0.43	1.86	downregulate stage
50	453666	AW015681	Hs.135229	ESTs, Moderately similar to AF107203 1 a	0.28	2.42	downregulate stage
	453698	AA037615	Hs.42746	ESTs	0.2	1.88	downregulate stage
	453702	AA037637	Hs.42128	ESTs	0.32	2.42	downregulate stage
	453725	W28543		gb:48c5 Human retina cDNA randomly prime	0.2	2.06	downregulate stage
	453950	AA156998	Hs.211568	eukaryotic translation Initiation factor	0.07	7.86	downregulate stage
55	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	0.16	2.49	downregulate stage
	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	0.41	2.45	downregulate stage
	454637	AW811613		gb:CM3-ST0157-300999-017-f05 ST0157 Homo	0.18	2.2	downregulate stage
	454750	AW866285		gb:QV4-SN0024-080400-167-a09 SN0024 Homo	0.49	2.05	downregulate stage
	455073	AW854829		gb:QV2-CT0261-201099-011-f01 CT0261 Homo	0.27	2.09	downregulate stage
60	455485	AA102287	Hs.26756	Homo sapiens cDNA: FLJ20896 fis, clone A	0.32	2.07	downregulate stage
	455611	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	0.15	2.87	downregulate stage
	456100	AI983981	Hs.189114	ESTs	0.4	2.5	downregulate stage
	456841	AA875863	Hs.152345	poliiovirus receptor-related 1 (herpesvir	0.35	1.9	downregulate stage
	457064	AA776743	Hs.191589	ESTs	0.17	2.34	downregulate stage
65	457108	N74724	Hs.108479	ESTs	0.48	2.1	downregulate stage
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	0.29	2.59	downregulate stage
	457625	T10073		gb:seq1293 b4HB3MA Col8-HAP-F1 Homo sapi	0.29	3.45	downregulate stage
	458482	AV648858	Hs.29488	ESTs	0.26	2.17	downregulate stage
	458622	AA972412	Hs.13755	f-box and WD-40 domain protein 2	0.51	1.95	downregulate stage
70	458841	W28965		gb:54d10 Human retina cDNA randomly prim	0.32	3.1	downregulate stage
	459037	AW439497	Hs.290656	EST	0.43	2.35	downregulate stage
	400762				0.71	0.4	early stage
	400937				1.2	0.26	early stage
	400977				0.63	0.48	early stage
75	401024				0.8	0.3	early stage
	401048				1.9	0.22	early stage
	401537				1.3	0.2	early stage
	401619				3.5	0.19	early stage

	402089			0.39	0.55	early stage
	402176			0.35	0.91	early stage
	402407			1	0.15	early stage
5	402430			0.28	1.25	early stage
	402435			2.15	0.21	early stage
	402522			1.8	0.14	early stage
	402546			0.17	1.66	early stage
	402604			0.41	0.66	early stage
10	402716			0.14	0.86	early stage
	402846			0.61	0.52	early stage
	402922			0.14	0.83	early stage
	403567			0.44	0.49	early stage
	403590			1	0.34	early stage
15	404336			0.49	0.44	early stage
	404345	AA730407	Hs.159156	0.38	0.4	early stage
	404501	AW247252	Hs.75514	0.32	0.8	early stage
	404594			0.37	0.91	early stage
	404874			1.87	0.26	early stage
	404881			0.36	0.5	early stage
20	404896	NM_000429	Hs.106845	1	0.36	early stage
	404999	U58196	Hs.296281	0.19	1.06	early stage
	405071			0.19	0.77	early stage
	405308			0.4	0.55	early stage
	405463			0.41	1	early stage
25	405580			1.89	0.19	early stage
	405600			0.22	0.63	early stage
	405720			0.37	0.61	early stage
	405863			0.53	0.26	early stage
	405887			0.24	1.1	early stage
30	405920			0.39	1.15	early stage
	406036			2.15	0.17	early stage
	406243			0.32	1.23	early stage
	406367			0.38	0.76	early stage
35	406834	AI318680		0.4	0.67	early stage
	406881	D16154		0.14	1.55	early stage
	407411	AF060170		0.39	0.69	early stage
	407639	AW205369	Hs.252936	0.61	0.34	early stage
	408112	AW451982	Hs.248613	0.2	0.54	early stage
40	408732	AL117490	Hs.47225	1	0.32	early stage
	409103	AF251237	Hs.112208	0.33	1.03	early stage
	409840	AW502122		0.56	0.28	early stage
	410128	AW904599		1.26	0.37	early stage
	411474	AW848427		1	0.14	early stage
45	412564	X83703	Hs.74019	0.36	0.44	early stage
	413266	BE300352		1.46	0.25	early stage
	413341	H78472	Hs.191325	0.41	0.48	early stage
	414055	AW818687	Hs.5366	0.33	0.67	early stage
	414170	AA335996	Hs.3743	1.15	0.21	early stage
50	414220	BE298094		0.16	0.52	early stage
	414276	BE297852		1.75	0.2	early stage
	414327	BE408145	Hs.185254	0.1	0.99	early stage
	414366	BE549143		1	0.31	early stage
	414376	BE393856	Hs.66915	0.18	0.96	early stage
55	414555	N98569	Hs.76422	0.48	0.67	early stage
	415199	AA161125	Hs.57893	0.75	0.72	early stage
	417304	H15635		0.6	0.58	early stage
	417371	N74613	Hs.269149	0.3	0.58	early stage
	418133	R43504	Hs.6181	1.28	0.29	early stage
60	419273	BE271180	Hs.293490	0.54	0.28	early stage
	419716	AA953770		0.45	0.66	early stage
	420390	AA330047	Hs.191187	1.45	0.12	early stage
	421745	AF205849	Hs.107740	0.33	0.71	early stage
	421813	BE048255		0.52	0.67	early stage
65	422669	H12402	Hs.119122	1	0.26	early stage
	422743	BE304678	Hs.119598	0.2	0.57	early stage
	422760	BE409561		0.41	0.64	early stage
	422880	AF228704	Hs.121524	3.75	0.1	early stage
	423457	F08208	Hs.155606	0.55	0.54	early stage
70	425349	AA425234	Hs.79886	1	0.21	early stage
	425360	BE547704		0.28	0.85	early stage
	426356	BE536836		0.31	0.69	early stage
	426521	AF161445	Hs.170219	0.11	0.69	early stage
	426670	AA383047	Hs.193718	1	0.55	early stage
	426699	AA383337	Hs.121269	0.33	0.71	early stage
75	427827	AA416577	Hs.189105	1.16	0.41	early stage
	428651	AF186478	Hs.188401	1.85	0.24	early stage
	430727	X75917	Hs.2654	0.78	0.46	early stage

	430750	AI650360	Hs.100256	ESTs	2.15	0.17	early stage
	430795	AW971398		gb:EST383487 MAGE resequences, MAGL Homo	1.95	0.21	early stage
	431900	AW972048	Hs.192534	ESTs	0.36	0.73	early stage
5	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	1.8	0.17	early stage
	432791	NM_014554	Hs.278949	sentin/SUMO-specific protease	2.8	0.15	early stage
	433404	T32982	Hs.102720	ESTs	2.2	0.13	early stage
	433782	AF090945		gb:Homo sapiens clone HQ0670	3.3	0.15	early stage
	433877	BE146567	Hs.257475	ESTs	0.65	0.7	early stage
10	434483	AA223646	Hs.57222	nurim (nuclear envelope membrane protein	0.38	0.49	early stage
	435752	AF230801	Hs.125180	growth hormone receptor	0.52	0.4	early stage
	436178	BE152396	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1.65	0.14	early stage
	436391	AJ227892	Hs.146274	ESTs	1.35	0.16	early stage
	436602	AI793222	Hs.166817	ESTs	0.17	1.46	early stage
	436777	AA731199	Hs.293130	ESTs	1	0.2	early stage
15	436813	AW975714	Hs.129004	ESTs	0.19	1.45	early stage
	438869	NM_014857	Hs.297661	Homo sapiens YAC clone 377A1 unknown mRN	0.96	0.2	early stage
	437169	AA309612	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	0.07	1.8	early stage
	438649	AA813136	Hs.143014	ESTs	1.38	0.19	early stage
20	438681	AW384815	Hs.149208	KIAA1555 protein	0.25	0.54	early stage
	438802	AA825976	Hs.136954	ESTs	1.8	0.14	early stage
	438887	R68857	Hs.265499	ESTs	1.05	0.32	early stage
	440128	AA952623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	1	0.19	early stage
	440397	AA884448	Hs.157239	ESTs	0.59	0.38	early stage
	440509	BE410132	Hs.134202	ESTs, Weakly similar to B41182 collagen	0.26	0.9	early stage
25	440605	Z40094	Hs.185698	ESTs	0.51	0.43	early stage
	442238	AW135374	Hs.270549	ESTs	1	0.18	early stage
	443258	AF169301	Hs.9098	sulfate transporter 1	0.85	0.49	early stage
	445739	AW136354	Hs.145303	ESTs	0.88	0.4	early stage
	447306	AI373163	Hs.170333	ESTs	0.15	0.8	early stage
30	447346	AI525135	Hs.210507	ESTs	1.35	0.27	early stage
	448265	N46272	Hs.26812	ESTs	0.47	0.26	early stage
	448578	AI560776	Hs.199854	ESTs	0.19	0.68	early stage
	448778	AF074913		gb:Homo sapiens transcription factor Pax	0.57	0.53	early stage
35	448871	BE616709		gb:601279937F1 NIH_MGC_39 Homo sapiens c	0.26	0.94	early stage
	449180	AI633836	Hs.195649	ESTs	0.46	0.45	early stage
	449213	BE616861		gb:601279056F1 NIH_MGC_39 Homo sapiens c	0.73	0.56	early stage
	449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens c	0.27	0.76	early stage
	449450	AL039852	Hs.256990	ESTs, Moderately similar to ALU7_HUMAN A	1	0.26	early stage
40	449815	AI671000	Hs.199739	ESTs	1.2	0.15	early stage
	450972	AW967906	Hs.194617	ESTs	0.28	0.83	early stage
	451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	0.35	0.77	early stage
	451283	H83979		gb:ys93d11.1.r1 Soares retina N2b5HR Homo	1	0.23	early stage
	451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from	0.16	1.37	early stage
45	452530	AI905518		gb:RC-BT091-210199-098 BT091 Homo sapien	1.35	0.21	early stage
	452550	AA026735		gb:ze93d05.r1 Soares_fetal_heart_NbH19W	0.44	0.6	early stage
	454121	AW090524	Hs.244967	ESTs	2.85	0.17	early stage
	454554	AW847505		gb:RCO-CT0210-280999-021-c10 CT0210 Homo	0.36	0.5	early stage
	454697	AW813728	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	0.43	0.6	early stage
50	454851	AW835127		gb:RC4-LT0011-100100-012-c07 LT0011 Homo	0.77	0.32	early stage
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	0.26	0.52	early stage
	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	1.7	0.18	early stage
	455970	AI733857	Hs.71483	ESTs	0.66	0.45	early stage
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	0.64	0.43	early stage
55	456450	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	0.38	0.76	early stage
	456526	AA782222	Hs.192008	ESTs	0.63	0.43	early stage
	456855	AF035528	Hs.153883	MAD (mothers against decapentaplegic, Dr	0.49	0.46	early stage
	456983	AI081687	Hs.170225	thymopolein	0.27	0.75	early stage
	457089	AA416556	Hs.98234	ESTs	0.34	0.48	early stage
60	458198	AI286100	Hs.192739	ESTs	0.47	0.48	early stage
	458425	AI084057	Hs.301149	ESTs	0.4	0.37	early stage
	458660	AI299739	Hs.99601	Homo sapiens cDNA FLJ12553 fis, clone NT	0.79	0.68	early stage
	458703	AW749121	Hs.282901	ESTs	1	0.23	early stage
	458767	T97083	Hs.148355	ESTs	1	0.17	early stage
65	459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens c	0.68	0.56	early stage
	400860				4.9	0.08	late stage
	408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.58	0.84	late stage
	408558	AW015759	Hs.235709	ESTs	1.26	0.45	late stage
	410077	AF097645	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	6.2	0.12	late stage
70	410295	AA741357	Hs.62041	nidogen (enactin)	0.77	0.86	late stage
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	1.45	0.27	late stage
	410614	AI091195	Hs.65029	growth arrest-specific 1	0.4	1.12	late stage
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	0.71	1.07	late stage
	411573	AB029000	Hs.70823	KIAA1077 protein	3.64	0.19	late stage
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	5.18	0.13	late stage
75	412178	AW898526		gb:RC6-NN0072-040500-011-E05 NN0072 Homo	7.55	0.08	late stage
	412429	AV650262	Hs.75765	GRO2 oncogene	3.37	0.15	late stage
	412652	AI801777	Hs.6774	ESTs	0.49	1.24	late stage

5	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.6	0.11	late stage
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.62	0.14	late stage
	414183	AW957445	Hs.301711	ESTs	3.18	0.16	late stage
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	0.81	0.73	late stage
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	0.37	0.99	late stage
10	414504	AW069181	Hs.293523	ESTs, Weakly similar to transformallon-r	0.97	0.65	late stage
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.84	0.1	late stage
	415116	AA160363	Hs.269956	ESTs	7.45	0.07	late stage
	415714	NM_002290	Hs.78672	laminin, alpha 4	0.49	1.39	late stage
	415822	D59243	Hs.30708	gb:HUM526E07B Clontech human placenta po	8.15	0.09	late stage
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	0.48	1.46	late stage
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.52	0.44	late stage
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2	0.39	late stage
	417733	AL048678	Hs.82503	syntrophin	0.2	2.67	late stage
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	4.56	0.12	late stage
20	417849	AW291587	Hs.82733	nidogen 2	1.81	0.38	late stage
	418005	AI185220	Hs.83164	collagen, type XV, alpha 1	0.97	0.74	late stage
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	1.21	0.56	late stage
	418875	W19971	Hs.233459	ESTs	2.63	0.33	late stage
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	7.65	0.07	late stage
25	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	0.91	0.82	late stage
	420411	AI581085	Hs.24678	ESTs	7.3	0.1	late stage
	420943	AI718702	Hs.105341	ESTs	7.05	0.07	late stage
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	0.99	0.42	late stage
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.1	0.08	late stage
30	421786	AI188653	Hs.21351	ESTs	8.15	0.08	late stage
	422414	AW875237	Hs.13701	ESTs	1.05	0.59	late stage
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	0.28	1.53	late stage
	422790	AA809875	Hs.25933	ESTs	2.69	0.28	late stage
	423057	AW961597	Hs.130816	ESTs	7.55	0.08	late stage
35	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	1.24	0.61	late stage
	423905	AW579950	Hs.135150	lung type-I cell membrane-associated gly	2.12	0.24	late stage
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	0.29	2.45	late stage
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	4.47	0.17	late stage
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.44	0.26	late stage
40	424839	AA740632	Hs.120850	ESTs	2.74	0.23	late stage
	426780	BE242284	Hs.172199	adenylate cyclase 7	8.55	0.09	late stage
	426974	AB002298	Hs.173035	KIAA0300 protein	1.56	0.36	late stage
	427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	0.72	1	late stage
	427882	AA540987	Hs.193767	ESTs	2.25	0.29	late stage
45	428065	AI634046	Hs.157313	ESTs	6.19	0.1	late stage
	428147	AW629965	Hs.234983	ESTs	8.42	0.08	late stage
	428585	AB007863	Hs.185140	KIAA0403 protein	6.85	0.08	late stage
	428825	AI084336	Hs.128783	ESTs	0.9	0.8	late stage
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively sp	1.59	0.39	late stage
50	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	0.77	0.49	late stage
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.92	0.3	late stage
	431319	AA873350	Hs.262476	gb:h64h02.s1 NCI_CGAP_Kid5 Homo sapiens	1.36	0.44	late stage
	431583	AL042613	Hs.285173	S-adenosylmethionine decarboxylase 1	4.69	0.17	late stage
	432314	AA533447	Hs.274368	ESTs	1.75	0.31	late stage
55	432331	W37862	Hs.257631	Homo sapiens mRNA; cDNA DKFZp586i1524 (f	0.35	1.58	late stage
	432559	AW452948	Hs.3337	ESTs	1.37	0.49	late stage
	433470	AW960564	Hs.283712	transmembrane 4 superfamily member 1	2.58	0.24	late stage
	433586	T85301	Hs.3337	gb:yd78d06.s1 Soares fetal liver spleen	5.06	0.11	late stage
	436428	AW245900	Hs.3337	hypothetical protein	8.25	0.09	late stage
60	436729	BE621807	Hs.124292	transmembrane 4 superfamily member 1	1.6	0.26	late stage
	438873	AI302471	Hs.221612	Homo sapiens cDNA: FLJ23123 fis, clone L	8.15	0.08	late stage
	439584	AA838114	Hs.6631	ESTs	8.6	0.09	late stage
	439653	AW021103	Hs.15798	hypothetical protein FLJ20373	2.21	0.27	late stage
	440524	R71264	Hs.7306	ESTs	3.44	0.21	late stage
65	440624	AF017987	Hs.106131	secreted frizzled-related protein 1	0.42	0.63	late stage
	441976	AA428403	Hs.8679	ESTs	8.5	0.09	late stage
	442739	NM_007274	Hs.150603	cytosolic acyl coenzyme A thioester hydr	7.95	0.06	late stage
	443852	AI679966	Hs.271687	ESTs	6.84	0.12	late stage
	443896	AI680242	Hs.10649	Homo sapiens cDNA FLJ13527 fis, clone PL	7.95	0.08	late stage
70	444212	AW503976	Hs.24144	basement membrane-induced gene	2.31	0.28	late stage
	444331	AW193342	Hs.93842	ESTs	0.32	1.64	late stage
	445142	AW978484	Hs.13131	Homo sapiens cDNA: FLJ22554 fis, clone H	2.52	0.24	late stage
	445701	AF055581	Hs.15432	lymphocyte adaptor protein	1.43	0.47	late stage
	446584	U53445	Hs.340	downregulated in ovarian cancer 1	0.54	1.39	late stage
75	447526	AL048753	Hs.19413	small inducible cytokine A2 (monocyte ch	1.43	0.43	late stage
	447744	AA313230	Hs.21905	S100 calcium-binding protein A12 (calgr	1.35	0.26	late stage
	447818	W79940	Hs.188614	ESTs	6.63	0.13	late stage
	449567	AI990790	Hs.25035	ESTs	4.7	0.13	late stage
	450455	AL117424	Hs.170121	chloride intracellular channel 4	0.64	1.31	late stage
	452239	AW379378	Hs.301921	protein tyrosine phosphatase, receptor t	0.59	1.18	late stage
	452698	NM_001295		ESTs	2.31	0.26	late stage

	453212	H15416	Hs.21865	ESTs	2.51	0.26	late stage
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarization	8.6	0.06	late stage
	400775	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	T2-T4 grade 3 papilloma marker
5	401508				1	1	T2-T4 grade 3 papilloma marker
	403092				1	1	T2-T4 grade 3 papilloma marker
	404232				1	1	T2-T4 grade 3 papilloma marker
	407020	U49973		gb:Human Tigger1 transposable element, c	1	1	T2-T4 grade 3 papilloma marker
	407345	AJ053836	Hs.169365	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	T2-T4 grade 3 papilloma marker
10	407420	AF084362		gb:Homo sapiens lipote-protein ligase B	1	1	T2-T4 grade 3 papilloma marker
	407577	AW131324	Hs.246759	ESTs, Weakly similar to KIAA1074 protein	1	1	T2-T4 grade 3 papilloma marker
	407666	AF071107	Hs.37501	MAD [mothers against decapentaplegic, Dr	1	1	T2-T4 grade 3 papilloma marker
	407916	L09234	Hs.603	ATPase, H+ transporting, lysosomal (vacu	1	1	T2-T4 grade 3 papilloma marker
	407936	AW118147	Hs.270935	ESTs	1	1	T2-T4 grade 3 papilloma marker
	408186	AW168847	Hs.250156	ESTs	1	1	T2-T4 grade 3 papilloma marker
15	408950	AA707814	Hs.7395	ESTs	1	1	T2-T4 grade 3 papilloma marker
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.2	0.12	T2-T4 grade 3 papilloma marker
	409045	AA635062	Hs.50094	Homo sapiens mRNA: cDNA DKFZp434O0515 (I	1	1	T2-T4 grade 3 papilloma marker
	409196	NM_001874	Hs.169765	carboxypeptidase M	1	1	T2-T4 grade 3 papilloma marker
20	409281	AA069998		gb:zm67b03.r1 Stratagene neuroepithelium	1	1	T2-T4 grade 3 papilloma marker
	410010	AW572853	Hs.257683	ESTs, Weakly similar to ALU3_HUMAN ALU S	1	0.5	T2-T4 grade 3 papilloma marker
	410157	AW593277	Hs.225056	ESTs	1	0.69	T2-T4 grade 3 papilloma marker
	411112	AW818158		gb:CM1-ST0277-161299-070-g07 ST0277 Homo	1	1	T2-T4 grade 3 papilloma marker
	411336	AW837675		gb:QV2-LT0039-260300-107-b04 LT0039 Homo	1	1	T2-T4 grade 3 papilloma marker
25	412051	T15872	Hs.268713	ESTs, Weakly similar to hypothetical pro	1	1	T2-T4 grade 3 papilloma marker
	413485	N52628		gb:yv37g11.s1 Soares fetal liver spleen	1	1	T2-T4 grade 3 papilloma marker
	413574	BE149158	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1	1	T2-T4 grade 3 papilloma marker
	413782	BE546104		gb:601072642F1 NIH_MGC_12 Homo sapiens c	1	1	T2-T4 grade 3 papilloma marker
	414749	H94622	Hs.193358	ESTs, Moderately similar to diabetes mel	1	1	T2-T4 grade 3 papilloma marker
30	415293	R49462	Hs.106541	ESTs	1	1	T2-T4 grade 3 papilloma marker
	415442	F12963	Hs.7045	GL004 protein	1	1	T2-T4 grade 3 papilloma marker
	416255	T87587	Hs.272082	ESTs	1	1	T2-T4 grade 3 papilloma marker
	417047	AA192640	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	1	1	T2-T4 grade 3 papilloma marker
	417181	L10123	Hs.1071	surfactant protein A binding protein	1	1	T2-T4 grade 3 papilloma marker
35	417367	N73877	Hs.171815	ESTs	1	1	T2-T4 grade 3 papilloma marker
	419721	NM_001650	Hs.288650	aquaporin 4	1	1	T2-T4 grade 3 papilloma marker
	420294	AA808259	Hs.196716	ESTs	1	0.65	T2-T4 grade 3 papilloma marker
	423589	AA328082	Hs.209569	ESTs, Weakly similar to thrombospondin t	1	1	T2-T4 grade 3 papilloma marker
	424549	AJ873205	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1	1	T2-T4 grade 3 papilloma marker
40	425458	H89317	Hs.182889	ESTs	1	1	T2-T4 grade 3 papilloma marker
	426475	AL134728		gb:DKFZp547A1890_r1 547 (synonym: hibr1)	1	1	T2-T4 grade 3 papilloma marker
	429453	AA453195	Hs.124222	ESTs	1	1	T2-T4 grade 3 papilloma marker
	431200	AF044923	Hs.250752	hook1 protein	1	1	T2-T4 grade 3 papilloma marker
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding pr	1	1	T2-T4 grade 3 papilloma marker
45	431944	AJ360891	Hs.143619	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432021	AA524470	Hs.58753	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432205	AJ806583	Hs.125291	ESTs	1	0.31	T2-T4 grade 3 papilloma marker
	432527	AW975028	Hs.102754	ESTs	1	1	T2-T4 grade 3 papilloma marker
	434069	AF116651	Hs.283058	hypothetical protein PRO0800	1	0.41	T2-T4 grade 3 papilloma marker
50	435278	AW994242	Hs.173495	ESTs	1	1	T2-T4 grade 3 papilloma marker
	435965	AJ034368	Hs.132650	ESTs	1	0.36	T2-T4 grade 3 papilloma marker
	436227	AA706937	Hs.120802	ESTs, Moderately similar to A26541 Na+/K	1	1	T2-T4 grade 3 papilloma marker
	436635	AW104325	Hs.272093	ESTs, Weakly similar to STK2_HUMAN SERIN	1	0.74	T2-T4 grade 3 papilloma marker
	436640	AA724411	Hs.156065	ESTs	1	1	T2-T4 grade 3 papilloma marker
55	436884	BE046657		gb:hna42e02.x1 NCL_CGAP_RDF2 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	437251	AW976082		gb:EST388191 MAGE resequences, MAGN Homo	1	1	T2-T4 grade 3 papilloma marker
	437348	AA749149	Hs.163114	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437769	AA767853	Hs.122895	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437771	AA811071	Hs.123349	ESTs	1	1	T2-T4 grade 3 papilloma marker
60	438347	AA909686	Hs.293397	ESTs	1	1	T2-T4 grade 3 papilloma marker
	439171	AA831133	Hs.294128	ESTs	1	0.95	T2-T4 grade 3 papilloma marker
	439914	AA854066	Hs.145394	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440399	AJ215527	Hs.125589	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440972	BE044588	Hs.276158	ESTs	1	1	T2-T4 grade 3 papilloma marker
65	442004	AA973568	Hs.128317	ESTs	1	1	T2-T4 grade 3 papilloma marker
	442270	BE565699	Hs.62005	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443413	AJ056457	Hs.221642	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443927	AW016726	Hs.134860	ESTs	1	1	T2-T4 grade 3 papilloma marker
	445442	N20392	Hs.42846	ESTs	1	1	T2-T4 grade 3 papilloma marker
70	445611	AW418497	Hs.145593	ESTs	1	0.49	T2-T4 grade 3 papilloma marker
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	1	1	T2-T4 grade 3 papilloma marker
	446552	AW470827	Hs.156241	ESTs	1	1	T2-T4 grade 3 papilloma marker
	447399	AJ815401	Hs.251967	Homo sapiens clone 785627 unknown mRNA	2.9	0.14	T2-T4 grade 3 papilloma marker
	449111	T83109	Hs.196180	ESTs	1	1	T2-T4 grade 3 papilloma marker
75	449232	AW192780	Hs.196080	ESTs	1	0.8	T2-T4 grade 3 papilloma marker
	451373	AJ792030		gb:os03e11.y5 NCL_CGAP_Lu5 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	452453	AJ902519		gb:QV-BT009-101198-051 BT009 Homo sapien	1	1	T2-T4 grade 3 papilloma marker
	452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1	0.67	T2-T4 grade 3 papilloma marker

5	452536	BE063380		gb:PM0-BT0275-291099-002-g10 BT0275 Homo	1.65	0.26	T2-T4 grade 3 papilloma marker
	452640	AA027115	Hs.100206	ESTs, Weakly similar to AAAAD_HUMAN ARYL	1	1	T2-T4 grade 3 papilloma marker
	452645	AI911325	Hs.212049	EST	1	1	T2-T4 grade 3 papilloma marker
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1	1	T2-T4 grade 3 papilloma marker
	453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: h1br2)	1	0.8	T2-T4 grade 3 papilloma marker
	453609	AL045301	Hs.13427	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453677	AL079389		gb:DKFZp434E2116_r1 434 (synonym: htes3)	1	0.77	T2-T4 grade 3 papilloma marker
	453704	R41806	Hs.100884	ESTs	1	1	T2-T4 grade 3 papilloma marker
10	455267	AW880861		gb:QV0-OT0033-070300-152-c12 OT0033 Homo	1	1	T2-T4 grade 3 papilloma marker
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	1	1	T2-T4 grade 3 papilloma marker
	456520	AW835416	Hs.29417	HCF-binding transcription factor Zhangfe	1	1	T2-T4 grade 3 papilloma marker
	456763	AJ271351	Hs.128180	B-cell translocation gene 4	1	0.71	T2-T4 grade 3 papilloma marker
	456912	AI458843	Hs.158112	protein tyrosine phosphatase, receptor I	1	1	T2-T4 grade 3 papilloma marker
15	457018	AA761820	Hs.250965	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457323	AW867813	Hs.201064	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457339	AW971949	Hs.291252	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457340	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	457507	AW300248	Hs.181693	ESTs	1	1	T2-T4 grade 3 papilloma marker
20	458106	AF086561	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	1	1	T2-T4 grade 3 papilloma marker
	458624	AI362790	Hs.181801	ESTs	1	0.34	T2-T4 grade 3 papilloma marker
	459396	AI907536	Hs.103869	ESTs	1	1	T2-T4 grade 3 papilloma marker
	401002				1	1	T2-T4 grade 3 solid tumor marker
	401866				1.35	0.14	T2-T4 grade 3 solid tumor marker
25	403615				1	1	T2-T4 grade 3 solid tumor marker
	403776				1	1	T2-T4 grade 3 solid tumor marker
	404113				1	0.43	T2-T4 grade 3 solid tumor marker
	404488				1	0.17	T2-T4 grade 3 solid tumor marker
	404653				1	1	T2-T4 grade 3 solid tumor marker
30	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (tr	1	0.24	T2-T4 grade 3 solid tumor marker
	406471				1	0.42	T2-T4 grade 3 solid tumor marker
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	2.75	0.05	T2-T4 grade 3 solid tumor marker
	407624	AW157431	Hs.248941	ESTs	3.05	0.15	T2-T4 grade 3 solid tumor marker
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	3.85	0.03	T2-T4 grade 3 solid tumor marker
35	409464	X69115	Hs.54488	zinc finger protein 37a (KOX 21)	1.15	0.29	T2-T4 grade 3 solid tumor marker
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	1	0.24	T2-T4 grade 3 solid tumor marker
	410025	BE220489	Hs.113592	ESTs	1	0.3	T2-T4 grade 3 solid tumor marker
	410589	AW770768	Hs.265717	ESTs	1	0.28	T2-T4 grade 3 solid tumor marker
	411840	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	1.05	0.15	T2-T4 grade 3 solid tumor marker
40	412198	AA937111	Hs.69165	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	412305	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	1	0.53	T2-T4 grade 3 solid tumor marker
	412753	AI065016	Hs.6390	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1	0.69	T2-T4 grade 3 solid tumor marker
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	1	0.29	T2-T4 grade 3 solid tumor marker
45	415027	D31010		gb:HUM12147 Human fetal lung Homo sapie	1	1	T2-T4 grade 3 solid tumor marker
	416099	H18626	Hs.22634	ESTs	1	0.74	T2-T4 grade 3 solid tumor marker
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8	0.12	T2-T4 grade 3 solid tumor marker
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	2.85	0.08	T2-T4 grade 3 solid tumor marker
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	1	0.2	T2-T4 grade 3 solid tumor marker
50	421243	AW873803	Hs.102876	pancreatic lipase	1	0.38	T2-T4 grade 3 solid tumor marker
	422660	AW297582	Hs.237062	ESTs	1.05	0.32	T2-T4 grade 3 solid tumor marker
	422834	AA318334		gb:EST20402 Retina II Homo sapiens cDNA	1	0.38	T2-T4 grade 3 solid tumor marker
	422972	N59319	Hs.145404	ESTs	1	0.61	T2-T4 grade 3 solid tumor marker
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	2.95	0.12	T2-T4 grade 3 solid tumor marker
55	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1	0.05	T2-T4 grade 3 solid tumor marker
	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on	1	0.35	T2-T4 grade 3 solid tumor marker
	425196	AL037915	Hs.155097	carbonic anhydrase II	2.75	0.05	T2-T4 grade 3 solid tumor marker
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1	0.09	T2-T4 grade 3 solid tumor marker
	430300	U60805	Hs.238648	oncostatin M receptor	1	0.25	T2-T4 grade 3 solid tumor marker
60	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	1	0.28	T2-T4 grade 3 solid tumor marker
	431277	AA501806	Hs.249965	ESTs	1	0.22	T2-T4 grade 3 solid tumor marker
	431750	AA514986	Hs.283705	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	434273	AA913143	Hs.26303	ESTs	1	0.41	T2-T4 grade 3 solid tumor marker
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.8	0.19	T2-T4 grade 3 solid tumor marker
65	436281	AW411194	Hs.120051	ESTs	2.05	0.14	T2-T4 grade 3 solid tumor marker
	437010	AA741368	Hs.291434	ESTs	2.4	0.17	T2-T4 grade 3 solid tumor marker
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.8	0.13	T2-T4 grade 3 solid tumor marker
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	1	0.3	T2-T4 grade 3 solid tumor marker
	438376	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HE	1	0.57	T2-T4 grade 3 solid tumor marker
	439370	AW274369	Hs.158853	ESTs	1	0.17	T2-T4 grade 3 solid tumor marker
70	440021	AW025498	Hs.270842	ESTs, Weakly similar to ALU8_HUMAN ALU S	1	0.65	T2-T4 grade 3 solid tumor marker
	440404	AI015881	Hs.125616	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	441523	AW514263	Hs.168872	ESTs, Weakly similar to ALUF_HUMAN IIII	1	1	T2-T4 grade 3 solid tumor marker
	442277	AW448914	Hs.202391	ESTs	2.4	0.15	T2-T4 grade 3 solid tumor marker
	442738	AW002370	Hs.131055	ESTs	1	0.29	T2-T4 grade 3 solid tumor marker
75	443297	AI049864	Hs.133029	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1	0.61	T2-T4 grade 3 solid tumor marker
	445550	AI242754	Hs.137306	ESTs	1	0.5	T2-T4 grade 3 solid tumor marker

	446149	BE242980	Hs.203181	ESTs	1	0.25	T2-T4 grade 3 solid tumor marker
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1	0.21	T2-T4 grade 3 solid tumor marker
	446434	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	1	1	T2-T4 grade 3 solid tumor marker
5	446928	AI694493	Hs.246916	ESTs	1	0.31	T2-T4 grade 3 solid tumor marker
	448591	AI540111	Hs.171261	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449121	AI915858	Hs.194980	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449539	W80363	Hs.58446	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	450451	AW591528	Hs.202072	ESTs	1	0.59	T2-T4 grade 3 solid tumor marker
10	450469	AI955049	Hs.281326	ESTs	1	0.43	T2-T4 grade 3 solid tumor marker
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1	0.05	T2-T4 grade 3 solid tumor marker
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	1.55	0.11	T2-T4 grade 3 solid tumor marker
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	1	0.95	T2-T4 grade 3 solid tumor marker
	451130	AI762250	Hs.211347	ESTs	3.65	0.15	T2-T4 grade 3 solid tumor marker
15	451412	AW136378	Hs.208060	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	1.35	0.22	T2-T4 grade 3 solid tumor marker
	452114	N22687	Hs.8236	ESTs	1	0.19	T2-T4 grade 3 solid tumor marker
	452743	AW965082	Hs.61455	ESTs	1	0.44	T2-T4 grade 3 solid tumor marker
	454622	U70071		gb:HSU70071 Human Homo sapiens cDNA clon	1	1	T2-T4 grade 3 solid tumor marker
20	455235	AW875951		gb:CM1-PT0013-131299-067-109 PT0013 Homo	1	0.31	T2-T4 grade 3 solid tumor marker
	457792	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	1	0.24	T2-T4 grade 3 solid tumor marker
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fascidin)	20.531	0.036	upregulate stage
	101193	L20861	Hs.152213	*wingless-type MMTV integration site fam	1	0.526	upregulate stage
	101724	M69225	Hs.620	bulbosus pemphigoid antigen 1 (230/240kD)	20.67	0.037	upregulate stage
25	101809	M86849	*Hs.323733	*gap junction protein, beta 2, 26kD (con	20.78	0.019	upregulate stage
	102154	U17760	Hs.75517	*laminin, beta 3 (nicein (125kD), kalini	18.848	0.042	upregulate stage
	102211	U23070	Hs.78776	putative transmembrane protein	2.092	0.28	upregulate stage
	102623	U66083	Hs.37110	*melanoma antigen, family A, 9"	1	0.306	upregulate stage
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.27	0.041	upregulate stage
30	103036	X54925	*Hs.83169	matrix metalloproteinase 1 (interstitial	13.63	0.034	upregulate stage
	103119	X63629	Hs.2877	*cadherin 3, type 1, P-cadherin (placent	7.296	0.054	upregulate stage
	103312	X82693	Hs.3185	*lymphocyte antigen 6 complex, locus D"	0.908	0.485	upregulate stage
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.928	0.219	upregulate stage
	103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.156	0.16	upregulate stage
35	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	1.642	0.516	upregulate stage
	107151	AA621169	Hs.8687	ESTs	2.421	0.174	upregulate stage
	107901	AA026418	*Hs.111758	keratin 6A	1.259	0.343	upregulate stage
	107922	AA028028	Hs.61460	*Homo sapiens Ig superfamily receptor LN	14.22	0.049	upregulate stage
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	11.13	0.039	upregulate stage
40	109424	AA227919	*Hs.85962	hyaluronan synthase 3	1.737	0.518	upregulate stage
	110906	N39584	Hs.17404	ESTs	20.93	0.021	upregulate stage
	112244	R51309	Hs.70823	KAA1077 protein	3.941	0.181	upregulate stage
	115060	AA253214	Hs.198249	*gap junction protein, beta 5 (connexin	1.932	0.502	upregulate stage
	115697	AA411502	Hs.63325	*transmembrane protease, serine 4"	7.394	0.101	upregulate stage
45	115978	AA447522	*Hs.69517	*Homo sapiens, clone MGC:5257, mRNA, com	1.667	0.445	upregulate stage
	116335	AA458830	Hs.41690	desmoolin 3	4.899	0.154	upregulate stage
	118314	N63402	Hs.46692	ESTs	9.75	0.069	upregulate stage
	118336	N63604	Hs.47166	HT021	4.601	0.197	upregulate stage
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1.95	0.123	upregulate stage
50	120486	AA253400	Hs.137569	tumor protein 63 kDa with strong homolog	4.191	0.211	upregulate stage
	121027	AA398470	Hs.99785	*Homo sapiens cDNA: FLJ21245 fis, clone	14.25	0.058	upregulate stage
	124059	F13673	Hs.283713	*ESTs, Weakly similar to ORF YGL050w [S.	4.99	0.168	upregulate stage
	125859	U31875	*Hs.152677	*Homo sapiens cDNA FLJ20338 fis, clone H	2.433	0.306	upregulate stage
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	4.34	0.14	upregulate stage
55	129041	H58873	*Hs.169902	*solute carrier family 2 (facilitated gl	2.003	0.455	upregulate stage
	129466	L42583	*Hs.111758	keratin 6A	11.584	0.042	upregulate stage
	130627	L23808	Hs.1695	matrix metalloproteinase 12 (macrophage	2.376	0.233	upregulate stage
	132349	Y00705	*Hs.181286	*serine protease inhibitor, Kazal type 1	5.4	0.132	upregulate stage
	132710	W93726	Hs.55279	*serine (or cysteine) proteinase inhibit	3.888	0.187	upregulate stage
60	133391	X57579	Hs.727	*inhibin, beta A (activin A, activin AB	1.517	0.334	upregulate stage
	134110	AA242758	*Hs.79136	*LIV-1 protein, estrogen regulated"	2.221	0.387	upregulate stage
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.85	0.03	upregulate stage
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.54	0.13	upregulate stage
	400346	AB041269	Hs.272263	Homo sapiens mRNA for keratin 19, parlia	8.95	0.07	upregulate stage
65	400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	10.7	0.06	upregulate stage
	400495				1	0.56	upregulate stage
	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.52	0.51	upregulate stage
	400528				3.47	0.23	upregulate stage
	400577				1	0.29	upregulate stage
70	400603				7.2	0.08	upregulate stage
	400644				1	1	upregulate stage
	400666				1.42	0.43	upregulate stage
	400750				8.7	0.1	upregulate stage
	400773				1.11	0.51	upregulate stage
75	400844				9.65	0.04	upregulate stage
	400845				2.3	0.28	upregulate stage
	400846				1.34	0.5	upregulate stage
	400880				9.4	0.06	upregulate stage

				1	1	upregulate stage
				1	0.51	upregulate stage
				7	0.08	upregulate stage
				1	0.17	upregulate stage
5				5.18	0.14	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				9.1	0.06	upregulate stage
				1.42	0.5	upregulate stage
10	M83738	Hs.147663	protein tyrosine phosphatase, non-recept	1	0.33	upregulate stage
				6.5	0.11	upregulate stage
				1	0.31	upregulate stage
				1	1	upregulate stage
				2.65	0.17	upregulate stage
15				12	0.05	upregulate stage
	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	9.15	0.08	upregulate stage
	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	8.75	0.09	upregulate stage
				1	1	upregulate stage
20				29.75	0.02	upregulate stage
				11.35	0.06	upregulate stage
				6.15	0.07	upregulate stage
	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/PL1-	1	0.69	upregulate stage
				3.15	0.15	upregulate stage
25				4.4	0.14	upregulate stage
				8.75	0.06	upregulate stage
				1	0.36	upregulate stage
				5.15	0.1	upregulate stage
				9.05	0.08	upregulate stage
30				1	1	upregulate stage
				9.6	0.07	upregulate stage
				9.85	0.09	upregulate stage
				9.4	0.09	upregulate stage
				1.07	0.65	upregulate stage
35				1	1	upregulate stage
				9.6	0.06	upregulate stage
				1.5	0.21	upregulate stage
				5.15	0.12	upregulate stage
40	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	upregulate stage
	R58624	Hs.2186	eukaryotic translation elongation factor	1.5	0.28	upregulate stage
				1	0.37	upregulate stage
				1	0.43	upregulate stage
				1.12	0.57	upregulate stage
	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene	0.86	1.08	upregulate stage
45				7.7	0.09	upregulate stage
				1.18	0.62	upregulate stage
				6.05	0.1	upregulate stage
				4.5	0.11	upregulate stage
				3.2	0.13	upregulate stage
50				10.7	0.05	upregulate stage
				10.35	0.08	upregulate stage
				1	1	upregulate stage
				2.45	0.34	upregulate stage
				1	1	upregulate stage
55				4.45	0.14	upregulate stage
				1.39	0.58	upregulate stage
	W28077	Hs.79389	nel (chicken)-like 2	1	1	upregulate stage
				9.15	0.08	upregulate stage
				1	1	upregulate stage
60				1	1	upregulate stage
				1.3	0.2	upregulate stage
				1	0.39	upregulate stage
				1	0.28	upregulate stage
				7.05	0.06	upregulate stage
65				1	0.33	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				0.89	0.9	upregulate stage
				2.74	0.26	upregulate stage
70				9.35	0.08	upregulate stage
				1	0.24	upregulate stage
				3.65	0.15	upregulate stage
				2.05	0.16	upregulate stage
75				1	1	upregulate stage
	AL035754	Hs.2474	tol-like receptor 1	1	0.18	upregulate stage
				1	0.56	upregulate stage
				1	0.22	upregulate stage
				9.65	0.08	upregulate stage

	405167			1	0.67	upregulate stage
	405170			1	0.48	upregulate stage
	405177			1	0.22	upregulate stage
5	405186			3.75	0.1	upregulate stage
	405258			8.85	0.09	upregulate stage
	405281			1	1	upregulate stage
	405379			1	0.87	upregulate stage
	405494			5	0.13	upregulate stage
	405520			1	0.95	upregulate stage
10	405526			8.96	0.08	upregulate stage
	405725			3.3	0.12	upregulate stage
	405738			0.86	0.69	upregulate stage
	405809			2.4	0.18	upregulate stage
	405838			1	0.22	upregulate stage
15	405906			2.6	0.12	upregulate stage
	406137			1.54	0.52	upregulate stage
	406187			3.2	0.14	upregulate stage
	406322			3.95	0.12	upregulate stage
	406360			4.1	0.1	upregulate stage
20	406397			1	0.24	upregulate stage
	406434			7.4	0.07	upregulate stage
	406467			9.1	0.07	upregulate stage
	406511			1	1	upregulate stage
25	406517	W28077	Hs.79389	1	1	upregulate stage
	406588			0.93	0.91	upregulate stage
	406651	Al559224	Hs.277477	10.1	0.07	upregulate stage
	406665	U22961	Hs.75442	1.08	0.81	upregulate stage
	406671	AA129547	Hs.285754	5.7	0.12	upregulate stage
30	406687	M31126	Hs.272620	1.95	0.3	upregulate stage
	406732	AA487229	Hs.2064	1	0.77	upregulate stage
	406747	Al925153	Hs.217493	3.6	0.14	upregulate stage
	406753	AA505665	Hs.217493	5.45	0.13	upregulate stage
	406815	AA833930	Hs.288036	3.65	0.09	upregulate stage
35	406850	Al624300	Hs.172928	1.29	0.62	upregulate stage
	406892	D55643		1	1	upregulate stage
	406944	J04742	Hs.247945	1	1	upregulate stage
	406950	L17325	Hs.278	1	0.36	upregulate stage
	406961	L77563		1	1	upregulate stage
40	406964	M21305	Hs.247946	42.25	0.01	upregulate stage
	406993	S83249		1	1	upregulate stage
	407017	U48697		1	1	upregulate stage
	407073	Y10510		1	0.53	upregulate stage
	407105	S64699	Hs.663	1	1	upregulate stage
45	407128	R83312	Hs.237260	1	1	upregulate stage
	407132	T02871	Hs.228523	1	0.45	upregulate stage
	407137	T97307	Hs.199067	14.3	0.05	upregulate stage
	407158	N49839		1	0.57	upregulate stage
	407175	T86603		1	0.31	upregulate stage
50	407186	AA435610		1	1	upregulate stage
	407189	AA598927		1	1	upregulate stage
	407192	AA609200		6.05	0.12	upregulate stage
	407195	C21124		1	1	upregulate stage
	407202	N58172	Hs.109370	3.7	0.16	upregulate stage
55	407204	R41933	Hs.140237	10.2	0.06	upregulate stage
	407205	R78910	Hs.272620	1.9	0.22	upregulate stage
	407211	T95828	Hs.230070	1	0.59	upregulate stage
	407346	Al090210	Hs.264106	1	1	upregulate stage
	407422	AF116633		1	0.22	upregulate stage
60	407494	U10072		4.1	0.13	upregulate stage
	407547	Y10259		2.45	0.19	upregulate stage
	407564	AA042860	Hs.103005	1	1	upregulate stage
	407603	AW955705	Hs.62604	1.18	0.73	upregulate stage
	407634	AW016569	Hs.301280	9.6	0.06	upregulate stage
65	407668	BE161086	Hs.279817	1	0.39	upregulate stage
	407709	AA456135	Hs.23023	6.8	0.12	upregulate stage
	407710	AW022727	Hs.23616	3.9	0.14	upregulate stage
	407725	BE388094	Hs.21857	9.97	0.07	upregulate stage
	407729	T40707	Hs.270862	9.2	0.09	upregulate stage
70	407774	AA084958		2.65	0.22	upregulate stage
	407788	BE514982	Hs.38991	2.1	0.34	upregulate stage
	407811	AW190902	Hs.40098	8.45	0.06	upregulate stage
	407813	AL120247	Hs.40109	9.1	0.08	upregulate stage
	407833	AW955632	Hs.66666	9.2	0.07	upregulate stage
75	407839	AA045144	Hs.161566	2.11	0.25	upregulate stage
	407853	AA336797	Hs.40499	1	0.34	upregulate stage
	407881	AW072003	Hs.40968	3.52	0.18	upregulate stage
	407882	Al241264	Hs.62772	1	0.26	upregulate stage

5	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	13.6	0.05	upregulate stage
	407911	AF104922	Hs.41565	growth differentiation factor 8	1	1	upregulate stage
	407912	AW104401	Hs.243489	ESTs, Weakly similar to AF151881.1 CGI-1	10.35	0.07	upregulate stage
	407935	U31986	Hs.41583	cartilage paired-class homeoprotein 1	4.25	0.12	upregulate stage
	407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	8.75	0.09	upregulate stage
10	407944	R34008	Hs.239727	desmocollin 2	9.2	0.06	upregulate stage
	407945	X69208	Hs.606	ATPase, Cu+++ transporting, alpha polypep	1.45	0.25	upregulate stage
	407946	AA226495	Hs.154292	ESTs	9.4	0.07	upregulate stage
	407949	W21874	Hs.247057	ESTs	3.32	0.2	upregulate stage
	407974	AW968123	Hs.146401	small inducible cytokine subfamily E, ma	3.55	0.14	upregulate stage
15	407983	U40371	Hs.41718	phosphodiesterase 1C, calmodulin-depende	8.95	0.07	upregulate stage
	407994	AW135309	Hs.244331	ESTs	4.5	0.12	upregulate stage
	408000	L11690	Hs.820	bullous pemphigoid antigen 1 (230/240kD)	2.89	0.19	upregulate stage
	408014	AA723782	Hs.41749	protein kinase, cGMP-dependent, type II	1.31	0.53	upregulate stage
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.6	0.17	upregulate stage
20	408046	AW139121	Hs.183643	ESTs	1	0.36	upregulate stage
	408053	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	10.75	0.05	upregulate stage
	408092	NM_007057	Hs.42650	ZW10 interactor	4.7	0.13	upregulate stage
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.5	0.14	upregulate stage
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic b	4.4	0.13	upregulate stage
25	408170	AW204516	Hs.31835	ESTs	5.85	0.13	upregulate stage
	408184	AW168741	Hs.22249	ESTs	1	1	upregulate stage
	408224	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo	1	0.44	upregulate stage
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.95	0.04	upregulate stage
	408241	AW176546		gb:MR0-CT0063-200899-001-a01 CT0063 Homo	2.8	0.17	upregulate stage
30	408268	AL138247		gb:DKFZp547D237_r1 547 (synonym: hfr1)	1	0.61	upregulate stage
	408277	AW177959		gb:IL3-HT0060-200899-008-D03 HT0060 Homo	1	1	upregulate stage
	408306	BE141991		gb:PM2-HT0134-220999-002-d10 HT0134 Homo	1	1	upregulate stage
	408352	AA053875	Hs.95310	ESTs	1	1	upregulate stage
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.15	0.08	upregulate stage
35	408393	AW015318	Hs.23165	ESTs	9.35	0.07	upregulate stage
	408396	AA330496	Hs.40840	ESTs	1	0.61	upregulate stage
	408442	R59608	Hs.21435	ESTs	1	1	upregulate stage
	408514	AW206559	Hs.255903	ESTs	1	0.34	upregulate stage
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1	0.33	upregulate stage
40	408617	R61736	Hs.124128	ESTs	2.75	0.14	upregulate stage
	408633	AW963372	Hs.45677	PRO2000 protein	3.14	0.25	upregulate stage
	408706	AW438503	Hs.256935	ESTs	8.45	0.09	upregulate stage
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	2.81	0.21	upregulate stage
	408725	AA131539	Hs.15669	ESTs	9.1	0.08	upregulate stage
45	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.1	0.11	upregulate stage
	408738	NM_014785	Hs.47313	KIAA0258 gene product	4.4	0.13	upregulate stage
	408739	W01556	Hs.238797	ESTs	5.65	0.11	upregulate stage
	408754	N31256	Hs.161623	ESTs	1	1	upregulate stage
	408765	AA057268	Hs.146013	ESTs	8.75	0.09	upregulate stage
50	408805	H69912	Hs.48269	vaccinia related kinase 1	4.95	0.12	upregulate stage
	408813	AI580090	Hs.48295	RNA helicase family	3.65	0.17	upregulate stage
	408817	AA524525	Hs.279864	PRO1996 protein	6.15	0.12	upregulate stage
	408849	BE219451	Hs.254919	ESTs	1	0.32	upregulate stage
	408902	AW014869	Hs.5510	ESTs	3.3	0.15	upregulate stage
55	408908	BE296227	Hs.48915	serine/threonine kinase 15	5.65	0.1	upregulate stage
	408916	AW295232	Hs.22893	ESTs	10	0.08	upregulate stage
	408933	AA058979	Hs.182133	ESTs, Highly similar to ADP-ribosylation	1	0.91	upregulate stage
	408943	NM_007070	Hs.49105	FKBP-associated protein	3.45	0.16	upregulate stage
	408950	BE158389	Hs.300976	ESTs	6.3	0.1	upregulate stage
60	409032	AW301807	Hs.297260	ESTs	8.4	0.08	upregulate stage
	409093	BE243834	Hs.50441	CGI-04 protein	1.71	0.49	upregulate stage
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	10.1	0.07	upregulate stage
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	11.85	0.05	upregulate stage
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	2.83	0.24	upregulate stage
65	409231	AA446644	Hs.692	tumor-associated calcium signal transduc	9.34	0.08	upregulate stage
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	8.7	0.09	upregulate stage
	409357	M73628	Hs.54415	casein, kappa	1.6	0.2	upregulate stage
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.57	0.56	upregulate stage
	409405	AA075869	Hs.126400	ESTs, Highly similar to RL39_HUMAN 60S R	2.6	0.12	upregulate stage
70	409408	AW387837		gb:MR4-ST0118-021299-021-r08 ST0118 Homo	4.3	0.15	upregulate stage
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	8.28	0.06	upregulate stage
	409509	AL036923	Hs.127006	ESTs	10.2	0.06	upregulate stage
	409566	AA078899		gb:zm94b01.r1 Stratagene colon HT29 (937	1	0.56	upregulate stage
	409575	AW419225	Hs.256247	ESTs	2.15	0.14	upregulate stage
75	409582	R27430	Hs.271565	ESTs	7.3	0.07	upregulate stage
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	3.78	0.19	upregulate stage
	409642	AW450809	Hs.257347	ESTs	9.55	0.07	upregulate stage
	409674	AI935146	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1	0.29	upregulate stage
	409691	T89983	Hs.246042	ESTs	1	1	upregulate stage
	409703	NM_006187	Hs.56009	Z'-oligoadenylate synthetase 3	2.22	0.36	upregulate stage
	409727	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.57	upregulate stage

409760	AA302840		gb:EST10534 Adipose tissue, white	9.95	0.06	upregulate stage
409789	BE256027	Hs.180946	ribosomal protein L5	1	0.83	upregulate stage
409794	AW885691		gb:RC4-OT0071-240300-013-b04 OT0071 Homo	1	1	upregulate stage
409977	AW805510	Hs.97056	hypothetical protein FLJ21634	9.65	0.07	upregulate stage
409985	AW291944	Hs.122139	ESTs	4.35	0.14	upregulate stage
409989	R37868	Hs.13333	ESTs	1	0.21	upregulate stage
409995	AW960597	Hs.30164	ESTs	5.05	0.12	upregulate stage
410013	AF067173	Hs.57904	mago-nashi (Drosophila) homolog, prolife	3.05	0.25	upregulate stage
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	3.15	0.09	upregulate stage
410071	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	2.5	0.18	upregulate stage
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	8	0.06	upregulate stage
410114	AW590540	Hs.271280	ESTs	5.1	0.14	upregulate stage
410117	AK001586	Hs.58650	hypothetical protein FLJ10724	1	1	upregulate stage
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	4.7	0.11	upregulate stage
410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	1	0.23	upregulate stage
410196	AI936442	Hs.59838	hypothetical protein FLJ10808	6.05	0.09	upregulate stage
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	5.55	0.12	upregulate stage
410259	AK000337	Hs.61485	hypothetical protein	10.1	0.07	upregulate stage
410276	AI554545	Hs.68301	ESTs	2.98	0.25	upregulate stage
410278	AW614396	Hs.282230	ESTs	1	0.28	upregulate stage
410325	AB023154	Hs.62264	KIAA0937 protein	6.85	0.13	upregulate stage
410356	BE244668	Hs.62643	dual adaptor of phosphotyrosine and 3-ph	1	1	upregulate stage
410388	AA831460	Hs.22039	hepatocyte nuclear factor 3, alpha	1	0.33	upregulate stage
410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific	1.07	0.78	upregulate stage
410420	AA224053	Hs.172405	ESTs, Moderately similar to I52835 H-NUC	1	0.14	upregulate stage
410429	AA310500	Hs.63657	hypothetical protein FLJ11005	11.25	0.07	upregulate stage
410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	9.6	0.08	upregulate stage
410475	AW749927		gb:QV0-BT0537-231299-049-f03 BT0537 Homo	9.8	0.08	upregulate stage
410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	11.3	0.06	upregulate stage
410501	AI675688	Hs.83286	ESTs	4.75	0.1	upregulate stage
410503	AW975746	Hs.188662	Homo sapiens cDNA: FLJ23421 fis, clone H	6.5	0.1	upregulate stage
410520	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	1	1	upregulate stage
410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	3.1	0.16	upregulate stage
410537	AW753108		gb:PM1-CT0247-080100-008-e10 CT0247 Homo	10.35	0.08	upregulate stage
410553	AW016824	Hs.68784	ESTs	1.67	0.41	upregulate stage
410560	N29220		gb:yx43b05.r1 Soares melanocyte 2NbHM Ho	9	0.07	upregulate stage
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	6.2	0.11	upregulate stage
410562	AW858528		gb:CM3-CT0341-150300-119-h11 CT0341 Homo	1	1	upregulate stage
410579	AK001828	Hs.64691	KIAA0483 protein	11.1	0.06	upregulate stage
410634	AW888653	Hs.268859	ESTs	1	1	upregulate stage
410664	NM_006033	Hs.65370	lipase, endothelial	3.95	0.1	upregulate stage
410668	BE379794	Hs.65403	hypothetical protein	1.82	0.41	upregulate stage
410730	AW368860	Hs.293950	ESTs	9.25	0.07	upregulate stage
410751	AA357918		gb:EST66726 Fetal lung III Homo sapiens	1	1	upregulate stage
410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	3.1	0.14	upregulate stage
410762	AF226053	Hs.66170	HSKM-B protein	5.55	0.1	upregulate stage
410764	AW978159	Hs.250164	ESTs, Weakly similar to coded for by C.	1	0.2	upregulate stage
410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT	1.75	0.25	upregulate stage
410794	AA248010	Hs.154669	ESTs	1	0.67	upregulate stage
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.2	0.17	upregulate stage
410844	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo	1	0.8	upregulate stage
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	6.5	0.12	upregulate stage
410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	9.35	0.08	upregulate stage
410973	AW812278		gb:RC0-ST0174-211099-011-h12 ST0174 Homo	1	1	upregulate stage
410976	R36207	Hs.25092	ESTs	8.35	0.1	upregulate stage
410997	AW812877		gb:RC3-ST0186-300100-017-e04 ST0186 Homo	1	1	upregulate stage
410998	W28247	Hs.82007	KIAA0094 protein	2.45	0.18	upregulate stage
411035	AA857218	Hs.297007	ESTs	4.05	0.14	upregulate stage
411110	H93000		gb:yyv07f01.s1 Soares fetal liver spleen	1	0.36	upregulate stage
411132	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	1	1	upregulate stage
411137	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	3.65	0.18	upregulate stage
411157	AW819867		gb:QV0-ST0294-070300-151-f02 ST0294 Homo	3.2	0.2	upregulate stage
411159	AW820178		gb:QV0-ST0294-100400-185-e07 ST0294 Homo	1	0.27	upregulate stage
411170	AW820503		gb:QV2-ST0298-140200-042-b05 ST0298 Homo	1	1	upregulate stage
411193	AW821484		gb:IL2-ST0311-211299-028-F12 ST0311 Homo	1	0.24	upregulate stage
411242	BE146808		gb:QV4-HT0222-181099-013-g03 HT0222 Homo	2.55	0.26	upregulate stage
411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	9.62	0.09	upregulate stage
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.4	0.32	upregulate stage
411282	AW995011		gb:QV0-BN0040-170300-161-d07 BN0040 Homo	1	1	upregulate stage
411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	3.25	0.12	upregulate stage
411294	AW859729	Hs.42680	ESTs	1	1	upregulate stage
411327	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo	1	0.37	upregulate stage
411338	AW731782	Hs.116122	ESTs, Weakly similar to unnamed protein	5	0.13	upregulate stage
411339	BE164598		gb:RC3-HT0470-120200-013-b10 HT0470 Homo	1	0.25	upregulate stage
411383	AA001394	Hs.69749	KIAA0087 gene product	3.6	0.18	upregulate stage
411387	AW842339	Hs.130815	hypothetical protein FLJ21870	8.75	0.09	upregulate stage
411400	AA311919	Hs.69851	GAR1 protein	12.1	0.07	upregulate stage

5	411425	AW846012		gb:RC2-CT0163-230999-003-E01 CT0163 Homo	1	0.74	upregulate stage
	411461	AW847937		gb:IL3-CT0213-210200-042-002 CT0213 Homo	1	1	upregulate stage
	411526	AW850327		gb:IL3-CT0219-221199-029-008 CT0219 Homo	1	1	upregulate stage
	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo	2.8	0.17	upregulate stage
	411568	BE144593		gb:MR0-HT0167-141199-002-004 HT0167 Homo	1	1	upregulate stage
10	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.55	0.14	upregulate stage
	411605	AW006831	Hs.20479	ESTs	9.6	0.08	upregulate stage
	411626	AW793453	Hs.71109	KIAA1229 protein	1	1	upregulate stage
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.1	0.11	upregulate stage
	411643	AI924519	Hs.192570	Homo sapiens cDNA: FLJ22028 fis, clone H	1	0.28	upregulate stage
15	411653	AF070578	Hs.711158	Homo sapiens clone 24674 mRNA sequence	8.9	0.08	upregulate stage
	411727	AW858443		gb:CM0-CT0341-260100-160-010 CT0341 Homo	1	1	upregulate stage
	411771	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	2.6	0.14	upregulate stage
	411787	AW863568		gb:MR3-SN0010-240300-102-c10 SN0010 Homo	1	1	upregulate stage
	411788	AW897793		gb:CM1-NN0063-280400-203-007 NN0063 Homo	3.7	0.15	upregulate stage
20	411826	AW947946		gb:PM0-MT0011-240300-001-a09 MT0011 Homo	3.25	0.13	upregulate stage
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	1	1	upregulate stage
	411860	T89420		gb:yd98f04s1 Soares fetal liver spleen	1	0.22	upregulate stage
	411874	AA096106	Hs.20403	ESTs	5.75	0.11	upregulate stage
	411917	AW876360	Hs.3592	Homo sapiens cDNA: FLJ22555 fis, clone H	1	0.33	upregulate stage
25	411928	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	4.75	0.12	upregulate stage
	411932	AW876548		gb:RC3-PT0028-190100-012-h02 PT0028 Homo	1	0.38	upregulate stage
	411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	3.82	0.23	upregulate stage
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	4.65	0.15	upregulate stage
	411991	X58822	Hs.73010	interferon, omega 1	2.45	0.14	upregulate stage
30	412040	D85519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	4.6	0.14	upregulate stage
	412088	AI689496	Hs.108932	ESTs	2.82	0.18	upregulate stage
	412134	AW895560		gb:QV4-NN0038-270400-187-g08 NN0038 Homo	6.4	0.1	upregulate stage
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	17.05	0.04	upregulate stage
	412231	AW902491	Hs.289088	heat shock 90kD protein 1, alpha	1	0.91	upregulate stage
35	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1	1	upregulate stage
	412327	AW937355		gb:QV3-DT0043-211299-044-a08 DT0043 Homo	1	1	upregulate stage
	412357	AW939537		gb:QV1-DT0072-110200-066-005 DT0072 Homo	1	0.24	upregulate stage
	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	1	0.41	upregulate stage
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo	1	0.22	upregulate stage
40	412529	BE271224	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	4.45	0.14	upregulate stage
	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13345 fis, clone OV	9.3	0.08	upregulate stage
	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	4.25	0.14	upregulate stage
	412547	W27161		gb:23a12 Human retina cDNA randomly prim	1	1	upregulate stage
	412559	T31474		gb:EST33147 Human Embryo Homo sapiens cD	1	0.26	upregulate stage
45	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPL)	12.05	0.05	upregulate stage
	412648	AA115211	Hs.69658	EST	1	0.28	upregulate stage
	412668	AA456195	Hs.10056	ESTs	10.75	0.07	upregulate stage
	412671	AW977734		gb:EST389963 MAGE resequences, MAGO Homo	2.65	0.3	upregulate stage
	412673	AL042957	Hs.31845	ESTs	4.6	0.11	upregulate stage
50	412723	AA648459	Hs.179912	ESTs	2.55	0.11	upregulate stage
	412739	AA116018	Hs.271809	Homo sapiens cDNA: FLJ22406 fis, clone H	1.6	0.24	upregulate stage
	412744	N31101		gb:ys2a03r1 Soares melanocyte 2NbHM Homo	2	0.23	upregulate stage
	412778	AA120882	Hs.159244	ESTs	1	1	upregulate stage
	412811	H06382	Hs.21400	ESTs	1	0.49	upregulate stage
55	412838	D61870		gb:HUM218F11B Clontech human aorta polyA	1	0.34	upregulate stage
	412854	BE004149	Hs.31161	ESTs	1	1	upregulate stage
	413075	D59828	Hs.70953	ESTs	1	0.77	upregulate stage
	413109	AW389845	Hs.110855	ESTs	3.93	0.1	upregulate stage
	413117	BE066107	Hs.138484	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.22	upregulate stage
60	413119	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	1	0.87	upregulate stage
	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	5.45	0.12	upregulate stage
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	2.54	0.19	upregulate stage
	413228	AA127518	Hs.195870	ESTs	1	1	upregulate stage
	413273	U75679	Hs.75257	Hairpin binding protein, histone	5.05	0.11	upregulate stage
65	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.45	0.5	upregulate stage
	413294	BE144034		gb:MR0-HT0165-191199-004-a02 HT0165 Homo	1	1	upregulate stage
	413324	V00571	Hs.75294	corticotropin releasing hormone	6.95	0.03	upregulate stage
	413342	AA128535		gb:z124e04.r1 Soares_pregnant uterus_NbH	1	1	upregulate stage
	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	3	0.18	upregulate stage
70	413707	BE158679		gb:CM0-HT0395-280100-169-c04 HT0395 Homo	1	0.28	upregulate stage
	413743	BE161004		gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	1	upregulate stage
	413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	22.7	0.03	upregulate stage
	413785	AW613780	Hs.13500	ESTs	9.9	0.07	upregulate stage
	413792	BE166924		gb:CM4-HT0501-240300-519-011 HT0501 Homo	1	1	upregulate stage
75	413804	T64682		gb:yc48b02.r1 Stralagena liver (937224)	0.99	0.75	upregulate stage
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.55	0.17	upregulate stage
	413854	BE174300	Hs.44581	heat shock protein hsp70-related protein	1.25	0.24	upregulate stage
	413918	AW015898	Hs.71245	ESTs	4	0.11	upregulate stage
	413968	AW500374	Hs.64056	ESTs	10.85	0.07	upregulate stage
	414091	T83742		gb:yd57g02s1 Soares fetal liver spleen	8.9	0.1	upregulate stage
	414099	U11313	Hs.75760	sterol carrier protein 2	10.3	0.06	upregulate stage

	414116	AA587370	Hs.71584	ESTs	1	1	upregulate stage
	414127	AI431863	Hs.135270	ESTs	2.85	0.13	upregulate stage
	414169	AA136169	Hs.149335	ESTs	8.95	0.09	upregulate stage
5	414275	AW970254	Hs.889	Charot-Leyden crystal protein	7.05	0.05	upregulate stage
	414304	AI621276	Hs.165998	OKFZP564M2423 protein	1	0.24	upregulate stage
	414338	N80751	Hs.301471	ESTs	10.3	0.08	upregulate stage
	414447	AA147549	Hs.109909	ESTs	3.4	0.16	upregulate stage
	414494	AA768491	Hs.6783	Homo sapiens cDNA: FLJ22724 fis, clone H	3.4	0.18	upregulate stage
10	414520	AA148806	Hs.204046	ESTs	1	0.21	upregulate stage
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.1	0.18	upregulate stage
	414575	H11257	Hs.295233	ESTs	3.1	0.15	upregulate stage
	414597	H67472	Hs.34274	ESTs	4.6	0.11	upregulate stage
	414643	H46177	Hs.119316	ESTs	1	0.28	upregulate stage
15	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	7.75	0.08	upregulate stage
	414661	T97401	Hs.21929	ESTs	1	0.26	upregulate stage
	414683	S78296	Hs.76888	interlexin neuronal intermediate filamen	2.72	0.25	upregulate stage
	414735	BE458016	Hs.281904	ESTs	1	0.38	upregulate stage
	414737	AI160386	Hs.125087	ESTs	5.5	0.1	upregulate stage
20	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.19	0.24	upregulate stage
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.45	0.49	upregulate stage
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	4.65	0.13	upregulate stage
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.7	0.46	upregulate stage
	414833	T07114		gb:EST05003 Fetal brain, Striatogene (cat	4.5	0.13	upregulate stage
25	414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.36	0.22	upregulate stage
	414885	AA157531	Hs.269276	ESTs	2.7	0.21	upregulate stage
	414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fis, clone PL	0.87	0.69	upregulate stage
	414985	C17372		gb:C17372 Clontech human aorta polyA+ mR	1	0.42	upregulate stage
	415025	AW207091	Hs.72307	ESTs	5.3	0.06	upregulate stage
30	415033	D31476	Hs.301448	Homo sapiens cDNA FLJ12152 fis, clone MA	1	1	upregulate stage
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF5_HUMAN TRANS	6.05	0.1	upregulate stage
	415068	Z19448	Hs.131887	ESTs, Weakly similar to ORF YNL227c [S.c	4.5	0.13	upregulate stage
	415095	D59592	Hs.34745	ESTs	1	0.44	upregulate stage
	415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3	2.27	0.29	upregulate stage
35	415104	D60076		gb:HUM084E10A Clontech human fetal brain	3.95	0.13	upregulate stage
	415114	D60468		gb:HUM111A06B Clontech human fetal brain	2.05	0.2	upregulate stage
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	5.8	0.05	upregulate stage
	415139	AW975942	Hs.48524	ESTs	1.15	0.21	upregulate stage
	415148	Z36953	Hs.48527	ESTs	2.5	0.2	upregulate stage
40	415153	C03508	Hs.7000	ESTs	8.95	0.09	upregulate stage
	415178	D80503		gb:HUM080A02B Human fetal brain (TFujiwa	1	0.15	upregulate stage
	415217	H23983	Hs.26922	ESTs	1	0.31	upregulate stage
	415227	AW821113	Hs.72402	ESTs	6.3	0.11	upregulate stage
	415238	R37780	Hs.21422	ESTs	1	1	upregulate stage
45	415241	F02208	Hs.27214	ESTs	1	1	upregulate stage
	415295	R41450	Hs.6546	ESTs	1	0.63	upregulate stage
	415296	F05086		gb:HSC01A011 normalized infant brain cDN	5.65	0.1	upregulate stage
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	8.15	0.09	upregulate stage
	415330	Z44693	Hs.21422	ESTs	3	0.2	upregulate stage
50	415336	T77664	Hs.78362	Human clone 23839 mRNA sequence	1	0.87	upregulate stage
	415337	Z44881	Hs.9012	ESTs	8.8	0.07	upregulate stage
	415352	F06565		gb:HSC1CG051 normalized infant brain cDN	1	1	upregulate stage
	415364	F06771		gb:HSC1KD031 normalized infant brain cDN	1	1	upregulate stage
	415371	R15239		gb:YB9b02.r1 Soares infant brain 1NIB H	5.1	0.13	upregulate stage
55	415412	F08049	Hs.52132	ESTs	4.25	0.16	upregulate stage
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.1	0.15	upregulate stage
	415462	R52692	Hs.12698	ESTs	4.65	0.11	upregulate stage
	415496	R37637	Hs.12286	ESTs	5.4	0.13	upregulate stage
	415509	R40000	Hs.91968	ESTs	1	0.44	upregulate stage
60	415511	AI732617	Hs.182362	ESTs	9.3	0.03	upregulate stage
	415542	R13474	Hs.290263	ESTs	9.7	0.08	upregulate stage
	415569	Z43930		gb:HSC1OH121 normalized infant brain cDN	1	0.74	upregulate stage
	415600	F12664		gb:HSC3CG021 normalized infant brain cDN	1	0.43	upregulate stage
	415616	F12945	Hs.12294	ESTs	1	1	upregulate stage
65	415626	Z43847		gb:HSC1MC051 normalized infant brain cDN	1	1	upregulate stage
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	1	0.26	upregulate stage
	415750	AA167712		gb:zq39g08.s1 Striatogene hNT neuron (937	1	0.83	upregulate stage
	415786	AW419196	Hs.257924	Homo sapiens cDNA FLJ13782 fis, clone PL	9	0.08	upregulate stage
	415788	AW628686	Hs.73851	KIAA0217 protein	5.2	0.11	upregulate stage
70	415790	R23574	Hs.23545	ESTs	1	1	upregulate stage
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.25	0.12	upregulate stage
	415837	H05279	Hs.21758	ESTs	1	0.57	upregulate stage
	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	8.05	0.07	upregulate stage
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	12.2	0.06	upregulate stage
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	12.2	0.06	upregulate stage
75	415948	AA262226		gb:z24h06.r1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	415979	H16427	Hs.271501	ESTs	4.85	0.13	upregulate stage
	415989	AI267700	Hs.111128	ESTs	4.45	0.08	upregulate stage

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1	1	upregulate stage
	416052	R12816	Hs.21164	ESTs	1.45	0.24	upregulate stage
	416053	H16359	Hs.130648	ESTs	4.35	0.14	upregulate stage
5	416061	R45516	Hs.26119	ESTs	1	1	upregulate stage
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	4.72	0.17	upregulate stage
	416097	BE387371	Hs.301304	Homo sapiens cDNA: FLJ21017 fis, clone C	5.75	0.11	upregulate stage
	416111	AA038313	Hs.79018	chromatin assembly factor 1, subunit A (8.4	0.09	upregulate stage
	416135	AW473656	Hs.45119	ESTs	2.29	0.2	upregulate stage
10	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610.1 inner	5.1	0.13	upregulate stage
	416173	R52782		gb:yg99d09.r1 Soares Infant brain 1N1B H	3.7	0.12	upregulate stage
	416195	AW131940	Hs.104030	ESTs	1.1	0.16	upregulate stage
	416196	W51955	Hs.73372	ESTs	3.25	0.14	upregulate stage
	416203	H27794	Hs.269055	ESTs	1	0.32	upregulate stage
15	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.15	0.12	upregulate stage
	416226	N55342	Hs.34372	ESTs	2.35	0.21	upregulate stage
	416239	AL038450	Hs.48948	ESTs	4.05	0.14	upregulate stage
	416241	N52639	Hs.32583	ESTs	5	0.09	upregulate stage
	416254	H51703	Hs.13640	ESTs	1	0.95	upregulate stage
20	416269	AA177138	Hs.161671	ESTs	4.07	0.2	upregulate stage
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	1.84	0.45	upregulate stage
	416280	H44180	Hs.181789	ESTs	1	1	upregulate stage
	416309	R84694	Hs.79194	cAMP responsive element binding protein	9.35	0.08	upregulate stage
	416324	H47983	Hs.1870	phenylalanine hydroxylase	5.15	0.13	upregulate stage
25	416332	H91284	Hs.244461	ESTs	1	1	upregulate stage
	416343	H49213		gb:yy19e04.r1 Soares fetal liver spleen	1	1	upregulate stage
	416353	T77127	Hs.191297	ESTs, Moderately similar to ALU6_HUMAN A	1.46	0.59	upregulate stage
	416395	R94575		gb:yy173e10.s1 Soares fetal liver spleen	9.2	0.09	upregulate stage
	416437	N48990	Hs.37204	ESTs	4.15	0.12	upregulate stage
30	416476	H58137	Hs.268639	ESTs	1	0.22	upregulate stage
	416537	T99086	Hs.144904	nuclear receptor co-repressor 1	5.45	0.12	upregulate stage
	416539	Y07909	Hs.79368	epithelial membrane protein 1	9.45	0.09	upregulate stage
	416575	W02414	Hs.38383	ESTs	4.95	0.1	upregulate stage
	416624	H69044		gb:yy77h05.s1 Soares fetal liver spleen	1	0.22	upregulate stage
35	416644	H70701	Hs.269135	ESTs	5.65	0.12	upregulate stage
	416658	U03272	Hs.79432	fibulin 2 (congenital contractural ara	9.65	0.05	upregulate stage
	416682	R99700	Hs.36152	ESTs	1	0.25	upregulate stage
	416690	H84078	Hs.108551	ESTs	5.35	0.13	upregulate stage
	416709	R99369	Hs.283108	hemoglobin, gamma G	5.4	0.13	upregulate stage
40	416712	N68576	Hs.81602	ESTs	1	0.25	upregulate stage
	416715	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.32	upregulate stage
	416731	T58115	Hs.10336	ESTs	1	0.4	upregulate stage
	416734	H81213	Hs.14825	ESTs	3.8	0.16	upregulate stage
	416735	R11275	Hs.194485	ESTs	11.5	0.06	upregulate stage
45	416738	N29218	Hs.40290	ESTs	1	0.42	upregulate stage
	416856	N27833	Hs.269028	ESTs	2.6	0.22	upregulate stage
	416883	AW140128	Hs.184902	ESTs	11.3	0.07	upregulate stage
	416923	N32498	Hs.42829	ESTs	1	0.61	upregulate stage
	416936	N21352	Hs.42987	ESTs, Weakly similar to ORF2 [Musculus	1	1	upregulate stage
50	417018	M16038	Hs.80887	v-yas-1 Yamaguchi sarcoma viral related	11.3	0.05	upregulate stage
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.04	0.15	upregulate stage
	417134	N51220	Hs.269068	ESTs	1	0.24	upregulate stage
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	1.98	0.32	upregulate stage
	417218	AA005247	Hs.285754	mal proto-oncogene (hepatocyte growth fa	2.95	0.21	upregulate stage
55	417265	AL121359	Hs.281117	ESTs	1	0.3	upregulate stage
	417283	N62840	Hs.48648	ESTs	1.05	0.27	upregulate stage
	417308	H60720	Hs.81892	KIAA0101 gene product	9.2	0.09	upregulate stage
	417320	AA195667	Hs.287324	ESTs	2.8	0.16	upregulate stage
	417396	T98987		gb:ye66f02.r1 Soares fetal liver spleen	1	1	upregulate stage
60	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.75	0.09	upregulate stage
	417409	BE272506	Hs.82109	syndecan 1	1.92	0.44	upregulate stage
	417448	AA203135	Hs.130186	ESTs	6.45	0.1	upregulate stage
	417453	H73183	Hs.129885	ESTs, Moderately similar to unnamed prot	4.65	0.13	upregulate stage
65	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.59	0.49	upregulate stage
	417540	AA203600	Hs.152250	ESTs	1	1	upregulate stage
	417576	AA339449	Hs.82285	phosphoribosylglycnamide formyltransfer	5.65	0.1	upregulate stage
	417581	R26968	Hs.24104	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.15	0.09	upregulate stage
	417596	R07343	Hs.226823	ESTs	4.35	0.14	upregulate stage
	417599	AA204688	Hs.136201	ESTs, Weakly similar to ALU7_HUMAN ALU S	0.94	0.9	upregulate stage
70	417620	R02530	Hs.191198	ESTs	9.1	0.07	upregulate stage
	417638	R12490	Hs.189779	ESTs	1	0.32	upregulate stage
	417650	T05870	Hs.100640	ESTs	1	0.22	upregulate stage
	417715	AW869587	Hs.86366	ESTs	6.31	0.09	upregulate stage
	417720	AA205625	Hs.208067	ESTs	4.65	0.11	upregulate stage
75	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	4.15	0.13	upregulate stage
	417750	AI267720	Hs.260523	neuroblastoma RAS viral (v-ras) oncogene	9.98	0.08	upregulate stage
	417780	Z43482	Hs.82772	collagen, type XI, alpha 1	2.3	0.14	upregulate stage
	417789	R50978	Hs.267054	ESTs	1.05	0.19	upregulate stage

	417791	AW965339	Hs.111471	ESTs	5.35	0.1	upregulate stage
	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kD)	1	1	upregulate stage
	417898	AA826198	Hs.291851	ESTs	2.15	0.21	upregulate stage
5	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone L	3.7	0.13	upregulate stage
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.57	0.5	upregulate stage
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	17.9	0.02	upregulate stage
	418027	AB037807	Hs.83293	hypothetical protein	6.6	0.09	upregulate stage
	418030	BE207573	Hs.83321	neuromedin B	12.2	0.04	upregulate stage
10	418068	AW971155	Hs.293902	ESTs, Weakly similar to prollyl 4-hydroxy	4.26	0.14	upregulate stage
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.21	0.15	upregulate stage
	418134	AA397769	Hs.86617	ESTs	1	0.3	upregulate stage
	418153	R13696	Hs.112830	ESTs	1	0.3	upregulate stage
	418180	BE618087	Hs.83724	Human clone 23773 mRNA sequence	8.79	0.09	upregulate stage
15	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	3.75	0.13	upregulate stage
	418203	X54942	Hs.83758	CDC28 protein kinase 2	13.85	0.04	upregulate stage
	418216	AA662240	Hs.283099	AF15q14 protein	9.75	0.07	upregulate stage
	418235	AW994005	Hs.172572	hypothetical protein FLJ20093	10.75	0.05	upregulate stage
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	5.25	0.12	upregulate stage
20	418259	AA215404	Hs.137289	ESTs	11.5	0.07	upregulate stage
	418268	AA810599	Hs.86643	ESTs	1	0.43	upregulate stage
	418296	C01566	Hs.86571	ESTs	1	0.45	upregulate stage
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	9.04	0.08	upregulate stage
	418379	AA218940	Hs.137516	fidgetin-like 1	3.25	0.15	upregulate stage
25	418422	AW440068	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	8.95	0.1	upregulate stage
	418454	AA315308	Hs.85266	gbr:EST187095 Colon carcinoma (HCC) cell	2.5	0.15	upregulate stage
	418462	BE001596	Hs.85266	Integrin, beta 4	1.33	0.59	upregulate stage
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	1.21	0.71	upregulate stage
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma	2.69	0.23	upregulate stage
30	418480	AA223929	Hs.86902	ESTs	1	1	upregulate stage
	418498	T78248	Hs.85701	gb:yd79f05.r1 Soares fetal liver spleen	1	0.47	upregulate stage
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.4	0.14	upregulate stage
	418546	AA224827	Hs.85701	gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.72	0.23	upregulate stage
	418573	AA225188	Hs.85701	gb:nc21h04.r1 NCI_CGAP_Pr1 Homo sapiens	9.95	0.07	upregulate stage
35	418577	AA225247	Hs.269300	ESTs, Weakly similar to B34087 hypothell	1	0.77	upregulate stage
	418578	U92459	Hs.86204	glutamate receptor, metabotropic 8	1	1	upregulate stage
	418590	AI732672	Hs.252507	ESTs	1	0.59	upregulate stage
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	4.75	0.13	upregulate stage
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	1	0.23	upregulate stage
40	418624	AI734080	Hs.104211	ESTs	7.95	0.09	upregulate stage
	418651	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	3	0.15	upregulate stage
	418663	AK001100	Hs.87013	Homo sapiens cDNA FLJ10238 fis, clone HE	17.2	0.04	upregulate stage
	418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	1	1	upregulate stage
	418686	Z36830	Hs.87268	annexin A8	2.11	0.3	upregulate stage
45	418687	R61650	Hs.22581	ESTs	6.75	0.07	upregulate stage
	418693	AI750878	Hs.87409	thrombospondin 1	4.5	0.08	upregulate stage
	418704	AA227235	Hs.83286	ESTs	1	0.33	upregulate stage
	418712	Z42183	Hs.83286	gb:HSC08F041 normalized infant brain cDN	1	0.91	upregulate stage
50	418717	AI334430	Hs.86984	ESTs	4.7	0.12	upregulate stage
	418723	AA504428	Hs.10487	ESTs, Weakly similar to Weak similarity	5.85	0.1	upregulate stage
	418738	AW388633	Hs.6682	ESTs	3.6	0.09	upregulate stage
	418752	AL133556	Hs.88144	hypothetical protein FLJ12476	1	1	upregulate stage
	418757	AI864193	Hs.169728	Homo sapiens cDNA FLJ13150 fis, clone NT	9.15	0.09	upregulate stage
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	9.25	0.08	upregulate stage
55	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.83	0.43	upregulate stage
	418876	AA740616	Hs.293874	ESTs	11.3	0.06	upregulate stage
	418903	AW969665	Hs.154848	ESTs	1	1	upregulate stage
	418915	AI474778	Hs.118977	ESTs	4.75	0.12	upregulate stage
	418939	AW630803	Hs.89497	lamin B1	2.6	0.13	upregulate stage
60	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.45	0.53	upregulate stage
	418976	AA933082	Hs.126883	ESTs	1	0.23	upregulate stage
	419059	T86216	Hs.89584	gb:yd84a05.r1 Soares fetal liver spleen	1	0.38	upregulate stage
	419078	M93119	Hs.89584	Insulinoma-associated 1	1.25	0.18	upregulate stage
	419121	AA374372	Hs.89526	parathyroid hormone-like hormone	1	1	upregulate stage
65	419169	AW851980	Hs.262346	ESTs, Weakly similar to ORF2: function u	1.59	0.3	upregulate stage
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	3.55	0.05	upregulate stage
	419218	AI248073	Hs.188723	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.27	upregulate stage
	419226	AI342491	Hs.87413	ESTs	1	0.37	upregulate stage
	419235	AW470411	Hs.288433	neurotrophin	11.9	0.07	upregulate stage
70	419286	AA236005	Hs.221303	ESTs	4.85	0.14	upregulate stage
	419327	AA521504	Hs.190179	ESTs	1	1	upregulate stage
	419355	AA428520	Hs.90061	progesterone binding protein	10.6	0.06	upregulate stage
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.84	0.47	upregulate stage
	419413	AA237040	Hs.87589	ESTs	1	1	upregulate stage
	419436	AA991639	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	6.6	0.1	upregulate stage
75	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.31	0.64	upregulate stage
	419472	AW978038	Hs.87648	gb:EST390147 MAGE resequences, MAGO Homo	1	1	upregulate stage
	419475	AA243420	Hs.87648	ESTs	1.1	0.24	upregulate stage

	419477	AA826279		gb:cd03g07.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.56	upregulate stage
	419484	AA243474	Hs.272128	Homo sapiens cDNA FLJ13901 fis, clone TH	1	0.22	upregulate stage
	419506	N20812	Hs.42369	ESTs	1	1	upregulate stage
5	419554	AI732138	Hs.104318	ESTs	1	0.5	upregulate stage
	419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	1	0.91	upregulate stage
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.1	0.08	upregulate stage
	419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide exchan	1	1	upregulate stage
	419666	NM_014810	Hs.92200	KIAA0480 gene product	5.2	0.12	upregulate stage
10	419737	H24185	Hs.92918	hypothetical protein	11.7	0.07	upregulate stage
	419743	AW408762	Hs.127478	ESTs	6.1	0.09	upregulate stage
	419752	AA249573	Hs.152618	ESTs	1.8	0.17	upregulate stage
	419769	H27374	Hs.103483	ESTs	1	0.36	upregulate stage
	419805	AW966945		gb:EST379019 MAGE resequences, MAGJ Homo	1	0.34	upregulate stage
15	419807	R77402		gb:yf75f11.s1 Soares placenta Nb2HP Homo	1	0.67	upregulate stage
	419831	AW448930	Hs.5415	ESTs	7.05	0.1	upregulate stage
	419833	AA251131	Hs.220697	ESTs	1.25	0.53	upregulate stage
	419834	AA251139		gb:zs03g12.s1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	419923	AW081455	Hs.120219	ESTs	5.89	0.13	upregulate stage
20	419945	AW290975	Hs.118923	ESTs	1	0.24	upregulate stage
	419962	AA830111	Hs.291917	ESTs	1	1	upregulate stage
	419970	AW612022	Hs.263271	ESTs	9.15	0.09	upregulate stage
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.05	0.17	upregulate stage
	419998	AA252691		gb:zs26d09.r1 NCI_CGAP_GCB1 Homo sapiens	1	0.47	upregulate stage
25	420016	AW016908	Hs.88025	ESTs	1	0.8	upregulate stage
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.8	0.11	upregulate stage
	420076	AA827860	Hs.293717	ESTs	5.35	0.12	upregulate stage
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.3	0.11	upregulate stage
	420145	AA809860	Hs.256284	ESTs	1	1	upregulate stage
30	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	14.8	0.04	upregulate stage
	420161	AI683069	Hs.175319	ESTs	4.7	0.11	upregulate stage
	420184	AA188408	Hs.95565	hypothetical protein	4.35	0.15	upregulate stage
	420226	AA773709	Hs.152818	ubiquitin specific protease 8	3.1	0.16	upregulate stage
	420230	AL034344	Hs.298020	Homo sapiens cDNA FLJ11796 fis, clone HE	10.35	0.06	upregulate stage
	420236	AA256763	Hs.291111	ESTs	4.45	0.14	upregulate stage
35	420270	AA257990		gb:zs35h07.r1 NCI_CGAP_GCB1 Homo sapiens	10.05	0.08	upregulate stage
	420297	AI628272	Hs.88323	ESTs	9.45	0.09	upregulate stage
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	11.7	0.05	upregulate stage
	420392	AI242930	Hs.97393	KIAA0328 protein	1.7	0.22	upregulate stage
40	420413	AW971624	Hs.120605	ESTs	1	1	upregulate stage
	420445	AA262213	Hs.193514	ESTs	1	1	upregulate stage
	420471	AA262452	Hs.192268	ESTs	3.95	0.13	upregulate stage
	420479	AW183695	Hs.186572	ESTs	4.95	0.12	upregulate stage
	420493	AI635113	Hs.270366	Homo sapiens mRNA: cDNA DKFZp564H0616 (f	4.4	0.15	upregulate stage
45	420552	AK000492	Hs.98806	hypothetical protein	11.55	0.06	upregulate stage
	420572	AL035593	Hs.99016	Human DNA sequence from clone 310J6 on c	1.35	0.22	upregulate stage
	420643	W87731		gb:zh65g10.r1 Soares_fetal_liver_spleen_	1.25	0.25	upregulate stage
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	7.3	0.09	upregulate stage
	420654	AA279091	Hs.104420	ESTs	1	0.27	upregulate stage
50	420655	R74405	Hs.300886	ESTs	1	1	upregulate stage
	420717	AA284447	Hs.271887	ESTs	9	0.09	upregulate stage
	420734	AW972872	Hs.293736	ESTs	5.2	0.13	upregulate stage
	420756	AA411800	Hs.189900	ESTs	1	1	upregulate stage
	420789	AI670057	Hs.199882	ESTs	8.85	0.06	upregulate stage
55	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	4.6	0.12	upregulate stage
	420851	AA281062	Hs.250734	ESTs	8.35	0.08	upregulate stage
	420880	AI809621	Hs.105620	ESTs	1	1	upregulate stage
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	10.4	0.03	upregulate stage
	420928	AA281809		gb:zt10e01.r1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
60	420936	AA456112	Hs.99410	ESTs	8.71	0.07	upregulate stage
	420947	AA491044	Hs.47196	ESTs	1	0.38	upregulate stage
	421017	AW979181	Hs.293221	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	upregulate stage
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.26	0.62	upregulate stage
	421070	AA283185	Hs.19327	ESTs	2.2	0.14	upregulate stage
65	421100	AW351839	Hs.124690	Homo sapiens cDNA: FLJ21763 fis, clone C	1.69	0.28	upregulate stage
	421102	AI470093	Hs.89217	ESTs	2.65	0.19	upregulate stage
	421103	AI625835	Hs.27104	ESTs	6	0.1	upregulate stage
	421114	AW975051	Hs.293156	ESTs	4.7	0.12	upregulate stage
	421118	AI471925	Hs.89257	ESTs	1	0.39	upregulate stage
70	421155	H87879	Hs.102257	lysyl oxidase	1.15	0.18	upregulate stage
	421159	AW978316	Hs.136649	ESTs	1	0.44	upregulate stage
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.7	0.11	upregulate stage
	421218	NM_000499	Hs.72312	cytochrome P450, subfamily I (aromatic c	0.07	2.55	upregulate stage
	421221	AW276914	Hs.300877	ESTs	8.75	0.07	upregulate stage
75	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	1.64	0.49	upregulate stage
	421261	AA600853	Hs.98133	ESTs	10.9	0.07	upregulate stage
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	2.65	0.16	upregulate stage
	421278	AI387919	Hs.99691	ESTs	1	0.56	upregulate stage

5	421280	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
	421282	AA286914	Hs.183299	ESTs	9	0.08	upregulate stage
	421306	AA806207	Hs.125889	ESTs	1	0.95	upregulate stage
	421308	AA687322	Hs.192843	ESTs	2.85	0.15	upregulate stage
	421373	AA808229	Hs.167771	ESTs	2.45	0.14	upregulate stage
10	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.6	0.26	upregulate stage
	421381	AA361752		gb:EST71314 T-cell lymphoma Homo sapiens	5.05	0.09	upregulate stage
	421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens	6.55	0.1	upregulate stage
	421433	AI829192	Hs.134805	ESTs	9.9	0.07	upregulate stage
	421451	AA291377	Hs.50831	ESTs	11.9	0.06	upregulate stage
15	421491	H99999	Hs.42736	ESTs	3	0.2	upregulate stage
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.51	0.32	upregulate stage
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	9	0.09	upregulate stage
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	5.75	0.12	upregulate stage
	421673	H54384	Hs.36892	ESTs	1	1	upregulate stage
20	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	9.45	0.07	upregulate stage
	421708	AW754341		gb:CM0-CT0341-181299-130-h12 CT0341 Homo	1	0.47	upregulate stage
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.97	0.33	upregulate stage
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	7.05	0.1	upregulate stage
	421869	AB003592	Hs.109050	contactin 6	1	1	upregulate stage
25	421925	S80310	Hs.109620	acidic epidermal glycoprotein-like 1	1	1	upregulate stage
	421948	L42583	Hs.111758	keratin 6A	51.9	0.01	upregulate stage
	421958	AA357185	Hs.109918	ras homolog gene family, member H	10.17	0.07	upregulate stage
	421991	NM_014918	Hs.110488	KIAA0990 protein	4.5	0.17	upregulate stage
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	6.5	0.08	upregulate stage
30	422072	AB018255	Hs.111138	KIAA0712 gene product	9.2	0.08	upregulate stage
	422094	AF129535	Hs.272027	F-box only protein 5	6.95	0.09	upregulate stage
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.66	0.17	upregulate stage
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.95	0.1	upregulate stage
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.8	0.16	upregulate stage
35	422204	AA339015		gb:EST44247 Fetal brain I Homo sapiens c	1	1	upregulate stage
	422261	AA307595	Hs.119908	nucleolar protein NOP5/NOP58	1	1	upregulate stage
	422271	AB038995	Hs.114159	RAB-8b protein	5.04	0.16	upregulate stage
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	3.46	0.24	upregulate stage
	422282	AF019225	Hs.114309	apolipoprotein L	4.54	0.14	upregulate stage
40	422322	AB022192	Hs.115240	peroxisome biogenesis factor 13	1	0.53	upregulate stage
	422330	D30783	Hs.115263	epiregulin	4.45	0.06	upregulate stage
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.25	0.19	upregulate stage
	422406	AF025441	Hs.116206	Opa-interacting protein 5	9.5	0.07	upregulate stage
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.35	0.04	upregulate stage
45	422491	AA338548	Hs.117546	neurofilin	0.64	1.24	upregulate stage
	422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.6	0.11	upregulate stage
	422505	AL120862	Hs.124165	ESTs	2.8	0.14	upregulate stage
	422508	AJ000327	Hs.117852	ATP-binding cassette, sub-family D (ALD)	5.25	0.14	upregulate stage
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.57	0.31	upregulate stage
50	422540	AI050751	Hs.22895	Homo sapiens cDNA: FLJ23548 fis, clone L	1	0.59	upregulate stage
	422588	AA312730		gb:EST183651 Monocytes, stimulated II Ho	3	0.14	upregulate stage
	422678	AA247778	Hs.119155	Homo sapiens mRNA; cDNA DKFZp434B249 (fr	10.7	0.07	upregulate stage
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.1	0.13	upregulate stage
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.94	0.1	upregulate stage
55	422823	D89974	Hs.121102	vanin 2	10	0.07	upregulate stage
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	1	0.27	upregulate stage
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.2	0.08	upregulate stage
	422964	AW439476	Hs.256895	ESTs	11.75	0.07	upregulate stage
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	3.05	0.14	upregulate stage
60	423001	AA320014	Hs.208603	ESTs	9.1	0.09	upregulate stage
	423090	BE387529	Hs.123536	melanoma antigen, family E, 1, cancer/te	1	0.49	upregulate stage
	423100	AA323114		gb:EST25873 Cerebellum II Homo sapiens c	1	1	upregulate stage
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	2.8	0.19	upregulate stage
	423156	AA131493	Hs.124752	fibroblast growth factor 12B	1	0.27	upregulate stage
65	423198	M81933	Hs.1634	cell division cycle 25A	8.95	0.07	upregulate stage
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.2	0.57	upregulate stage
	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	9.75	0.07	upregulate stage
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	4.95	0.12	upregulate stage
	423309	BE006775	Hs.126782	sushi-repeat protein	1.58	0.34	upregulate stage
70	423347	AI660412	Hs.234557	ESTs	1	0.45	upregulate stage
	423359	NM_014170	Hs.127496	HSPC135 protein	1	0.69	upregulate stage
	423368	AA364195		gb:EST75015 Pineal gland II Homo sapiens	1	0.95	upregulate stage
	423389	AI471609	Hs.54347	ESTs	3.95	0.14	upregulate stage
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.62	0.43	upregulate stage
75	423441	R68649	Hs.278359	absent in melanoma 1 like	6.25	0.1	upregulate stage
	423453	AW450737	Hs.128791	CGI-09 protein	8.45	0.09	upregulate stage
	423500	AF020763	Hs.129705	clone 1900 unknown protein	1	0.8	upregulate stage
	423578	AW960454	Hs.222830	ESTs	11.94	0.07	upregulate stage
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.4	0.17	upregulate stage
	423632	AA328824		gb:EST32358 Embryo, 12 week I Homo sapie	1	0.71	upregulate stage
	423642	AW452650	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	8.35	0.1	upregulate stage

5	423644	AA329048		gb:EST32875 Embryo, 12 week I Homo sapie	1	0.43	upregulate stage
	423648	AK000456	Hs.130546	hypothetical protein FLJ20449	10.4	0.07	upregulate stage
	423651	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	5.75	0.1	upregulate stage
	423654	AI674253	Hs.35828	ESTs	3.15	0.18	upregulate stage
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	29.7	0.02	upregulate stage
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.1	0.16	upregulate stage
	423745	AI809797	Hs.43222	ESTs	1	0.5	upregulate stage
	423748	AJ149048	Hs.30211	hypothetical protein FLJ22313	4.25	0.13	upregulate stage
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	1.18	0.71	upregulate stage
	423758	AA338153	Hs.82124	laminin, beta 1	1	1	upregulate stage
15	423774	L39064	Hs.1702	interleukin 9 receptor	3.08	0.15	upregulate stage
	423818	AA332439		gb:EST36554 Embryo, 8 week I Homo sapien	1	0.38	upregulate stage
	423827	AI472828	Hs.172625	ESTs	1	0.43	upregulate stage
	423837	AW937063		gb:PM3-DT0037-231299-001-g11 DT0037 Homo	1.44	0.55	upregulate stage
	423912	BE091233		gb:PM0-BT0726-300300-001-H07 BT0726 Homo	1	1	upregulate stage
20	423938	AL049328	Hs.135642	Homo sapiens mRNA; cDNA DKFZp564E026 (fr	1	1	upregulate stage
	423942	AF209704	Hs.135723	glycolipid transfer protein	11.65	0.05	upregulate stage
	423944	T91433	Hs.128291	phosphodiesterase 10A	1	0.45	upregulate stage
	423946	AL137344	Hs.135892	Homo sapiens mRNA; cDNA DKFZp76111311 (f	1	1	upregulate stage
	423956	W82803	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	5.35	0.09	upregulate stage
25	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	8.8	0.06	upregulate stage
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	3.14	0.19	upregulate stage
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6	0.26	upregulate stage
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	1.8	0.22	upregulate stage
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	9.1	0.06	upregulate stage
30	424087	N69333	Hs.21638	ESTs	1	1	upregulate stage
	424193	AK002005	Hs.142868	Homo sapiens cDNA FLJ11143 fis, clone PL	1	0.23	upregulate stage
	424353	AA339646		gb:EST44755 Fetal brain I Homo sapiens c	1	1	upregulate stage
	424364	AW383226	Hs.201189	ESTs, Weakly similar to DRPLA [H.sapiens	2.18	0.33	upregulate stage
	424406	D54120	Hs.146409	wingless-type MMTV integration site fami	2.05	0.17	upregulate stage
35	424420	BE614743	Hs.146688	prostaglandin E synthase	1.19	0.67	upregulate stage
	424425	AB031480	Hs.146824	SPR1 protein	1.42	0.54	upregulate stage
	424486	BE002477	Hs.278714	chloride intracellular channel 6	1	0.27	upregulate stage
	424490	AJ278016	Hs.55565	ankyrin repeat domain 3	2.02	0.39	upregulate stage
	424492	AI133482	Hs.165210	ESTs	3.15	0.14	upregulate stage
40	424505	AA446131	Hs.124918	Homo sapiens cDNA FLJ13186 fis, clone NT	11.55	0.05	upregulate stage
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	2.65	0.23	upregulate stage
	424575	AL110217	Hs.150751	DKFZP572C163 protein	1	1	upregulate stage
	424583	AF017445	Hs.150926	fructose-1-phosphate guanylyltransferase	1.8	0.26	upregulate stage
	424589	AW854298		gb:RC3-CT0254-100500-211-c03 CT0254 Homo	0.85	0.94	upregulate stage
45	424602	AK002055	Hs.301129	Homo sapiens clone Z3859 mRNA sequence	2.85	0.2	upregulate stage
	424625	AW904466	Hs.151310	PDZ domain protein (Drosophila InaD-like	1	0.4	upregulate stage
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.41	0.52	upregulate stage
	424643	AF241850	Hs.151428	rel finger protein 2	9.75	0.07	upregulate stage
	424649	BE242035	Hs.151461	embryonic ectoderm development	5.85	0.13	upregulate stage
50	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	1	0.56	upregulate stage
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.42	0.52	upregulate stage
	424690	BE538356	Hs.151777	Human translation initiation factor eIF-	4.3	0.1	upregulate stage
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.85	0.11	upregulate stage
	424702	AF250237	Hs.152009	G protein-coupled receptor 85	1	1	upregulate stage
55	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.05	0.09	upregulate stage
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	1.04	0.59	upregulate stage
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.11	0.65	upregulate stage
	424749	NM_002451	Hs.152817	methylthioadenosine phosphorylase	1	1	upregulate stage
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	18.5	0.03	upregulate stage
60	424841	AI280215	Hs.96885	ESTs	1	1	upregulate stage
	424860	W60828	Hs.153529	Homo sapiens clone 24540 mRNA sequence	1	1	upregulate stage
	424878	H57111	Hs.221132	ESTs	9.45	0.07	upregulate stage
	424879	AA348013	Hs.159354	ESTs	10.7	0.07	upregulate stage
	424888	AA348126	Hs.24882	ESTs	2.8	0.21	upregulate stage
65	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene e)-related k	7.75	0.07	upregulate stage
	424930	AA885344	Hs.96910	ESTs	1.45	0.38	upregulate stage
	424948	AA348810	Hs.190503	ESTs	3.2	0.12	upregulate stage
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	8.75	0.09	upregulate stage
	424993	F07625		gb:HSC2CF021 normalized infant brain cDN	1	1	upregulate stage
70	425020	U09368	Hs.154205	zinc finger protein 140 (clone pTZ-39)	1	1	upregulate stage
	425024	R39235	Hs.12407	ESTs	2.65	0.13	upregulate stage
	425057	AA826434	Hs.96944	ESTs	1	0.22	upregulate stage
	425068	AL048716	Hs.154387	KIAA0103 gene product	9.5	0.07	upregulate stage
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.66	0.52	upregulate stage
75	425191	AF052146	Hs.155085	Homo sapiens clone 24653 mRNA sequence	1	0.32	upregulate stage
	425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	7.05	0.1	upregulate stage
	425234	AW152225	Hs.165909	ESTs	19.7	0.04	upregulate stage
	425239	BE567924	Hs.155244	pre-mRNA splicing factor similar to S. c	1	0.69	upregulate stage
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	10.45	0.05	upregulate stage
	425304	AA463844	Hs.31339	fibroblast growth factor 11	1.57	0.51	upregulate stage
	425316	AA354977	Hs.191565	ESTs, Moderately similar to NSD1 protein	5.05	0.12	upregulate stage

	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	14.7	0.05	upregulate stage
	425362	AA355936		gb:EST64410 Jurkat T-cells V1 Homo sap	1	1	upregulate stage
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kd)	8.24	0.09	upregulate stage
5	425403	AL023753	Hs.156406	Human DNA sequence from clone 1193H6 on	1	0.22	upregulate stage
	425415	M13903	Hs.157091	involucrin	1.19	0.55	upregulate stage
	425420	BE536911	Hs.234545	ESTs, Weakly similar to AF155135 1 novel	2.85	0.13	upregulate stage
	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	9	0.07	upregulate stage
	425465	L18964	Hs.1904	protein kinase C, iota	9.6	0.07	upregulate stage
10	425467	R16484	Hs.190075	ESTs	1	0.83	upregulate stage
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.2	0.15	upregulate stage
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	1	1	upregulate stage
	425608	AA360486	Hs.92448	ESTs	4.7	0.14	upregulate stage
	425614	AI334963	Hs.156256	ESTs	2.65	0.14	upregulate stage
15	425641	D79758	Hs.143355	Homo sapiens cDNA FLJ13207 fis, clone NT	4.86	0.1	upregulate stage
	425660	AA521184	Hs.105504	ESTs	1	0.31	upregulate stage
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	1.25	0.19	upregulate stage
	425672	AA361483		gb:EST70790 T-cell lymphoma Homo sapiens	1	1	upregulate stage
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript)	3.96	0.13	upregulate stage
20	425726	AF085808	Hs.159330	uroplakin 3	0.92	0.79	upregulate stage
	425742	AJ001454	Hs.159425	testican 3	1	1	upregulate stage
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	1	0.39	upregulate stage
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.89	0.44	upregulate stage
	425843	BE313280	Hs.159627	death associated protein 3	3.1	0.15	upregulate stage
25	425852	AK001504	Hs.159651	death receptor 6	1.72	0.47	upregulate stage
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.95	0.68	upregulate stage
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	1	0.34	upregulate stage
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	14.3	0.04	upregulate stage
	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	11.75	0.05	upregulate stage
30	426108	AA622037	Hs.166468	programmed cell death 5	3.23	0.18	upregulate stage
	426115	H08895	Hs.166733	leucylcystinyl aminopeptidase	1	0.32	upregulate stage
	426168	NM_003152	Hs.167503	signal transducer and activator of trans	1.97	0.4	upregulate stage
	426257	AL137201	Hs.168625	KIAA0979 protein	1	0.29	upregulate stage
	426261	AW242243	Hs.168670	peroxisomal fatty acylated protein	2.8	0.16	upregulate stage
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	14.75	0.04	upregulate stage
	426451	AI908165	Hs.169946	GATA-binding protein 3	3.05	0.28	upregulate stage
	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	1	0.36	upregulate stage
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.17	0.05	upregulate stage
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	1.15	0.47	upregulate stage
40	426561	AA381437		gb:EST94514 Activated T-cells I Homo sap	5.65	0.11	upregulate stage
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	11.05	0.05	upregulate stage
	426731	AW303411	Hs.130332	ESTs	2.4	0.21	upregulate stage
	426759	AI590401	Hs.21213	ESTs	9.5	0.06	upregulate stage
	426786	AA319798	Hs.172247	eukaryotic translation elongation factor	9.25	0.09	upregulate stage
45	426788	U66815	Hs.172280	SWI/SNF related, matrix associated, acti	5.63	0.14	upregulate stage
	426818	AA554827	Hs.124841	ESTs, Weakly similar to ALU5_HUMAN ALU S	9	0.08	upregulate stage
	426824	D87717	Hs.172652	KIAA0013 gene product	1	0.87	upregulate stage
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	8.95	0.09	upregulate stage
	426921	AA037145	Hs.172665	cleavage stimulation factor, 3' pre-RNA,	1	0.19	upregulate stage
50	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.15	0.72	upregulate stage
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	11.06	0.06	upregulate stage
	427071	AA397958	Hs.192719	ESTs	5.75	0.08	upregulate stage
	427126	AA620613	Hs.191827	ESTs	2.55	0.18	upregulate stage
	427134	AA398409	Hs.173561	EST	3.4	0.18	upregulate stage
55	427142	AA398510	Hs.133148	ESTs	1	0.25	upregulate stage
	427259	AA400096		gb:zu69107.s1 Soares_testis_NHT Homo sap	1	0.22	upregulate stage
	427308	D26067	Hs.174905	KIAA0033 protein	5.9	0.1	upregulate stage
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	6.12	0.11	upregulate stage
	427356	AW023482	Hs.97849	ESTs	2.7	0.13	upregulate stage
60	427370	AI243615	Hs.97740	ESTs	3.6	0.14	upregulate stage
	427376	AA401533	Hs.19440	ESTs	2.1	0.16	upregulate stage
	427387	BE244966	Hs.177584	3-oxoacid CoA transferase	1	0.39	upregulate stage
	427470	AW999924	Hs.178357	Homo sapiens cDNA FLJ13657 fis, clone PL	3.4	0.16	upregulate stage
	427519	AW085233	Hs.180696	ESTs	8.23	0.1	upregulate stage
65	427521	AW973352	Hs.299056	ESTs	7.75	0.1	upregulate stage
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	5.7	0.15	upregulate stage
	427566	AI743515		gb:wf72b08.x2 Soares_NFL_T_GBC_S1 Homo s	1	1	upregulate stage
	427581	NM_014788	Hs.179703	KIAA0129 gene product	11.45	0.06	upregulate stage
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.25	0.16	upregulate stage
70	427603	AI090838	Hs.98006	ESTs	1	1	upregulate stage
	427646	AI678042	Hs.271953	ESTs	5.7	0.11	upregulate stage
	427652	AI673025	Hs.43874	ESTs	1	0.34	upregulate stage
	427742	AA411880	Hs.190688	ESTs	2.4	0.16	upregulate stage
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regl	9.13	0.08	upregulate stage
75	427839	AA608823	Hs.98244	ESTs	1.9	0.19	upregulate stage
	427878	C05766	Hs.181022	CGI-07 protein	4.1	0.14	upregulate stage
	427922	AK001934	Hs.181112	HSPC126 protein	2.6	0.19	upregulate stage
	427933	AW974643	Hs.190571	ESTs	4.55	0.14	upregulate stage

	427934	AA810541	Hs.291866	ESTs	1	1	upregulate stage
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.15	0.1	upregulate stage
	427961	AW293165	Hs.143134	ESTs	4.85	0.11	upregulate stage
5	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.55	0.13	upregulate stage
	428003	AL110200	Hs.181384	Homo sapiens mRNA; cDNA DKFZp586B0922 (f	1.45	0.36	upregulate stage
	428004	AA449563	Hs.300270	ESTs	3.95	0.12	upregulate stage
	428010	AA806554	Hs.185375	ESTs	1	0.38	upregulate stage
	428057	AI343641	Hs.185798	ESTs	10.1	0.06	upregulate stage
10	428058	AI821625	Hs.191602	ESTs	1	0.5	upregulate stage
	428071	AF212848	Hs.182339	els homologous factor	6.4	0.09	upregulate stage
	428182	BE386042	Hs.293317	ESTs, Weakly similar to JM27 [H.sapiens]	1	0.23	upregulate stage
	428192	AA424051		gb:zv80d03.s1 Soares_total_fetus_Nb2HF8_	2.45	0.16	upregulate stage
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	9.25	0.04	upregulate stage
15	428403	AI393048	Hs.239894	leucine rich repeat (in FLI) Interactin	9.94	0.06	upregulate stage
	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	1	1	upregulate stage
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.43	0.16	upregulate stage
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.2	0.07	upregulate stage
	428529	AW262022	Hs.106278	Homo sapiens cDNA FLJ12839 fis, clone NT	1	1	upregulate stage
20	428576	AW009330	Hs.167621	ESTs	1	0.3	upregulate stage
	428605	AB037662	Hs.188756	KIAA1441 protein	9.25	0.09	upregulate stage
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.8	0.08	upregulate stage
	428685	AF131853	Hs.189527	Homo sapiens clone 25016 mRNA sequence	1	1	upregulate stage
	428716	AL122118	Hs.190614	Homo sapiens mRNA; cDNA DKFZp43401221 (f	1	0.65	upregulate stage
25	428763	AW070204	Hs.178176	ESTs	1.6	0.23	upregulate stage
	428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	9.6	0.08	upregulate stage
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	5.45	0.11	upregulate stage
	428839	AI767756	Hs.82302	ESTs	10	0.06	upregulate stage
	428881	AI298368	Hs.98918	ESTs	1.4	0.18	upregulate stage
30	428954	AF100781	Hs.194678	WNT1 Inducible signaling pathway protein	1	1	upregulate stage
	428988	AA442900	Hs.27947	ESTs	3.05	0.13	upregulate stage
	429042	AW015489	Hs.235920	ESTs	1	0.56	upregulate stage
	429057	AF156557	Hs.194816	stromatin-like protein 1	0.95	0.93	upregulate stage
	429066	AA868555	Hs.178222	ESTs	6	0.11	upregulate stage
35	429072	AI376228	Hs.108043	Friend leukemia virus integration 1	1	1	upregulate stage
	429083	Y09397	Hs.227817	BCL2-related protein A1	11.12	0.03	upregulate stage
	429091	AA935658	Hs.187939	ESTs	8.9	0.08	upregulate stage
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	4.1	0.17	upregulate stage
	429127	AA749382	Hs.107233	ESTs	1	0.23	upregulate stage
40	429135	AA446966	Hs.99090	ESTs, Moderately similar to similar to K	1	1	upregulate stage
	429170	NM_001394	Hs.23359	dual specificity phosphatase 4	8.6	0.08	upregulate stage
	429174	BE559598	Hs.197803	KIAA0160 protein	8.4	0.05	upregulate stage
	429236	AA448407		gb:zv68d11.s1 Soares_testis_NHT Homo sap	1	0.36	upregulate stage
45	429268	AA205386	Hs.198481	RAR-related orphan receptor B	2.9	0.16	upregulate stage
	429300	AB011108	Hs.198891	serine/threonine-protein kinase PRP4 hom	4.25	0.15	upregulate stage
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	2.95	0.11	upregulate stage
	429344	R94038	Hs.199538	inhibin, beta C	2.91	0.28	upregulate stage
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.19	0.68	upregulate stage
	429376	AI867889	Hs.43227	ESTs	1	1	upregulate stage
50	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	8.15	0.07	upregulate stage
	429450	AA824451	Hs.94292	Homo sapiens cDNA: FLJ23311 fis, clone H	3.3	0.17	upregulate stage
	429472	AW452421	Hs.15652	ESTs	1	1	upregulate stage
	429482	AF076974	Hs.203952	transformation/transcription domain-asso	1.52	0.59	upregulate stage
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.9	0.15	upregulate stage
55	429572	AW295375	Hs.39474	ESTs	1	0.95	upregulate stage
	429584	AI817785	Hs.183037	protein kinase, cAMP-dependent, regulato	6.55	0.1	upregulate stage
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	1	1	upregulate stage
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.6	0.14	upregulate stage
	429601	AI804293	Hs.119406	ESTs, Weakly similar to AF143946 1 trans	1.36	0.58	upregulate stage
60	429602	AA521463	Hs.183424	ESTs	1	0.34	upregulate stage
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	10.8	0.07	upregulate stage
	429629	BE501732	Hs.30822	Homo sapiens cDNA FLJ13010 fis, clone NT	3.4	0.12	upregulate stage
	429631	AA455612	Hs.136710	EST	1	1	upregulate stage
	429644	AA455892	Hs.156379	ESTs	3.4	0.15	upregulate stage
65	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	4.45	0.17	upregulate stage
	429664	L20433	Hs.211588	POU domain, class 4, transcription facto	1.17	0.74	upregulate stage
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.19	0.22	upregulate stage
	429689	AI383469	Hs.159300	ESTs	4.4	0.1	upregulate stage
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.25	0.13	upregulate stage
70	429813	AW139678	Hs.180791	ESTs	1	0.95	upregulate stage
	429828	AB019494	Hs.225767	IDN3 protein	4.2	0.14	upregulate stage
	429838	AW904907	Hs.108241	ESTs, Weakly similar to The KIAA0191 gen	3.25	0.14	upregulate stage
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	1	0.36	upregulate stage
	429913	AA460608	Hs.99552	ESTs	1.35	0.2	upregulate stage
75	429917	H80572		gb:yu76c02.r1 Soares fetal liver spleen	4.8	0.13	upregulate stage
	429921	AA526911	Hs.102756	ESTs	1	0.63	upregulate stage
	429950	AW081608	Hs.105053	ESTs	3.7	0.13	upregulate stage
	429971	AF079550	Hs.227098	glial cells missing (Drosophila) homolog	1	0.83	upregulate stage

	429979	AA463338		gb:zx97a10.r1 Soares_NhHMPu_S1 Homo sapi	1	0.32	upregulate stage
	429982	AW449534	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	9.45	0.08	upregulate stage
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.78	0.58	upregulate stage
	430020	AI539029	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	1	0.36	upregulate stage
5	430021	AA463913	Hs.221160	ESTs	1	0.56	upregulate stage
	430049	AW277085	Hs.99619	ESTs	3.55	0.17	upregulate stage
	430060	NM_002941	Hs.301198	roundabout (axon guidance receptor, Dros	1	0.59	upregulate stage
	430076	AA465115		gb:aa32c11.r1 NCL_CGAP_GCB1 Homo sapiens	5.4	0.12	upregulate stage
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to contains similar	3.6	0.13	upregulate stage
	430184	AB013802	Hs.234790	contactin 5	1	1	upregulate stage
	430195	AW969308	Hs.188594	ESTs	9.15	0.1	upregulate stage
	430279	R85974	Hs.16279	ESTs	1.2	0.52	upregulate stage
	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	4.05	0.15	upregulate stage
15	430291	AV660345	Hs.238126	CGI-49 protein	7.2	0.08	upregulate stage
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	11.9	0.06	upregulate stage
	430350	BE169639		gb:PM1-HT0527-280200-005-a05 HT0527 Homo	7.1	0.09	upregulate stage
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9	0.11	upregulate stage
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.56	0.2	upregulate stage
20	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	10.5	0.08	upregulate stage
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	11.2	0.06	upregulate stage
	430519	AF129534	Hs.49210	F-box only protein 4	5.35	0.11	upregulate stage
	430550	AK000062	Hs.243756	hypothetical protein FLJ20055	1	1	upregulate stage
	430551	BE065227		gb:RC1-BT0314-310300-015-b06 BT0314 Homo	1	1	upregulate stage
25	430553	AA481269	Hs.178381	ESTs	1	0.45	upregulate stage
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.75	0.14	upregulate stage
	430630	AW269920	Hs.2521	cystatin A (stefin A)	2.52	0.25	upregulate stage
	430634	AI860651	Hs.26685	ESTs	1.24	0.61	upregulate stage
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.79	0.47	upregulate stage
30	430640	AA482636		gb:zv29c06.r1 Soares ovary tumor NbHOT H	9.15	0.08	upregulate stage
	430665	BE350122	Hs.157367	ESTs	9.4	0.08	upregulate stage
	430726	AL031224	Hs.247850	Human DNA sequence from clone 336H9 on c	1	0.27	upregulate stage
	430733	AW975920	Hs.283361	ESTs	3.5	0.13	upregulate stage
	430781	AW088127	Hs.278636	ESTs	1	1	upregulate stage
35	430791	AA485293	Hs.272068	ESTs, Moderately similar to allanin	1.61	0.42	upregulate stage
	430817	AA487242	Hs.185105	ESTs	1	1	upregulate stage
	430888	BE155293	Hs.76064	ribosomal protein L27a	3.05	0.17	upregulate stage
	430918	NM_000843	Hs.248131	glutamate receptor, metabotropic 6	9.05	0.09	upregulate stage
	430926	L05597	Hs.248136	5-hydroxytryptamine (serotonin) receptor	1	0.91	upregulate stage
40	430994	AA490346	Hs.40530	ESTs	1.03	0.89	upregulate stage
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 3	24.8	0.03	upregulate stage
	431023	AI283133	Hs.178925	ESTs	2.55	0.15	upregulate stage
	431030	AA830525	Hs.291988	ESTs	1	0.47	upregulate stage
	431041	AA490987	Hs.105276	ESTs	1	0.35	upregulate stage
45	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.65	0.45	upregulate stage
	431082	AA491600	Hs.161942	ESTs	9.85	0.06	upregulate stage
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	43.15	0.01	upregulate stage
	431146	Z83850	Hs.250649	Human DNA sequence from PAC 82J11 and co	1	0.4	upregulate stage
	431173	AW971198	Hs.294068	ESTs	6.3	0.12	upregulate stage
50	431245	AA496933	Hs.191687	ESTs	1	1	upregulate stage
	431253	R06428	Hs.226351	ESTs	1	0.8	upregulate stage
	431267	AW969661	Hs.124047	ESTs	1	0.31	upregulate stage
	431287	BE044989	Hs.274901	ESTs	1	1	upregulate stage
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	10.8	0.06	upregulate stage
55	431332	AA503297	Hs.117108	ESTs	6.55	0.1	upregulate stage
	431343	AW970503	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HE	5.65	0.09	upregulate stage
	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.68	0.52	upregulate stage
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.12	0.47	upregulate stage
	431381	AA577114	Hs.105727	ESTs	1	0.36	upregulate stage
60	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	3.72	0.13	upregulate stage
	431494	AA991355	Hs.129808	ESTs	2.75	0.18	upregulate stage
	431510	AA580082	Hs.112264	ESTs	3.75	0.13	upregulate stage
	431560	BE244135	Hs.260238	hypothetical protein FLJ10842	9.1	0.08	upregulate stage
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.5	0.11	upregulate stage
65	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	8.2	0.08	upregulate stage
	431610	AK000972	Hs.264363	hypothetical protein FLJ10110	5.4	0.1	upregulate stage
	431613	AA018515	Hs.264482	Apg12 (autophagy 12, S. cerevisiae)-like	5.8	0.11	upregulate stage
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	1.3	0.59	upregulate stage
	431663	NM_016569	Hs.267182	TBX3-iso protein	1.6	0.52	upregulate stage
70	431670	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	1	1	upregulate stage
	431689	AA305688	Hs.267695	UDP-Gal-betaGlcNAc beta 1,3-galactosyltr	9.1	0.05	upregulate stage
	431691	AI208511	Hs.292510	ESTs	4.15	0.12	upregulate stage
	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	4.2	0.13	upregulate stage
	431694	AW970112	Hs.292697	ESTs	1	0.83	upregulate stage
75	431726	NM_015361	Hs.268053	KJAA0029 protein	10.1	0.07	upregulate stage
	431736	AI912234	Hs.151245	ESTs	9.9	0.08	upregulate stage
	431753	X76029	Hs.2841	neuromedin U	1	0.23	upregulate stage
	431781	AA515474	Hs.99908	nuclear receptor coactivator 4	1	0.36	upregulate stage

5	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	1	0.65	upregulate stage
	431814	BE256242	Hs.270847	della-tubulin	3.35	0.18	upregulate stage
	431817	X65233	Hs.271079	zinc finger protein 80 (pT17)	1	1	upregulate stage
	431828	AA572994		gb:nrm33f12.s1 NCL CGAP_Lip2 Homo sapiens	4	0.12	upregulate stage
	431890	AJ700238	Hs.187486	ESTs	1	1	upregulate stage
10	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit)	2.89	0.27	upregulate stage
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1	0.18	upregulate stage
	431951	AI086335	Hs.136470	ESTs	6.4	0.11	upregulate stage
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.09	0.07	upregulate stage
	431989	AW972870	Hs.291069	ESTs	1	0.23	upregulate stage
15	431992	NM_002742	Hs.2891	protein kinase C, mu	3.9	0.15	upregulate stage
	432015	AL157504	Hs.159115	ESTs	6.05	0.09	upregulate stage
	432023	AW273128	Hs.214188	ESTs	0.99	0.86	upregulate stage
	432028	AJ272208	Hs.272354	interleukin 1 receptor accessory protein	1	0.48	upregulate stage
	432039	AF220217	Hs.272374	Homo sapiens rsec15-like protein mRNA, p	1	0.24	upregulate stage
20	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	1.38	0.64	upregulate stage
	432069	AW975868	Hs.294100	ESTs	4.25	0.15	upregulate stage
	432072	N62937	Hs.269109	ESTs	5.9	0.09	upregulate stage
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	7.9	0.08	upregulate stage
	432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	1	0.28	upregulate stage
25	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.5	0.25	upregulate stage
	432169	Y00971	Hs.2910	phosphonobosyl pyrophosphate synthetase	6.1	0.11	upregulate stage
	432215	AL076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.44	0.29	upregulate stage
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	15	0.02	upregulate stage
	432235	AA531129	Hs.190297	ESTs	9.57	0.06	upregulate stage
30	432237	AK001926	Hs.274132	hypothetical protein FLJ11064	1	0.44	upregulate stage
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	4.3	0.1	upregulate stage
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.95	0.15	upregulate stage
	432338	AA534197	Hs.272693	ESTs	1	1	upregulate stage
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.97	0.4	upregulate stage
35	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.16	0.58	upregulate stage
	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	3.75	0.16	upregulate stage
	432410	X68561	Hs.2982	Sp4 transcription factor	1	1	upregulate stage
	432415	T16971	Hs.289014	ESTs	7.3	0.07	upregulate stage
	432432	AA541323	Hs.115831	ESTs	5.35	0.13	upregulate stage
40	432435	BE218886	Hs.282070	ESTs	5.35	0.1	upregulate stage
	432441	AW292425	Hs.163484	ESTs	19.4	0.04	upregulate stage
	432518	AI675836	Hs.94319	ESTs	1	0.59	upregulate stage
	432580	X82018	Hs.3053	zinc finger protein with interaction dom	9.15	0.08	upregulate stage
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	10.15	0.05	upregulate stage
45	432614	AA557153	Hs.185853	ESTs	1	0.33	upregulate stage
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	10.5	0.07	upregulate stage
	432661	AW973823	Hs.283526	ESTs	1	1	upregulate stage
	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein	1	0.16	upregulate stage
	432669	AL043482	Hs.267115	ESTs	4.15	0.12	upregulate stage
50	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	10.24	0.06	upregulate stage
	432678	AA923424	Hs.135567	ESTs	1	0.69	upregulate stage
	432690	AF181490	Hs.278627	prenylcysteine lyase	4.55	0.12	upregulate stage
	432724	X98266		gb:h.sapiens mRNA for ligase like protei	1	1	upregulate stage
	432758	NM_014091	Hs.278920	PRO1510 protein	1	1	upregulate stage
55	432773	NM_014124	Hs.278935	PRO0255 protein	1	1	upregulate stage
	432789	D26361	Hs.3104	KIAA0042 gene product	3.46	0.22	upregulate stage
	432829	W60377	Hs.57772	ESTs	1.33	0.43	upregulate stage
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.5	0.14	upregulate stage
	432900	BE178025	Hs.7942	hypothetical protein FLJ20080	1	0.3	upregulate stage
60	432917	NM_014125	Hs.279812	PRO0327 protein	6.33	0.12	upregulate stage
	432935	AW270239	Hs.213709	ESTs	3.85	0.11	upregulate stage
	432953	AA572859	Hs.225791	ESTs	1	0.19	upregulate stage
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	29.9	0.03	upregulate stage
	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1	0.59	upregulate stage
65	433129	AA577814		gb:nrm24d03.s1 NCL CGAP_Gas1 Homo sapiens	1	1	upregulate stage
	433159	AB035898	Hs.150587	kinesin-like protein 2	6	0.1	upregulate stage
	433201	AB040896	Hs.211104	KIAA1463 protein	9.2	0.09	upregulate stage
	433211	H11850	Hs.12808	MARK	1.6	0.45	upregulate stage
	433218	AI040372	Hs.278894	KIAA1482 protein	1	0.44	upregulate stage
70	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	5.45	0.12	upregulate stage
	433230	AW136134	Hs.220277	ESTs	7.3	0.09	upregulate stage
	433237	AB040930	Hs.297021	Homo sapiens cDNA FLJ13211 fis, clone NT	1	1	upregulate stage
	433365	AF026944	Hs.293797	ESTs	4.95	0.08	upregulate stage
	433371	T25451		gb:PTH188 HTCDL1 Homo sapiens cDNA 573	4.75	0.12	upregulate stage
75	433394	AI907753	Hs.93810	cerebral cavernous malformations 1	4.5	0.11	upregulate stage
	433424	R68252	Hs.163566	ESTs	1	1	upregulate stage
	433440	AF052127		gb:Homo sapiens clone 23850 mRNA sequenc	1	1	upregulate stage
	433452	AW296906	Hs.142669	ESTs	9.82	0.08	upregulate stage
	433455	AA593447	Hs.124296	ESTs	9.45	0.08	upregulate stage
	433457	AI420457	Hs.50955	ESTs	1.11	0.74	upregulate stage
	433479	AW511459	Hs.245972	ESTs	3.35	0.13	upregulate stage

	433484	BE264397	Hs.148674	ESTs	1	0.27	upregulate stage
	433515	AA595800	Hs.190246	ESTs	3.05	0.14	upregulate stage
	433602	AJ769948	Hs.24906	ESTs	1	1	upregulate stage
5	433613	AA836126	Hs.5669	ESTs	2.8	0.12	upregulate stage
	433625	AW955674	Hs.161762	ESTs	1	0.53	upregulate stage
	433658	L03678	Hs.156110	immunoglobulin kappa constant	9.65	0.05	upregulate stage
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	7.9	0.08	upregulate stage
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.7	0.11	upregulate stage
10	433735	AA608955	Hs.109653	ESTs	8.95	0.08	upregulate stage
	433895	AI287912	Hs.3628	mitogen-activated protein kinase kinase	4.43	0.16	upregulate stage
	433904	AI399956	Hs.208956	ESTs	5.5	0.12	upregulate stage
	433929	AI375499	Hs.27379	ESTs	7	0.09	upregulate stage
	433966	AF113017	Hs.284301	PRO1268 protein	7.95	0.08	upregulate stage
	433967	AF113018	Hs.284302	PRO1621 protein	2.65	0.1	upregulate stage
15	434006	AF113688		gb:Homo sapiens clone FLB4630	7.85	0.08	upregulate stage
	434037	AF115601	Hs.283048	hypothetical protein PRO0128	8.81	0.09	upregulate stage
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.35	0.09	upregulate stage
	434085	AF116673	Hs.250029	hypothetical protein PRO1925	1	1	upregulate stage
20	434092	AA625155		gb:at70d06.r1 Soares_NhHMPu_S1 Homo sapi	1	1	upregulate stage
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	11.5	0.06	upregulate stage
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.55	0.11	upregulate stage
	434192	AW387314	Hs.34371	ESTs	1.65	0.22	upregulate stage
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	7.85	0.09	upregulate stage
	434217	AW014795	Hs.23349	ESTs	3.8	0.13	upregulate stage
25	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	5.95	0.11	upregulate stage
	434271	AA897778	Hs.201677	ESTs	1	0.38	upregulate stage
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.45	0.07	upregulate stage
	434322	AI125686	Hs.152727	ESTs	2.65	0.18	upregulate stage
30	434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.61	upregulate stage
	434354	AW974912	Hs.292783	ESTs	1	1	upregulate stage
	434398	AA121098	Hs.3838	serum-inducible kinase	10.7	0.08	upregulate stage
	434464	BE053921	Hs.295971	ESTs	10.15	0.07	upregulate stage
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	7.6	0.09	upregulate stage
	434484	W79839	Hs.104336	hypothetical protein	5.1	0.15	upregulate stage
35	434513	AF143888	Hs.18213	Homo sapiens clone IMAGE:121736 mRNA seq	1	1	upregulate stage
	434534	H90477	Hs.41407	ESTs	1	0.18	upregulate stage
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	12.4	0.06	upregulate stage
	434569	AI311295	Hs.58609	ESTs	1.75	0.38	upregulate stage
	434575	AI133446	Hs.299964	ESTs	9.7	0.06	upregulate stage
40	434627	AI221894	Hs.39311	ESTs	1.65	0.17	upregulate stage
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	9	0.07	upregulate stage
	434663	AA641972	Hs.130058	ESTs	4.55	0.15	upregulate stage
	434731	AA648049	Hs.121518	ESTs	8.5	0.1	upregulate stage
	434765	AA831115	Hs.190473	ESTs	1	0.71	upregulate stage
45	434773	AA648962	Hs.152947	ESTs	10.55	0.08	upregulate stage
	434792	AA649253	Hs.132458	ESTs	5.45	0.11	upregulate stage
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1	0.34	upregulate stage
	434876	AF160477	Hs.245781	Homo sapiens Ig superfamily receptor LNI	1.4	0.57	upregulate stage
50	434909	AI479212	Hs.17283	hypothetical protein FLJ10890	1	0.91	upregulate stage
	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	4.9	0.13	upregulate stage
	434939	AF161422	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1	1	upregulate stage
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	10.75	0.07	upregulate stage
	434970	AW272262	Hs.250468	ESTs	9.05	0.08	upregulate stage
55	434980	AW770553	Hs.293640	ESTs	4.95	0.14	upregulate stage
	434997	AW975155	Hs.292163	ESTs	1	0.36	upregulate stage
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.16	0.71	upregulate stage
	435030	AI203316	Hs.148655	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.95	0.14	upregulate stage
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.31	0.2	upregulate stage
60	435061	AI651474	Hs.163944	ESTs	1.4	0.2	upregulate stage
	435080	AI831760	Hs.155111	ESTs	9.05	0.08	upregulate stage
	435087	AW975241	Hs.23567	ESTs	1	1	upregulate stage
	435108	AW975018	Hs.287440	Homo sapiens cDNA FLJ11692 fis, clone HE	1	0.2	upregulate stage
	435136	R27299	Hs.10172	ESTs	8.9	0.07	upregulate stage
65	435159	AA668879	Hs.116649	ESTs	1.35	0.25	upregulate stage
	435162	AI911044	Hs.213893	ESTs	1	1	upregulate stage
	435166	AI391470	Hs.158618	ESTs	5.5	0.12	upregulate stage
	435212	AW300100	Hs.164185	ESTs	1	1	upregulate stage
	435237	AI026836	Hs.114689	ESTs	8.75	0.1	upregulate stage
70	435255	W87434	Hs.105015	ESTs, Moderately similar to ALU1_HUMAN A	3.4	0.14	upregulate stage
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.2	0.14	upregulate stage
	435257	AA677026	Hs.191217	ESTs	4.5	0.12	upregulate stage
	435298	AA677696	Hs.189196	ESTs	1	1	upregulate stage
	435307	W90610	Hs.192003	ESTs	1	0.87	upregulate stage
	435347	AW014873	Hs.116963	ESTs	2.45	0.14	upregulate stage
75	435382	N54493		gb:yy40g05.s1 Soares fetal liver spleen	1	0.56	upregulate stage
	435408	H07897	Hs.4302	ESTs	0.84	0.97	upregulate stage
	435491	T98543	Hs.191900	ESTs	1	0.3	upregulate stage

	435525	AI831297	Hs.123310	ESTs	3.25	0.15	upregulate stage
	435597	AW305188	Hs.163027	ESTs	1	0.57	upregulate stage
	435637	AF220051	Hs.110853	uncharacterized hematopoietic stem/proge	8.76	0.09	upregulate stage
5	435647	AI653240	Hs.49823	ESTs	3.19	0.25	upregulate stage
	435738	AA699633	Hs.269543	ESTs	2.9	0.16	upregulate stage
	435762	AW043836	Hs.212460	ESTs	1	1	upregulate stage
	435809	H90213	Hs.191330	ESTs	1.25	0.23	upregulate stage
	435826	AI554089	Hs.117880	ESTs	6.55	0.08	upregulate stage
10	435854	AJ278120	Hs.4996	DKFZP564D166 protein	2.76	0.29	upregulate stage
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.25	upregulate stage
	435981	H74319	Hs.188620	ESTs	6.35	0.11	upregulate stage
	435990	AI015862	Hs.131793	ESTs	4.25	0.08	upregulate stage
	435999	AA703271	Hs.269903	ESTs, Moderately similar to ALU1_HUMAN A	1	1	upregulate stage
15	436016	AA806465	Hs.121536	ESTs	1.45	0.23	upregulate stage
	436023	T81819		gbyd95f05.s1 Soares fetal liver spleen	9.15	0.07	upregulate stage
	436052	AI021983	Hs.271432	ESTs	1	0.23	upregulate stage
	436115	AW512033	Hs.102004	ESTs	1.9	0.21	upregulate stage
	436118	AI221173	Hs.145080	ESTs	1	1	upregulate stage
20	436120	AI248193	Hs.119860	ESTs	9.61	0.08	upregulate stage
	436149	AI754308	Hs.159452	ESTs	2.4	0.19	upregulate stage
	436156	AA705466	Hs.119900	ESTs	1	0.26	upregulate stage
	436170	AW450381	Hs.14529	ESTs	1	0.91	upregulate stage
	436202	AA706315	Hs.192057	ESTs	1	1	upregulate stage
25	436246	AW450963	Hs.119991	ESTs	3.85	0.11	upregulate stage
	436274	AA732755	Hs.120299	ESTs	2.85	0.13	upregulate stage
	436282	R91913	Hs.272104	ESTs	3.95	0.11	upregulate stage
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	6	0.09	upregulate stage
	436300	AA831601	Hs.275736	ESTs	1	1	upregulate stage
30	436326	BE085238	Hs.181244	major histocompatibility complex, class	2.49	0.28	upregulate stage
	436360	AI962796	Hs.136754	ESTs	2.4	0.17	upregulate stage
	436363	AA843926	Hs.124434	ESTs	3.35	0.1	upregulate stage
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1	0.67	upregulate stage
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	4	0.15	upregulate stage
35	436408	AW274577	Hs.252954	ESTs	9.1	0.09	upregulate stage
	436422	AA716141	Hs.147027	ESTs	1	0.26	upregulate stage
	436429	AA357003	Hs.17546	hypothetical protein FLJ23499	1	1	upregulate stage
	436463	H06502	Hs.6656	ESTs	5.45	0.12	upregulate stage
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-split	7.75	0.07	upregulate stage
40	436507	AA721209	Hs.201630	ESTs	2.45	0.18	upregulate stage
	436518	AA766433	Hs.122864	ESTs	3.15	0.21	upregulate stage
	436522	AA721381	Hs.129876	ESTs	4.75	0.1	upregulate stage
	436578	AI091435	Hs.134859	ESTs	3.4	0.12	upregulate stage
	436670	AI690021	Hs.201536	ESTs	6.85	0.11	upregulate stage
45	436740	AW975133		gb:EST387239 MAGE resequences, MAGN Homo	7.4	0.09	upregulate stage
	436764	AW976004	Hs.291731	ESTs	1	1	upregulate stage
	436785	AA745597	Hs.291400	ESTs	1	1	upregulate stage
	436823	AW749865	Hs.293645	ESTs	4.6	0.12	upregulate stage
	436831	AA830173	Hs.291918	ESTs	1.6	0.27	upregulate stage
50	436839	AA767346	Hs.291614	ESTs	1	1	upregulate stage
	436844	AA766458	Hs.122812	ESTs	1.5	0.28	upregulate stage
	436853	BE328074	Hs.148661	ESTs	5.05	0.14	upregulate stage
	436860	H12751	Hs.5327	PRO1914 protein	8.95	0.08	upregulate stage
	436925	AA742327	Hs.292687	ESTs	1	1	upregulate stage
55	437044	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.61	0.5	upregulate stage
	437087	AA745563		gb:ny60e04.s1 NCI_CGAP_Pr18 Homo sapiens	1	1	upregulate stage
	437144	AL049466	Hs.7859	ESTs	1	0.31	upregulate stage
	437170	R49202	Hs.181694	ESTs	8.7	0.08	upregulate stage
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	4.4	0.05	upregulate stage
60	437207	T27503	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	1.4	0.22	upregulate stage
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	5.65	0.09	upregulate stage
	437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.45	upregulate stage
	437257	AI283085	Hs.290931	ESTs, Weakly similar to unknown [S.cerev	3.8	0.14	upregulate stage
	437258	AL041243	Hs.174104	ESTs	9.72	0.08	upregulate stage
65	437267	AW511443	Hs.258110	ESTs	4.25	0.12	upregulate stage
	437274	AA747965		gb:nx79a10.s1 NCI_CGAP_Ew1 Homo sapiens	1	0.19	upregulate stage
	437288	AA748182	Hs.160377	ESTs	1	0.61	upregulate stage
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	3.1	0.17	upregulate stage
	437324	AL162077		gb:Homo sapiens mRNA; cDNA DKFZp761A219	1	0.25	upregulate stage
70	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.95	0.07	upregulate stage
	437356	BE622396	Hs.284252	Homo sapiens mRNA; cDNA DKFZp762O1615 (f	1	1	upregulate stage
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	9.15	0.09	upregulate stage
	437471	AL390169		gb:Homo sapiens mRNA; cDNA DKFZp547D064	1	1	upregulate stage
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	1.1	0.56	upregulate stage
75	437567	AW627990	Hs.288954	Homo sapiens cDNA: FLJ21466 fis, clone C	1	1	upregulate stage
	437575	AW954355	Hs.36529	ESTs	10.25	0.06	upregulate stage
	437717	AA804765	Hs.132853	ESTs	1	0.77	upregulate stage
	437722	AW292947	Hs.122872	ESTs	9.75	0.05	upregulate stage

	437752	AA767376	Hs.291631	ESTs	6.7	0.08	upregulate stage
	437770	AA767881	Hs.122897	ESTs	2.57	0.24	upregulate stage
	437798	AW811767		gb:RC2-ST0165-300999-011-g02 ST0165 Homo	1	1	upregulate stage
	437799	RS1083	Hs.90787	ESTs	1	1	upregulate stage
5	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	0.3	upregulate stage
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.8	0.08	upregulate stage
	437887	AA811524	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	3.8	0.17	upregulate stage
	437889	AA830524	Hs.124357	ESTs	1	0.69	upregulate stage
	437937	AJ917222	Hs.121655	ESTs	1	0.38	upregulate stage
10	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kd12 Homo sapien	1.37	0.52	upregulate stage
	437983	AJ303023	Hs.30211	hypothetical protein FLJ22313	8.82	0.08	upregulate stage
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	9	0.09	upregulate stage
	438032	BE045824	Hs.152992	ESTs	5.65	0.13	upregulate stage
	438069	N80701	Hs.33790	ESTs	3.25	0.13	upregulate stage
15	438077	AA777330	Hs.50429	ESTs	1	1	upregulate stage
	438081	H49546	Hs.298964	ESTs	3.75	0.11	upregulate stage
	438102	AA777793	Hs.137580	xylulokinase (H. Influenzae) homolog	1	1	upregulate stage
	438112	W85729	Hs.194279	ESTs	1	0.33	upregulate stage
	438113	AJ467908	Hs.8882	ESTs	1.21	0.55	upregulate stage
20	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	11.75	0.07	upregulate stage
	438144	AA778894	Hs.118364	ESTs	1	1	upregulate stage
	438153	AI268632	Hs.146159	ESTs	1	1	upregulate stage
	438171	AW976507	Hs.293515	ESTs	2.82	0.24	upregulate stage
25	438271	L21934	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1	1	upregulate stage
	438290	AA843719	Hs.122341	ESTs	3.9	0.13	upregulate stage
	438321	AA576635	Hs.6153	CGI-48 protein	9.4	0.08	upregulate stage
	438325	AA804258	Hs.123229	ESTs	4.65	0.11	upregulate stage
	438334	AA806992	Hs.291686	ESTs	1	1	upregulate stage
30	438366	AA805760		gb:ns43f01.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
	438370	AA843242	Hs.48523	ESTs	4	0.14	upregulate stage
	438374	AA321866	Hs.6193	Homo sapiens mRNA; cDNA DKFZp434C1717 (f	1	0.84	upregulate stage
	438377	AA806070	Hs.291716	ESTs	1	0.24	upregulate stage
	438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	5.65	0.11	upregulate stage
35	438401	AL046321	Hs.197484	ESTs	1	1	upregulate stage
	438403	AA806607	Hs.292206	ESTs	2.75	0.14	upregulate stage
	438412	AA805776	Hs.130814	ESTs	1	1	upregulate stage
	438448	AA807344	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	1	0.34	upregulate stage
	438451	AJ081972	Hs.220261	ESTs	5.7	0.09	upregulate stage
40	438473	H07986	Hs.136901	ESTs	1	1	upregulate stage
	438487	AI684733	Hs.88820	HDCMC28P protein	1	0.21	upregulate stage
	438529	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	1	0.36	upregulate stage
	438534	AW204052	Hs.123644	ESTs	1	0.37	upregulate stage
	438693	AA814360	Hs.249595	ESTs	3.55	0.15	upregulate stage
45	438698	AW297855	Hs.125815	ESTs	3.12	0.22	upregulate stage
	438728	AA815202	Hs.25657	ESTs	1	0.67	upregulate stage
	438746	AI885815	Hs.184727	ESTs	1.5	0.35	upregulate stage
	438805	AA826048	Hs.117887	ESTs	9.35	0.07	upregulate stage
	438812	AA826199	Hs.44287	ESTs	1	0.57	upregulate stage
50	438817	AI023799	Hs.163242	ESTs	4.2	0.08	upregulate stage
	438886	AA827728	Hs.126705	ESTs, Weakly similar to AF149422 2 unkno	4.05	0.12	upregulate stage
	438913	AI380429	Hs.172445	ESTs	5.4	0.11	upregulate stage
	438950	H23789	Hs.144530	ESTs	1	1	upregulate stage
	438961	H42135	Hs.101848	ESTs	7.85	0.08	upregulate stage
55	438990	AF085890		gb:Homo sapiens full length insert cDNA	1	0.83	upregulate stage
	439026	R98978	Hs.117767	ESTs	1	0.27	upregulate stage
	439052	AF085917	Hs.37921	ESTs	1	0.22	upregulate stage
	439057	H59623	Hs.271561	ESTs	1	1	upregulate stage
	439176	AI446444	Hs.190394	ESTs	5.8	0.12	upregulate stage
60	439179	AA831250	Hs.292693	ESTs	1	1	upregulate stage
	439183	AW970600		gb:EST382681 MAGE resequences, MAGK Homo	4.5	0.13	upregulate stage
	439208	AK000299	Hs.180952	dynactin p62 subunit	11.9	0.06	upregulate stage
	439212	AF087995	Hs.134877	ESTs	11.4	0.07	upregulate stage
	439223	AW238299	Hs.23945	ESTs	2.79	0.26	upregulate stage
65	439312	AA833902	Hs.270745	ESTs	8.9	0.08	upregulate stage
	439330	AF086147		gb:Homo sapiens full length insert cDNA	1	0.19	upregulate stage
	439351	W37688	Hs.55158	ESTs, Weakly similar to weak similarity	1	0.31	upregulate stage
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.9	0.15	upregulate stage
	439444	AI277652	Hs.54578	ESTs	11	0.07	upregulate stage
70	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.21	0.05	upregulate stage
	439476	AA836340	Hs.165490	ESTs	1	0.65	upregulate stage
	439492	AF086310	Hs.103159	ESTs	5.43	0.1	upregulate stage
	439527	AW298119	Hs.202536	ESTs	5.25	0.1	upregulate stage
	439550	H10438		gb:ym08d10.s1 Soares infant brain 1NIB H	3.2	0.18	upregulate stage
75	439560	BE555647	Hs.74899	hypothetical protein FLJ12820	1.81	0.32	upregulate stage
	439565	AF086386	Hs.145599	ESTs	8.96	0.07	upregulate stage
	439592	AF086413	Hs.58399	ESTs	1	1	upregulate stage
	439605	AF086431	Hs.134805	ESTs	9.15	0.09	upregulate stage

	439606	W79123	Hs.58561	ESTs, Weakly similar to KI01_HUMAN PROBA	8.45	0.06	upregulate stage
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.43	0.14	upregulate stage
	439780	AL109688		gb:Homo sapiens mRNA full length insert	5	0.09	upregulate stage
5	439851	AI149520	Hs.144453	ESTs	2.75	0.21	upregulate stage
	439862	AI571647	Hs.146170	hypothetical protein FLJ22969	6.3	0.11	upregulate stage
	439926	AW014875	Hs.137007	ESTs	33.5	0.02	upregulate stage
	439942	AW993791	Hs.94881	ESTs	9.9	0.08	upregulate stage
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.59	0.15	upregulate stage
10	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.95	0.07	upregulate stage
	439987	AA860116	Hs.223232	ESTs	2.45	0.17	upregulate stage
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.75	0.07	upregulate stage
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.68	0.41	upregulate stage
	440012	AA861072		gtrak32e05.s1 Scores_testis_NHT Homo sap	1	1	upregulate stage
15	440126	AA975145	Hs.66194	ESTs	1	1	upregulate stage
	440194	R43809	Hs.22688	ESTs	1	1	upregulate stage
	440228	AF125392	Hs.7089	insulin induced protein 2	1	1	upregulate stage
	440249	AI246590	Hs.125325	ESTs	1.74	0.44	upregulate stage
	440284	AA912032	Hs.181059	ESTs	1	1	upregulate stage
20	440334	BE276112	Hs.7165	zinc finger protein 259	9.45	0.09	upregulate stage
	440348	AW015802	Hs.47023	ESTs	1	0.33	upregulate stage
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.75	0.16	upregulate stage
	440366	F08229	Hs.125273	ESTs	3.5	0.12	upregulate stage
	440462	T71629	Hs.100554	ESTs	1.54	0.52	upregulate stage
25	440527	AV657117	Hs.184164	ESTs	3.75	0.14	upregulate stage
	440613	AI733034	Hs.137079	ESTs	3.9	0.11	upregulate stage
	440705	AA904244	Hs.153205	ESTs	3.9	0.14	upregulate stage
	440856	AW993377	Hs.130390	ESTs	8.95	0.09	upregulate stage
	440899	AW449445	Hs.172690	diacylglycerol kinase, alpha (80kD)	2.55	0.2	upregulate stage
30	440917	AA909851	Hs.160025	ESTs	1	0.17	upregulate stage
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	8.9	0.09	upregulate stage
	440994	AI160011	Hs.193341	ESTs	1.29	0.58	upregulate stage
	441092	T99289	Hs.126556	EST	4.9	0.11	upregulate stage
	441107	AA917075	Hs.190520	ESTs	5.9	0.09	upregulate stage
35	441131	AI733222	Hs.126632	ESTs	9.55	0.09	upregulate stage
	441143	AI027604	Hs.159650	ESTs	3.8	0.13	upregulate stage
	441205	AW137827	Hs.176904	ESTs	4.75	0.12	upregulate stage
	441206	BE552314	Hs.131823	ESTs, Weakly similar to TERA HUMAN [H.s]	1	1	upregulate stage
	441264	AA927170	Hs.23290	ESTs	4.3	0.14	upregulate stage
40	441318	AI078234	Hs.176130	ESTs	1.74	0.45	upregulate stage
	441334	AI700529	Hs.117954	ESTs	1	1	upregulate stage
	441346	AA931077	Hs.186889	Homo sapiens cDNA FLJ12021 fis, clone HE	1	1	upregulate stage
	441378	AA931826	Hs.126846	ESTs	4.5	0.1	upregulate stage
	441383	AW294408	Hs.222058	ESTs	1	1	upregulate stage
45	441421	AA356792	Hs.301786	ESTs	1	0.24	upregulate stage
	441470	BE503874	Hs.301986	ESTs	0.63	0.93	upregulate stage
	441474	AW274946	Hs.144476	ESTs	1	1	upregulate stage
	441484	AA935481	Hs.58972	ESTs	1	0.33	upregulate stage
	441485	AI792988	Hs.189133	ESTs	4.25	0.1	upregulate stage
50	441508	AW015203	Hs.232237	ESTs	1	1	upregulate stage
	441562	AW578981	Hs.52184	hypothetical protein FLJ20618	4.05	0.12	upregulate stage
	441599	AW473362	Hs.127221	ESTs	1	0.29	upregulate stage
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	8.75	0.08	upregulate stage
	441616	BE569122	Hs.74111	RNA-binding protein (autoantigenic)	1.14	0.71	upregulate stage
55	441643	AI740504	Hs.205128	ESTs	1	0.33	upregulate stage
	441677	AW271702	Hs.93739	ESTs	1	0.28	upregulate stage
	441693	AA384673	Hs.7943	RPB5-mediating protein	1	0.43	upregulate stage
	441703	AW390054	Hs.192843	ESTs	9.85	0.08	upregulate stage
	441732	AW298818	Hs.127341	ESTs	4.6	0.14	upregulate stage
60	441759	C16126	Hs.161377	ESTs	4.55	0.13	upregulate stage
	441762	AW592203	Hs.144769	ESTs	1	0.83	upregulate stage
	441790	AW294909	Hs.132208	ESTs	9	0.08	upregulate stage
	441794	AW197794	Hs.253338	ESTs	4.5	0.12	upregulate stage
	441799	AW252276	Hs.127872	ESTs	1	0.22	upregulate stage
65	441801	AW242799	Hs.211874	ESTs	8	0.06	upregulate stage
	441904	AI633205	Hs.128104	ESTs	2	0.19	upregulate stage
	441955	AA972327	Hs.142903	ESTs	0.87	0.96	upregulate stage
	441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone H	9.17	0.07	upregulate stage
	441990	T66139	Hs.113631	ESTs	3.55	0.12	upregulate stage
70	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.65	0.14	upregulate stage
	442030	W67167	Hs.109080	ESTs	1	0.35	upregulate stage
	442064	AI422867	Hs.88594	ESTs	8.8	0.08	upregulate stage
	442071	BE048433	Hs.276043	ESTs	9.15	0.09	upregulate stage
	442093	AA976049	Hs.128454	ESTs	1	1	upregulate stage
	442194	AA984389	Hs.205088	ESTs	1	0.63	upregulate stage
75	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone H	9.9	0.08	upregulate stage
	442203	AI921423	Hs.250146	ESTs	1	1	upregulate stage
	442214	AI681733	Hs.129003	ESTs	2.2	0.26	upregulate stage

5	442216	AI733468	Hs.129006	ESTs	1	1	upregulate stage
	442295	AI827248	Hs.224388	Homo sapiens cDNA FLJ11469 fis, clone HE	1.49	0.31	upregulate stage
	442319	BE048144	Hs.177677	CGI-102 protein	1	0.29	upregulate stage
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	22.95	0.03	upregulate stage
	442510	AF150179	Hs.249890	ESTs	1	0.63	upregulate stage
10	442518	AF150226		gb:AF150226 Human mRNA from cd34+ stem c	1	1	upregulate stage
	442539	AL119506	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	1	0.23	upregulate stage
	442552	R20624	Hs.83572	son of sevenless (Drosophila) homolog 1	9	0.08	upregulate stage
	442562	BE379584	Hs.34789	ESTs	6.55	0.1	upregulate stage
	442564	AI590207	Hs.188378	ESTs	1	1	upregulate stage
15	442577	AA292998	Hs.163900	ESTs	1.41	0.52	upregulate stage
	442590	AI002686	Hs.130313	ESTs	1	0.36	upregulate stage
	442597	AI499214	Hs.130825	ESTs	1	1	upregulate stage
	442611	BE077155	Hs.177537	ESTs	4.35	0.15	upregulate stage
	442612	AI005233	Hs.130631	ESTs	1	0.28	upregulate stage
20	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	7.85	0.09	upregulate stage
	442642	R51853	Hs.226429	ESTs	1	1	upregulate stage
	442650	AW138174	Hs.130651	ESTs	4.1	0.09	upregulate stage
	442696	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	2.65	0.16	upregulate stage
	442712	BE465168	Hs.131011	ESTs	2.51	0.23	upregulate stage
25	442760	BE075297	Hs.10067	ESTs, Weakly similar to KIAA1205 protein	8	0.1	upregulate stage
	442769	AW243058	Hs.131155	ESTs	1	0.3	upregulate stage
	442785	AW296625	Hs.131188	ESTs	1	0.27	upregulate stage
	442806	AW294522	Hs.149991	ESTs	9.6	0.08	upregulate stage
	442856	H56735	Hs.282958	Homo sapiens cDNA FLJ13611 fis, clone PL	4.3	0.11	upregulate stage
30	442861	AA243837	Hs.57787	ESTs	3.9	0.12	upregulate stage
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.85	0.15	upregulate stage
	442879	AF032922	Hs.8813	synlaxin binding protein 3	3.95	0.14	upregulate stage
	442883	AW195774	Hs.253199	ESTs	1	1	upregulate stage
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	11.55	0.07	upregulate stage
35	442966	AI394036	Hs.132237	ESTs, Weakly similar to dual specificity	2.95	0.16	upregulate stage
	442980	AA857025	Hs.8878	kinesin-like 1	1	0.24	upregulate stage
	442992	AI914699	Hs.13297	ESTs	6.1	0.14	upregulate stage
	442994	AI026718	Hs.16954	ESTs	8.9	0.07	upregulate stage
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	5.7	0.11	upregulate stage
40	443113	AI040885	Hs.132908	ESTs	3.9	0.14	upregulate stage
	443119	AA312264	Hs.7980	ESTs, Moderately similar to ALU4_HUMAN A	8.73	0.08	upregulate stage
	443171	BE281128	Hs.9030	TONDU	3.18	0.22	upregulate stage
	443211	AI128388	Hs.143655	ESTs	6.55	0.08	upregulate stage
	443242	BE243910	Hs.9082	nucleoporin p54	11.05	0.06	upregulate stage
45	443243	AI452496	Hs.132056	ESTs	8.9	0.09	upregulate stage
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	10.95	0.05	upregulate stage
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	3.75	0.2	upregulate stage
	443299	AI733642	Hs.133042	ESTs	1	0.69	upregulate stage
	443362	AI053464	Hs.166505	ESTs	2.9	0.16	upregulate stage
50	443383	AI792453	Hs.166507	ESTs	5	0.14	upregulate stage
	443411	AW134566	Hs.65320	ESTs	1	0.59	upregulate stage
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.68	0.31	upregulate stage
	443447	AI094222	Hs.166572	ESTs	1	0.38	upregulate stage
	443542	AI927065	Hs.146040	ESTs	5.65	0.13	upregulate stage
55	443557	AV645987	Hs.145681	ESTs	1	1	upregulate stage
	443584	AI807036	Hs.101619	ESTs	1	0.36	upregulate stage
	443606	AI078654	Hs.199424	ESTs	1.15	0.33	upregulate stage
	443634	H73972	Hs.134460	ESTs	3.05	0.16	upregulate stage
	443640	AI872643	Hs.134218	ESTs	3.65	0.12	upregulate stage
60	443715	AI583187	Hs.9700	cyclin E1	5.65	0.11	upregulate stage
	443799	AA150320	Hs.9800	protein kinase Njmu-R1	1.8	0.19	upregulate stage
	443899	AW842283	Hs.79933	cyclin I	4.65	0.13	upregulate stage
	443917	AW503739	Hs.72325	Human DNA sequence from clone RP1-187J11	1	1	upregulate stage
	443919	AI091284	Hs.135224	ESTs	8.05	0.07	upregulate stage
65	443967	AW294013	Hs.200942	ESTs	5.55	0.13	upregulate stage
	443977	AL120986	Hs.150627	ESTs	4	0.14	upregulate stage
	443979	AV647366	Hs.282365	ESTs	1	1	upregulate stage
	444020	R92962	Hs.35052	ESTs	10.45	0.08	upregulate stage
	444105	AW189097	Hs.166597	ESTs	6.29	0.1	upregulate stage
70	444129	AW294292	Hs.256212	ESTs	1	0.77	upregulate stage
	444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	1.64	0.48	upregulate stage
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.12	0.81	upregulate stage
	444166	AV648429	Hs.282393	ESTs	1	1	upregulate stage
	444270	AI138580	Hs.255220	EST	1	0.47	upregulate stage
75	444271	AW452569	Hs.149804	ESTs	3.2	0.12	upregulate stage
	444282	AI138955		gb:qd79b07.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444333	AI262567	Hs.253801	trinucleotide repeat containing 15	1	0.77	upregulate stage
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.9	0.06	upregulate stage
	444378	R41339	Hs.12569	ESTs	1	0.32	upregulate stage
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.85	0.26	upregulate stage
	444431	AW513324	Hs.42280	ESTs	6.27	0.12	upregulate stage

	444437	AI377961	Hs.44041	ESTs	9.9	0.07	upregulate stage
	444444	AI149332	Hs.14855	ESTs	1.16	0.47	upregulate stage
	444525	AW593778	Hs.259699	ESTs	1	0.5	upregulate stage
5	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.6	0.15	upregulate stage
	444599	AI174377	Hs.143796	ESTs	1	0.44	upregulate stage
	444646	AI184565		gb:qd60b08.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444649	AW207523	Hs.197628	ESTs	9.35	0.06	upregulate stage
	444675	AI186380	Hs.244621	ESTs	9.88	0.08	upregulate stage
10	444698	AI188139	Hs.147050	ESTs	1	0.36	upregulate stage
	444743	AA045648	Hs.11817	nucleoside diphosphate linked moi	2.1	0.15	upregulate stage
	444762	AI733700	Hs.143883	ESTs	3.9	0.14	upregulate stage
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.44	0.53	upregulate stage
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.65	0.07	upregulate stage
15	444838	AV651680	Hs.208558	ESTs	4.84	0.14	upregulate stage
	444849	AI199438	Hs.148480	ESTs	3.05	0.17	upregulate stage
	444950	AI950256	Hs.224875	ESTs	1	0.51	upregulate stage
	445027	AV652692	Hs.282498	ESTs	11.1	0.08	upregulate stage
	445091	AI652154	Hs.147294	ESTs	1	1	upregulate stage
20	445098	AL050272	Hs.12305	DKFZP566B183 protein	9.75	0.07	upregulate stage
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	10.9	0.07	upregulate stage
	445250	AI597838	Hs.175621	ESTs	9.8	0.08	upregulate stage
	445258	AI635931	Hs.147613	ESTs	3.05	0.13	upregulate stage
	445390	AI222165	Hs.144923	ESTs	10.6	0.06	upregulate stage
25	445396	BE181792		gb:CV1-HT0639-070500-193-g06 HT0639 Homo	1	0.29	upregulate stage
	445413	AA151342	Hs.12677	CGI-147 protein	4.65	0.12	upregulate stage
	445436	AI224105	Hs.151408	ESTs	1.35	0.22	upregulate stage
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	10.7	0.07	upregulate stage
	445483	AI307150	Hs.148845	ESTs	1	1	upregulate stage
30	445496	AB007860	Hs.12802	development and differentiation enhancin	12.05	0.06	upregulate stage
	445525	BE149866	Hs.14831	ESTs	10.65	0.06	upregulate stage
	445527	W39694	Hs.83286	ESTs	4.85	0.1	upregulate stage
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.7	0.06	upregulate stage
	445546	AW468821	Hs.156054	ESTs	4.2	0.13	upregulate stage
	445576	AI793233	Hs.145608	ESTs	1	0.31	upregulate stage
35	445623	AI245366	Hs.149158	ESTs	1	1	upregulate stage
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.7	0.13	upregulate stage
	445668	AI557114	Hs.181591	EST	1	0.34	upregulate stage
	445766	AI623607	Hs.282977	Homo sapiens cDNA FLJ13490 fis, clone PL	1	0.23	upregulate stage
40	445770	AL119499	Hs.13285	neuronal potassium channel alpha subunit	1	1	upregulate stage
	445778	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	9.7	0.07	upregulate stage
	445787	AI253167	Hs.145395	ESTs, Weakly similar to ALUC_HUMAN !!!	3.1	0.13	upregulate stage
	445814	H92020	Hs.101624	ESTs	1	1	upregulate stage
	445818	BE045321	Hs.136017	ESTs	1	1	upregulate stage
45	445829	AI452457	Hs.145526	ESTs	1	0.37	upregulate stage
	445832	AI261545		gb:qx30a07.x1 NCI_CGAP_Kid11 Homo sapien	3.21	0.22	upregulate stage
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	5.25	0.12	upregulate stage
	445880	AV655474	Hs.131058	ESTs	1.05	0.27	upregulate stage
	445883	AF070559	Hs.13413	Homo sapiens clone 24463 mRNA sequence	1	1	upregulate stage
50	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.25	0.15	upregulate stage
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	8.85	0.08	upregulate stage
	446019	AI362520	Hs.94133	ESTs	9.75	0.08	upregulate stage
	446054	AB014537	Hs.13604	KIAA0637 gene product	10.25	0.07	upregulate stage
	446062	AA211738	Hs.282974	ESTs, Weakly similar to transformation-r	1	1	upregulate stage
55	446080	AI221741	Hs.117777	ESTs	9.75	0.09	upregulate stage
	446082	AI274139	Hs.156452	ESTs	1.37	0.4	upregulate stage
	446099	T93096	Hs.17126	ESTs	2.4	0.31	upregulate stage
	446119	D29527		gb:HUMNK667 Human epidermal keratinocyte	1	1	upregulate stage
60	446120	N26080	Hs.43741	ESTs	1	0.31	upregulate stage
	446126	AW085909	Hs.47413	ESTs	9.35	0.08	upregulate stage
	446127	AA333608	Hs.13980	ubiquitously transcribed tetrapeptid	1	0.25	upregulate stage
	446152	AI292036	Hs.150028	ESTs	4.7	0.12	upregulate stage
	446196	AI744888	Hs.149470	ESTs	1	0.83	upregulate stage
	446229	AI744954	Hs.14449	KIAA1609 protein	2.4	0.36	upregulate stage
65	446248	AI283014	Hs.149638	ESTs	1	1	upregulate stage
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	10.85	0.07	upregulate stage
	446303	X77244	Hs.14732	malic enzyme 1, NADP(+)-dependent, cytos	1	1	upregulate stage
	446312	BE087853		gb:QV1-BT0681-290400-181-h05 BT0681 Homo	11.75	0.06	upregulate stage
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	6.45	0.1	upregulate stage
70	446356	AI816736	Hs.14896	DHHC1 protein	8.9	0.08	upregulate stage
	446362	AW612481	Hs.255914	ESTs	7.6	0.1	upregulate stage
	446398	AI681317	Hs.150074	ESTs	1	1	upregulate stage
	446411	AI298828	Hs.153439	ESTs	1	0.37	upregulate stage
	446474	AI301227	Hs.150186	ESTs	3.35	0.13	upregulate stage
75	446501	AI302616	Hs.150819	ESTs	4.25	0.12	upregulate stage
	446507	AA325554	Hs.15164	nuclear DNA-binding protein	11.25	0.06	upregulate stage
	446526	H89616	Hs.296290	Homo sapiens cDNA FLJ13357 fis, clone PL	10.25	0.07	upregulate stage
	446555	AV659046	Hs.201847	ESTs	1	1	upregulate stage

	446577	AB040933	Hs.15420	KIAA1500 protein	1	0.51	upregulate stage
	446629	AJ436046	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone L	1	0.25	upregulate stage
	446636	AC002563	Hs.15767	cltron (rho-interacting, serine/threonin	2.54	0.28	upregulate stage
5	446682	AW205532	Hs.211198	ESTs	4	0.18	upregulate stage
	446701	AK001621	Hs.15921	hypothetical protein FLJ10759	1.32	0.69	upregulate stage
	446718	AV660019	Hs.282676	ESTs	1	1	upregulate stage
	446719	W39500	Hs.47305	ESTs, Weakly similar to LONN_HUMAN MITOC	9.65	0.07	upregulate stage
	446720	AI439136	Hs.140546	ESTs	4.55	0.12	upregulate stage
10	446765	AV660348	Hs.282688	ESTs	1	0.91	upregulate stage
	446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	11.2	0.06	upregulate stage
	446821	W03766	Hs.301482	ESTs	8.9	0.09	upregulate stage
	446830	BE179030	Hs.64239	Human DNA sequence from clone RP5-1174N9	10.65	0.07	upregulate stage
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	14.05	0.05	upregulate stage
15	446853	AV660630	Hs.87627	disrupter of silencing 10	9.7	0.09	upregulate stage
	446880	AJ811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT	11.05	0.06	upregulate stage
	446922	BE175605		gb:RC5-HT0580-100500-022-H07 HT0580 Homo	2.75	0.16	upregulate stage
	446950	AA305800	Hs.293454	ESTs, Weakly similar to Similarity to Ye	9.6	0.06	upregulate stage
	446988	AW339533	Hs.272108	ESTs	1	0.29	upregulate stage
20	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	1.75	0.51	upregulate stage
	447052	AV661911	Hs.282735	ESTs	1	1	upregulate stage
	447065	AI829014	Hs.158678	ESTs	1	0.25	upregulate stage
	447069	AI359927	Hs.157722	ESTs	1	0.4	upregulate stage
	447078	AW885727	Hs.301570	ESTs	4.4	0.13	upregulate stage
25	447080	AJ418781	Hs.300144	ESTs	1	0.31	upregulate stage
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.55	0.12	upregulate stage
	447118	AB014599	Hs.17411	KJAA0699 protein	10.15	0.07	upregulate stage
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor	6.2	0.12	upregulate stage
	447154	H52284	Hs.293545	ESTs	1	0.24	upregulate stage
30	447159	AI685286	Hs.280386	EST	1.25	0.25	upregulate stage
	447215	BE617056	Hs.283000	ESTs	2.4	0.16	upregulate stage
	447228	AW192200	Hs.158188	ESTs	1	0.29	upregulate stage
	447258	BE047911		gb:tz44a05.y1 NCI_CGAP_Bm52 Homo sapien	1.15	0.23	upregulate stage
	447286	AW197097	Hs.183858	transcriptional intermediary factor 1	1	1	upregulate stage
35	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1	1	upregulate stage
	447334	AA515032	Hs.91109	ESTs	9.15	0.08	upregulate stage
	447342	AI199268	Hs.19322	ESTs	5.95	0.09	upregulate stage
	447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	2.11	0.33	upregulate stage
	447376	AI376747		gb:tc35h05.x1 Soares_tota_fetus_Nb2HF8_	1	0.33	upregulate stage
40	447397	BE247676	Hs.18442	E-1 enzyme	5.3	0.14	upregulate stage
	447430	AI742989	Hs.206112	ESTs	3.65	0.13	upregulate stage
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	9.2	0.08	upregulate stage
	447519	U46258	Hs.23448	ESTs	14.4	0.05	upregulate stage
	447522	BE143888		gb:MR0-HT0165-081199-001-b04 HT0165 Homo	1.7	0.18	upregulate stage
45	447578	AA912347	Hs.136585	ESTs	1.5	0.3	upregulate stage
	447606	AI588954	Hs.170995	ESTs	2.7	0.16	upregulate stage
	447688	N87079	Hs.19235	NADH dehydrogenase (ubiquinone) 1 beta s	4.55	0.12	upregulate stage
	447701	BE619526	Hs.255527	ESTs, Weakly similar to unnamed protein	1.63	0.46	upregulate stage
	447741	AI421737	Hs.167253	ESTs	1	1	upregulate stage
50	447748	AI422023	Hs.161338	ESTs	3.9	0.11	upregulate stage
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.44	0.59	upregulate stage
	447881	BE620886	Hs.23037	ESTs	12.15	0.06	upregulate stage
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALUC_HUMAN !!!!	8.9	0.08	upregulate stage
	447977	AI457097	Hs.255906	ESTs	1	1	upregulate stage
55	447978	AI457098	Hs.280848	ESTs	1	1	upregulate stage
	447982	H22953	Hs.137551	ESTs	4.25	0.13	upregulate stage
	448032	AW511770	Hs.246868	ESTs	1	1	upregulate stage
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.22	0.29	upregulate stage
60	448058	AI458998	Hs.170424	ESTs	1	0.51	upregulate stage
	448062	AW295923	Hs.255472	ESTs	5.9	0.08	upregulate stage
	448138	AW847925	Hs.170736	ESTs	1	1	upregulate stage
	448154	AL120320	Hs.203230	ESTs	9.85	0.07	upregulate stage
	448165	NM_005591	Hs.202379	metollic recombination (S. cerevisiae) 11	7.3	0.09	upregulate stage
	448168	AW605999	Hs.22549	hypothetical protein FLJ12799	1	0.77	upregulate stage
65	448236	AA890449	Hs.20766	oxysterol 7alpha-hydroxylase	1	0.47	upregulate stage
	448256	BE614149	Hs.20814	CGI-27 protein	11.95	0.07	upregulate stage
	448289	AW390251	Hs.202402	ESTs	1	0.47	upregulate stage
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	11	0.07	upregulate stage
	448357	N20169	Hs.108923	ESTs	1.34	0.61	upregulate stage
70	448408	AA322866	Hs.21107	neurolligin	1.7	0.24	upregulate stage
	448455	AI252625	Hs.269860	ESTs	8.8	0.09	upregulate stage
	448459	AW069838	Hs.171055	ESTs	1	0.27	upregulate stage
	448464	AI522053	Hs.196093	ESTs	10.35	0.06	upregulate stage
	448468	BE560361	Hs.171072	ESTs	1	1	upregulate stage
75	448502	AW805285	Hs.239699	ESTs	9.3	0.08	upregulate stage
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.75	0.13	upregulate stage
	448556	AW885606	Hs.6064	ESTs	9.8	0.08	upregulate stage
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.14	0.35	upregulate stage

	448632	BE614269	gb:601504311T1 NIH_MGC_71 Homo sapiens c	1	1	upregulate stage
	448643	AI557531	gb:pt2.1-06.D06.r tumor2 Homo sapiens cD	3.6	0.14	upregulate stage
	448649	T94590	Hs.222855	1.95	0.21	upregulate stage
5	448663	BE614599	Hs.106823	4.3	0.12	upregulate stage
	448680	AW245890	Hs.21753	0.97	0.93	upregulate stage
	448725	AA193251	Hs.40289	2.6	0.19	upregulate stage
	448729	BE614535	Hs.138580	3.25	0.16	upregulate stage
	448743	AB032962	Hs.21896	1.9	0.19	upregulate stage
10	448826	AI580252	Hs.293246	1.78	0.44	upregulate stage
	448914	AI927656	Hs.196459	2.75	0.19	upregulate stage
	448946	AI652855	Hs.155796	9.7	0.07	upregulate stage
	448958	AB020651	Hs.22653	1	0.18	upregulate stage
	448974	AL049390	Hs.22689	5.85	0.11	upregulate stage
	448979	AI611378	Hs.192610	1	1	upregulate stage
15	449008	AW578003	Hs.22826	5.2	0.11	upregulate stage
	449032	AA045573	Hs.22900	1	0.33	upregulate stage
	449053	AI625777	Hs.270344	5.73	0.12	upregulate stage
	449057	AB037784	Hs.22941	9.25	0.07	upregulate stage
20	449148	AW836577	Hs.287554	7.2	0.09	upregulate stage
	449203	AI634578	Hs.282121	7	0.1	upregulate stage
	449207	AL044222	Hs.23255	2.34	0.36	upregulate stage
	449219	AI637581	Hs.195012	1	1	upregulate stage
	449230	BE613348	Hs.23348	3.08	0.25	upregulate stage
25	449246	AW411209	Hs.23363	4.79	0.16	upregulate stage
	449318	AW236021	Hs.108788	2.8	0.16	upregulate stage
	449328	AI962493	Hs.197647	2.55	0.17	upregulate stage
	449343	AI151418	Hs.272458	4.75	0.12	upregulate stage
	449344	AI640355	protein phosphatase 3 (formerly 2B), cal	2.1	0.22	upregulate stage
30	449351	AW016537	Hs.200760	2.45	0.14	upregulate stage
	449370	AK002114	Hs.23495	1.55	0.14	upregulate stage
	449424	AW448937	Hs.197030	4.05	0.12	upregulate stage
	449425	AW103433	Hs.195684	4.6	0.12	upregulate stage
	449434	AW294858	Hs.197641	1	0.29	upregulate stage
	449437	AI702038	Hs.100057	2.38	0.34	upregulate stage
35	449474	AA019344	Hs.2055	5.9	0.12	upregulate stage
	449523	NM_000579	Hs.54443	6.45	0.1	upregulate stage
	449528	H63337	Hs.38178	2.85	0.18	upregulate stage
	449565	AI824925	Hs.197066	1	1	upregulate stage
40	449568	AL157479	Hs.23740	10.15	0.06	upregulate stage
	449518	AB07459	Hs.14356	11.7	0.06	upregulate stage
	449639	AA001968	Hs.59956	1	1	upregulate stage
	449666	AA002047	gb:zh84e05.r1 Soares_fetal_liver_spleen_	1.85	0.33	upregulate stage
	449704	AK000733	Hs.23900	2.82	0.3	upregulate stage
45	449722	BE280074	Hs.23960	6.44	0.12	upregulate stage
	449764	N93104	Hs.54895	1	1	upregulate stage
	449784	AW161319	Hs.12915	6.25	0.11	upregulate stage
	449829	N51440	Hs.47261	1	0.57	upregulate stage
	449843	R85337	Hs.24030	10.2	0.07	upregulate stage
50	449892	N73608	Hs.50309	6.5	0.1	upregulate stage
	449894	AK001578	Hs.24129	4.55	0.12	upregulate stage
	449919	AI674685	Hs.200141	5.3	0.11	upregulate stage
	450020	AI680684	Hs.282219	1	1	upregulate stage
	450033	R43010	Hs.269452	1	0.65	upregulate stage
55	450063	AI681509	Hs.277133	4.2	0.17	upregulate stage
	450083	AA131795	Hs.142001	3.9	0.16	upregulate stage
	450116	AA005355	Hs.222882	1	1	upregulate stage
	450121	AL040174	Hs.288927	1	1	upregulate stage
	450135	AI810816	Hs.201142	4.95	0.14	upregulate stage
60	450144	T63961	Hs.301851	2.75	0.13	upregulate stage
	450149	AW969781	Hs.293440	3.75	0.14	upregulate stage
	450151	AI088196	Hs.295233	2.51	0.28	upregulate stage
	450152	AI138635	Hs.22968	2.45	0.15	upregulate stage
	450195	AA007352	Hs.256042	4.1	0.14	upregulate stage
65	450221	AA328102	Hs.24641	1	0.3	upregulate stage
	450238	T89693	Hs.138777	12.2	0.07	upregulate stage
	450257	AW820313	gb:QV2-ST0296-150200-028-d02 ST0296 Homo	1	1	upregulate stage
	450313	AI038989	Hs.24809	4.35	0.15	upregulate stage
	450314	AA574309	Hs.283402	10.1	0.07	upregulate stage
70	450350	T97817	Hs.174880	3.65	0.1	upregulate stage
	450411	D61167	Hs.202156	1	0.67	upregulate stage
	450447	AF212223	Hs.25010	10.75	0.07	upregulate stage
	450448	D54299	Hs.36244	1	1	upregulate stage
	450449	AI696596	Hs.202068	1	1	upregulate stage
75	450506	NM_004460	Hs.418	11.45	0.05	upregulate stage
	450573	AW964334	gb:EST376407 MAGC resequences, MAGH Homo	1.2	0.2	upregulate stage
	450628	AW382884	Hs.204715	4.95	0.13	upregulate stage
	450636	AI703076	Hs.201959	1	0.69	upregulate stage

	450655	AI707846	Hs.279860	hypothetical protein FLJ20030	1	1	upregulate stage
	450654	AA808358	Hs.36830	ESTs	1	0.34	upregulate stage
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.51	0.09	upregulate stage
5	450722	AI732318	Hs.101120	ESTs	1	0.87	upregulate stage
	450751	AI733251	Hs.126853	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
	450772	BE326391	Hs.280146	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
	450800	BE395161	Hs.243963	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.7	0.08	upregulate stage
	450824	R09055	Hs.269204	ESTs	3.03	0.22	upregulate stage
10	450832	AW970602	Hs.105421	ESTs	6.15	0.08	upregulate stage
	450870	AA011471		gbz101h08.r1 Soares_fetal_liver_spleen_	1.15	0.23	upregulate stage
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	9.75	0.08	upregulate stage
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.32	0.26	upregulate stage
	451052	AA281504	Hs.24444	ESTs, Moderately similar to ALUE_HUMAN I	9.25	0.08	upregulate stage
15	451067	BE172186	Hs.180789	S164 protein	2.8	0.21	upregulate stage
	451088	AA015600	Hs.82415	ESTs	1	0.32	upregulate stage
	451094	AI949825	Hs.260395	ESTs	4.45	0.14	upregulate stage
	451096	BE383234	Hs.25925	Homo sapiens clone 23860 mRNA sequence	4.15	0.14	upregulate stage
	451126	H30600	Hs.40910	ESTs	1	1	upregulate stage
20	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	2.15	0.16	upregulate stage
	451166	T98171	Hs.185675	ESTs	9.26	0.08	upregulate stage
	451222	AA018386	Hs.64341	ESTs	1	0.36	upregulate stage
	451225	AI433694	Hs.293608	ESTs	9.19	0.08	upregulate stage
	451228	AI767166	Hs.207025	ESTs	1	1	upregulate stage
25	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	7.35	0.11	upregulate stage
	451266	AA016292	Hs.290849	ESTs	1	0.33	upregulate stage
	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H.s	1	1	upregulate stage
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	11.7	0.06	upregulate stage
	451291	R39288	Hs.6702	ESTs	1	1	upregulate stage
30	451326	AW296946	Hs.300967	ESTs	10.55	0.07	upregulate stage
	451347	AI288679	Hs.101139	ESTs	1	1	upregulate stage
	451359	H85334		gbys90e05.r1 Soares retina N2b5HR Homo	2.7	0.15	upregulate stage
	451365	AI791783		gbrop20h10.y5 NCI_CGAP_Co12 Homo sapiens	8.9	0.09	upregulate stage
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.45	0.19	upregulate stage
35	451440	AA017599	Hs.293817	ESTs	1	1	upregulate stage
	451487	AA018072		gbze51g02.r1 Soares retina N2b4HR Homo	5.7	0.1	upregulate stage
	451492	AA018119	Hs.297824	ESTs, Highly similar to C1K1_HUMAN VOLTA	1	1	upregulate stage
	451495	H86887		gb-y07a01.r1 Soares retina N2b5HR Homo	4.25	0.13	upregulate stage
	451535	AW970577		gb:EST382658 MAGE resequences, MAGK Homo	6.8	0.12	upregulate stage
40	451553	AA018454	Hs.269211	ESTs, Weakly similar to B34087 hypotheti	1	1	upregulate stage
	451562	H04150	Hs.107708	ESTs	4.65	0.11	upregulate stage
	451580	AW138195	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	1	0.42	upregulate stage
	451592	AI805416	Hs.213897	ESTs	2.8	0.17	upregulate stage
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	1	0.18	upregulate stage
45	451658	AW195351	Hs.250520	ESTs	9.55	0.07	upregulate stage
	451684	AF218751	Hs.26813	CDA14	3.7	0.15	upregulate stage
	451690	AW451469	Hs.209990	ESTs	10.86	0.07	upregulate stage
	451724	AI903765		gb:U1-BT037-301298-102 BT037 Homo sapien	8.65	0.09	upregulate stage
	451743	AW074266	Hs.23071	ESTs	2.17	0.35	upregulate stage
50	451794	AA019799	Hs.111911	ESTs	1	1	upregulate stage
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	6.5	0.11	upregulate stage
	451903	W19617	Hs.261003	ESTs, Moderately similar to B34087 hypot	2.2	0.21	upregulate stage
	451914	AI822115	Hs.270618	ESTs, Weakly similar to KIAA0822 protein	11.67	0.07	upregulate stage
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	11.65	0.06	upregulate stage
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	1	0.95	upregulate stage
55	451971	AA021185	Hs.226306	ESTs	1	1	upregulate stage
	451998	AW594129	Hs.213666	ESTs	1	0.26	upregulate stage
	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	1	0.21	upregulate stage
	452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repea	1.76	0.41	upregulate stage
60	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	8.9	0.07	upregulate stage
	452122	AF216833	Hs.1710	ATP-binding cassette, sub-family B (MDR/	1	0.47	upregulate stage
	452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	1	0.2	upregulate stage
	452179	H16725	Hs.27463	ESTs	3	0.13	upregulate stage
	452198	AI097560	Hs.61210	ESTs	1	0.28	upregulate stage
65	452206	AW340281	Hs.33074	ESTs, Moderately similar to ALU1_HUMAN A	12.4	0.07	upregulate stage
	452234	AW084176	Hs.223296	ESTs	6.8	0.09	upregulate stage
	452240	AI591147	Hs.61232	ESTs	3.75	0.07	upregulate stage
	452247	AL137432	Hs.28564	hypothetical protein DKFZp761E1824	3.9	0.15	upregulate stage
	452250	BE618654	Hs.28507	hypothetical protein A-211C6.1	8.75	0.09	upregulate stage
70	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	5.2	0.09	upregulate stage
	452266	AI767250	Hs.165240	ESTs	10.45	0.06	upregulate stage
	452277	AL049013	Hs.28783	KIAA1223 protein	8.9	0.05	upregulate stage
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.2	0.04	upregulate stage
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.5	0.13	upregulate stage
75	452328	AA805679	Hs.61271	ESTs	3.5	0.14	upregulate stage
	452331	AA598509	Hs.29117	H.sapiens mRNA for pur alpha extended 3'	11.75	0.07	upregulate stage
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	1.08	0.73	upregulate stage
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.15	0.07	upregulate stage

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1	0.17	upregulate stage
	452404	AW450675	Hs.212709	ESTs	3.63	0.2	upregulate stage
	452430	AF118083	Hs.29494	PRO1912 protein	1	0.41	upregulate stage
	452436	BE077546	Hs.31447	ESTs	10	0.07	upregulate stage
	452457	AW052499		gb:MR0-CT0065-100899-001-d02 CT0065 Homo	1	0.13	upregulate stage
10	452461	N78223	Hs.108106	transcription factor	8.1	0.06	upregulate stage
	452518	AA280722	Hs.24758	ESTs	9.3	0.08	upregulate stage
	452519	BE008701		gb:RC0-BN0132-270300-021-a03 BN0132 Homo	1	0.19	upregulate stage
	452524	AW135499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	1	0.45	upregulate stage
	452531	AA429462	Hs.293946	ESTs	2.94	0.22	upregulate stage
15	452547	AA335295	Hs.74120	adipose specific 2	1.51	0.53	upregulate stage
	452560	BE077084		gb:RCS-BT0603-220200-013-C07 BT0603 Homo	5.35	0.11	upregulate stage
	452571	W31518	Hs.34665	ESTs	2.55	0.11	upregulate stage
	452607	AJ160029	Hs.61438	ESTs	4.75	0.11	upregulate stage
	452677	BE167202	Hs.212065	ESTs	1	0.32	upregulate stage
20	452680	AW138410	Hs.45051	ESTs	1	1	upregulate stage
	452724	R84810	Hs.30464	cyclin E2	1	0.27	upregulate stage
	452738	AL133800		gb:DKFZp761A0614_r1 761 (synonym: hamy2)	3.45	0.15	upregulate stage
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ111344 fis, clone PL	3.05	0.16	upregulate stage
	452747	BE153855	Hs.61460	ESTs	2.54	0.28	upregulate stage
25	452761	BE244742	Hs.30532	CGI-77 protein	3.85	0.14	upregulate stage
	452825	AJ921523		gb:wo26d09.x1 NCI_CGAP_Gas4 Homo sapiens	1	1	upregulate stage
	452831	AW864089	Hs.135145	ESTs	2.4	0.19	upregulate stage
	452846	AA082160	Hs.204295	ESTs	8.9	0.08	upregulate stage
	452850	H23230	Hs.22481	ESTs	4.75	0.14	upregulate stage
30	452859	AJ300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.15	0.08	upregulate stage
	452862	AW378065	Hs.8687	ESTs	5.95	0.07	upregulate stage
	452899	M96739	Hs.30956	Human NSCL-1 mRNA sequence	1.04	0.9	upregulate stage
	452902	AJ926501	Hs.249729	ESTs	6.8	0.1	upregulate stage
	452909	NM_015368	Hs.30985	pannexin 1	5.6	0.1	upregulate stage
35	452931	AW190011	Hs.158006	hypothetical protein	1	0.53	upregulate stage
	452934	AA581322	Hs.4213	ESTs	1.44	0.55	upregulate stage
	452956	AW003578	Hs.231872	ESTs	1	0.22	upregulate stage
	452974	BE090803	Hs.61506	ESTs	1.75	0.18	upregulate stage
	453011	N62952	Hs.46473	ESTs	1	1	upregulate stage
40	453050	AW136479	Hs.224046	ESTs	1	0.39	upregulate stage
	453074	AA031813	Hs.271880	ESTs	1	1	upregulate stage
	453076	AJ978583	Hs.232161	ESTs	3.75	0.14	upregulate stage
	453123	AJ953718	Hs.221849	ESTs	6.6	0.11	upregulate stage
	453134	AA032211	Hs.118493	ESTs	1.68	0.42	upregulate stage
45	453135	T07886	Hs.31834	Homo sapiens clone 25129 mRNA sequence	1	1	upregulate stage
	453137	AJ954733	Hs.223640	ESTs	1	0.51	upregulate stage
	453144	AW268807	Hs.61646	ESTs	1	0.26	upregulate stage
	453153	N53893	Hs.24360	ESTs	5	0.13	upregulate stage
	453156	BE463762	Hs.223784	ESTs	2.8	0.15	upregulate stage
50	453204	R10799	Hs.191990	ESTs	9.5	0.05	upregulate stage
	453228	AW628325	Hs.232327	ESTs	1	1	upregulate stage
	453274	AA018511	Hs.32769	Homo sapiens mRNA full length insert cDN	1	1	upregulate stage
	453293	AA382267	Hs.10653	ESTs	8.4	0.09	upregulate stage
	453321	AJ984381	Hs.232521	ESTs	6.7	0.1	upregulate stage
55	453329	T97205	Hs.17998	ESTs	8.9	0.08	upregulate stage
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal kd	1	0.18	upregulate stage
	453437	H10751	Hs.79981	Human clone 23560 mRNA sequence	1	0.83	upregulate stage
	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	7.09	0.08	upregulate stage
	453459	BE047032	Hs.257789	ESTs	2.35	0.3	upregulate stage
60	453476	AJ840500	Hs.24633	SAM domain, SH3 domain and nuclear local	2.75	0.16	upregulate stage
	453651	AA971698	Hs.159397	x 010 protein	8.95	0.08	upregulate stage
	453653	AW505554	Hs.300284	ESTs	4.6	0.1	upregulate stage
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.4	0.1	upregulate stage
	453776	R15749	Hs.31677	ESTs	1	1	upregulate stage
65	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	1	0.95	upregulate stage
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.25	0.06	upregulate stage
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.75	0.12	upregulate stage
	453913	AW004683	Hs.233502	ESTs	3.65	0.14	upregulate stage
	453925	AW021088	Hs.181614	ESTs	3.7	0.13	upregulate stage
70	453931	AL121278	Hs.25144	ESTs	3.45	0.18	upregulate stage
	453945	NM_005171	Hs.36908	activating transcription factor 1	6.35	0.12	upregulate stage
	454032	W31790	Hs.194293	ESTs	6.15	0.07	upregulate stage
	454049	AW022885		gb:dl45e05.y1 Morton Fetal Cochlea Homo	2.8	0.15	upregulate stage
	454069	AW025160	Hs.34161	ESTs, Moderately similar to ALU1_HUMAN A	1	0.32	upregulate stage
75	454099	AW082974		gb:IL1-ST0041-020899-001-H08 ST0041 Homo	1	1	upregulate stage
	454111	AW081681	Hs.269064	ESTs	2.8	0.18	upregulate stage
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	9.4	0.05	upregulate stage
	454259	AL110136	Hs.47679	Homo sapiens mRNA; cDNA DKFZp564I112 (fr	6.2	0.11	upregulate stage
	454327	BE064097		gb:QV3-BT0297-231199-020-h08 BT0297 Homo	1	1	upregulate stage
	454331	AW372937		gb:QV3-BT0381-161299-042-a09 BT0381 Homo	1	0.43	upregulate stage
	454380	AW858722		gb:RC3-CT0347-281199-011-c04 CT0347 Homo	1	0.29	upregulate stage

5	454524	AW857191	gb:RC2-CT0304-080100-011-b12 CT0304 Homo	10.55	0.08	upregulate stage
	454592	AW810112	gb:MR4-ST0124-100400-006-e07 ST0124 Homo	1	0.37	upregulate stage
	454648	AW811960	gb:RC2-ST0168-240300-017-f09 ST0168 Homo	1	0.4	upregulate stage
	454687	AW814473	gb:MR3-ST0203-010200-109-c11 ST0203 Homo	1	1	upregulate stage
	454692	AW813350	gb:MR3-ST0192-100100-024-g07 ST0192 Homo	4.45	0.14	upregulate stage
10	454702	BE145915	gb:MR0-HT0208-221299-204-h08 HT0208 Homo	9.65	0.08	upregulate stage
	454729	AW817003	gb:QVO-ST0247-040100-081-f03 ST0247 Homo	1	0.8	upregulate stage
	454789	BE156314	gb:QVO-HT0367-150200-114-d02 HT0367 Homo	1	0.31	upregulate stage
	454797	BE161168	gb:PM0-HT0425-170100-002-a10 HT0425 Homo	4.1	0.14	upregulate stage
	454863	AW835610	gb:QV4-LT0016-090200-100-c02 LT0016 Homo	1	1	upregulate stage
15	454893	AW837753	gb:CM1-LT0042-310100-112-g03 LT0042 Homo	4.45	0.18	upregulate stage
	454898	AW838125	gb:QV2-LT0051-240300-097-e12 LT0051 Homo	1	1	upregulate stage
	454951	AW847464	gb:RC3-CT0208-270999-021-h12 CT0208 Homo	7.4	0.1	upregulate stage
	454956	AW847725	gb:IL3-CT0213-180200-041-H10 CT0213 Homo	1	0.23	upregulate stage
	455047	AW852530	gb:PM1-CT0243-071099-001-g06 CT0243 Homo	4.25	0.13	upregulate stage
20	455128	AW861555	gb:RC2-CT0321-110100-013-b05 CT0321 Homo	2.9	0.13	upregulate stage
	455201	AW847884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.15	0.16	upregulate stage
	455207	AW994394	gb:RC3-BN0036-060400-014-h12 BN0036 Homo	1	0.18	upregulate stage
	455331	AW897292	gb:CM0-NN0057-150400-338-b02 NN0057 Homo	1	0.87	upregulate stage
	455351	AW901942	gb:QVO-NN1022-100400-190-b04 NN1022 Homo	1	0.39	upregulate stage
25	455380	BE160188	gb:QV1-HT0413-010200-059-g05 HT0413 Homo	1.96	0.33	upregulate stage
	455414	AW936959	gb:RC1-DT0029-160200-013-f10 DT0029 Homo	1	1	upregulate stage
	455428	AW938204	gb:QVO-DT0048-170200-124-f01 DT0048 Homo	1	0.67	upregulate stage
	455573	BE004988	gb:MR2-BN0114-100500-020-b04 BN0114 Homo	1	1	upregulate stage
	455586	BE070794	gb:RC3-BT0501-130100-011-h02 BT0501 Homo	1	1	upregulate stage
30	455595	BE008343	gb:CM0-BN0154-080400-325-g10 BN0154 Homo	1	1	upregulate stage
	455610	BE011703	gb:CM3-BN0223-100500-177-h09 BN0223 Homo	6.05	0.12	upregulate stage
	455647	BE064415	gb:RC4-BT0311-241199-012-b03 BT0311 Homo	1	1	upregulate stage
	455650	BE064655	gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1	0.67	upregulate stage
	455657	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.87	0.4	upregulate stage
35	455669	BE065803	gb:RC2-BT0318-241199-011-g02 BT0318 Homo	2.85	0.2	upregulate stage
	455678	BE066007	gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.8	0.18	upregulate stage
	455761	BE080895	gb:QV1-BT0631-280200-084-e01 BT0631 Homo	1	0.48	upregulate stage
	455799	BE169911	Hs.14570 Homo sapiens cDNA: FLJ22530 fis, clone H	5.7	0.11	upregulate stage
	455831	BE144966	gb:RC6-HT0187-201099-031-c04 HT0187 Homo	1	1	upregulate stage
40	455874	BE152283	gb:QV4-HT0316-191199-039-b01 HT0316 Homo	1	0.67	upregulate stage
	455903	BE155185	gb:PM1-HT0350-231299-005-g05 HT0350 Homo	1	0.31	upregulate stage
	455938	BE159432	gb:MR0-HT0407-140200-009-e06 HT0407 Homo	2.4	0.15	upregulate stage
	455950	BE161004	gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	0.44	upregulate stage
	455951	BE161001	gb:PM0-HT0425-170100-002-f10 HT0425 Homo	1	0.38	upregulate stage
45	455965	BE167014	gb:CM2-HT0502-140200-088-d08 HT0502 Homo	1	1	upregulate stage
	455981	BE177000	gb:RC4-HT0587-070400-015-b07 HT0587 Homo	1	0.57	upregulate stage
	456034	AW450979	gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su	8.29	0.05	upregulate stage
	456046	R51494	Hs.71818 ESTs	3.15	0.17	upregulate stage
	456122	R11813	gb:YF53a04.r1 Soares Infant brain 1N18 H	1.3	0.31	upregulate stage
50	456212	N51636	gb:YF87b01.s1 Soares_multiple_sclerosis_	4.45	0.14	upregulate stage
	456265	AJ968210	Hs.173623 ESTs	1	0.34	upregulate stage
	456285	R67585	Hs.268748 ESTs	1	0.83	upregulate stage
	456320	AJ734064	Hs.136212 ESTs	1	1	upregulate stage
	456353	AJ042330	Hs.87128 ESTs, Weakly similar to similar to YBS4	5.15	0.11	upregulate stage
55	456486	AA676544	Hs.171545 HIV-1 Rev binding protein	1	0.27	upregulate stage
	456493	AA261830	gb:ZS17g09.r1 NCL_CGAP_GCB1 Homo sapiens	1	0.8	upregulate stage
	456504	AK000532	Hs.98491 Homo sapiens cDNA FLJ20525 fis, clone KA	1	0.29	upregulate stage
	456508	AA502764	Hs.123469 ESTs, Weakly similar to AF208855 1 BM-01	17.7	0.05	upregulate stage
	456519	AA279917	Hs.88678 ESTs, Weakly similar to Unknown [Hsaple	2.3	0.18	upregulate stage
60	456536	AW135986	Hs.257859 ESTs	9.45	0.05	upregulate stage
	456592	R91600	gb:YF10c02.r1 Soares fetal liver spleen	4.5	0.14	upregulate stage
	456621	T35958	Hs.107614 DKFZP564I1171 protein	1	0.2	upregulate stage
	456682	AW500321	Hs.246766 Homo sapiens cDNA FLJ12360 fis, clone MA	1	0.24	upregulate stage
	456726	H43102	Hs.144183 ESTs	1	0.69	upregulate stage
65	456736	AW248217	Hs.1619 achaete-scute complex (Drosophila) homol	0.89	0.91	upregulate stage
	456786	AK002084	Hs.132851 hypothetical protein FLJ11222	3.2	0.13	upregulate stage
	456800	AL118754	gb:DKFZp761P1910_r1 761 (synonym: hamy2)	1	0.69	upregulate stage
	456823	AL161979	Hs.146128 Homo sapiens mRNA; cDNA DKFZp761G1823 (f	8.95	0.07	upregulate stage
	456844	AJ264155	Hs.152981 CDP-diacylglycerol synthase (phosphatida	5.55	0.1	upregulate stage
70	456999	AA319798	Hs.172247 eukaryotic translation elongation factor	11.3	0.07	upregulate stage
	457015	AA688058	Hs.261544 ESTs	9.25	0.08	upregulate stage
	457030	AJ301740	Hs.173381 dihydropyrimidinase-like 2	2.65	0.17	upregulate stage
	457158	AA135370	Hs.188536 Homo sapiens cDNA: FLJ21635 fis, clone C	1	1	upregulate stage
	457190	AJ753247	Hs.29643 Homo sapiens cDNA FLJ13103 fis, clone NT	1	0.87	upregulate stage
75	457309	AF131843	Hs.239340 Homo sapiens clone 24587 mRNA sequence	2.6	0.15	upregulate stage
	457376	AJ026984	Hs.293662 ESTs	1	1	upregulate stage
	457402	AW452648	Hs.149342 activation-induced cytidine deaminase	2.9	0.16	upregulate stage
	457435	AW972024	Hs.154645 ESTs, Weakly similar to tyrosine kinase	1	0.36	upregulate stage
	457437	AW969732	gb:EST381810 MAGE resequences, MAGK Homo	2.5	0.14	upregulate stage
	457465	AW301344	Hs.195969 ESTs	6.3	0.1	upregulate stage
	457467	AW974815	Hs.292786 ESTs	1	1	upregulate stage

5	457474	AW972935		gb:EST385031 MAGE resequences, MAGM Homo	1	0.29	upregulate stage
	457530	AW973713	Hs.293596	ESTs	1	0.39	upregulate stage
	457637	AI288373	Hs.149875	ESTs	1	1	upregulate stage
	457643	AI375499	Hs.27379	ESTs	3.25	0.19	upregulate stage
	457650	AA649162	Hs.236456	ESTs	8.9	0.08	upregulate stage
10	457661	AA917801	Hs.128596	ESTs	0.96	0.9	upregulate stage
	457692	AA744046	Hs.133350	ESTs	1	1	upregulate stage
	457857	AW814892	Hs.273104	ESTs	1	1	upregulate stage
	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Homo sapiens	8.7	0.06	upregulate stage
	457902	AI624876	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.2	0.21	upregulate stage
15	457943	AA765625	Hs.155690	ESTs	3.55	0.1	upregulate stage
	457948	AI498640	Hs.159354	ESTs	2.65	0.19	upregulate stage
	457964	NM_016353	Hs.5943	rec	1.5	0.17	upregulate stage
	458004	AW976942	Hs.153057	ESTs	1	0.87	upregulate stage
	458027	L49054	Hs.85195	ESTs, Highly similar to U3.5(q25.1;p34	3.45	0.12	upregulate stage
20	458079	AI796870	Hs.54277	ESTs	11.5	0.05	upregulate stage
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	1	1	upregulate stage
	458171	AI420016	Hs.192090	ESTs	0.69	1.09	upregulate stage
	458172	BE007237		gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3	0.16	upregulate stage
	458186	AA904244	Hs.153205	ESTs	4.6	0.15	upregulate stage
25	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	3.1	0.16	upregulate stage
	458270	T66139	Hs.113631	ESTs	1	0.67	upregulate stage
	458282	AA984075	Hs.22580	alkylglycerone phosphate synthase	1	1	upregulate stage
	458287	AA987556	Hs.12867	ESTs	5.05	0.13	upregulate stage
	458580	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	1	0.28	upregulate stage
30	458586	AI683479	Hs.65390	ESTs	8.2	0.07	upregulate stage
	458608	AW444662	Hs.202247	ESTs	1	0.27	upregulate stage
	458632	AI744445	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	1.05	0.23	upregulate stage
	458663	AV658444	Hs.280776	Homo sapiens cDNA FLJ13684 fis, clone PL	5.05	0.13	upregulate stage
	458670	AI301987	Hs.233398	ESTs	8.9	0.08	upregulate stage
35	458680	N73773	Hs.282950	ESTs	1	0.23	upregulate stage
	458720	AV662037	Hs.124740	ESTs	1	0.3	upregulate stage
	458722	AA741545	Hs.282832	ESTs	3.2	0.11	upregulate stage
	458747	BE618395	Hs.257391	ESTs, Weakly similar to GTPase-activatin	3.3	0.14	upregulate stage
	458760	AI498631	Hs.111334	ferritin, light polypeptide	11	0.07	upregulate stage
40	458781	AI444821		gb:RET487 subtracted retina cDNA library	6.05	0.12	upregulate stage
	458801	N98648	Hs.276860	ESTs	4.45	0.13	upregulate stage
	458880	AA046742		gb:z48c09.r1 Soares retina N2b4HR Homo	9	0.08	upregulate stage
	458886	AI247487	Hs.103277	ESTs	1	0.3	upregulate stage
	458946	AA009716	Hs.42311	ESTs	8.7	0.08	upregulate stage
45	459023	AW968226	Hs.60798	ESTs	2.95	0.15	upregulate stage
	459028	AI940577		gb:IL5-HT0009-120799-001-G07 HT0009 Homo	2.6	0.17	upregulate stage
	459030	H86658	Hs.107699	ESTs, Weakly similar to hypothetical pro	1	1	upregulate stage
	459058	H85939	Hs.209605	ESTs	1	1	upregulate stage
	459128	AI902169		gb:IL-BT002-221198-051 BT002 Homo sapien	1	0.26	upregulate stage
50	459182	BE178517		gb:PM1-HT0603-090300-001-e09 HT0603 Homo	1	1	upregulate stage
	459204	AW194501	Hs.13219	ESTs	2.85	0.16	upregulate stage
	459256	AW967468	Hs.99821	Homo sapiens mRNA: cDNA DKFZp564C046 (fr	10.65	0.07	upregulate stage
	459319	NM_000059		gb:Homo sapiens breast cancer 2, early o	1	1	upregulate stage
	459395	Z30300	Hs.281935	ESTs	4.05	0.14	upregulate stage
55	459459	AA460445		gb:zx66h11.r1 Soares_tetal_fetus_Nb2HF8_	4.8	0.13	upregulate stage
	459464	AA854847		gb:aj77h02.s1 Soares_parathyroid_tumor_N	1	0.38	upregulate stage
	459492	AL118619		gb:DKFZp761E2410_r1 761 (synonym: hamy2)	1	1	upregulate stage
	459530	AW770811		gb:h49d07.x1 NCL_CGAP_Co17 Homo sapiens	1	1	upregulate stage
	401519				12.65	0.06	upregulate stage
60	402474				25.55	0.03	upregulate stage
	402727				16.25	0.05	upregulate stage
	405411				12.95	0.05	upregulate stage
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	14.42	0.03	upregulate stage
	406685	M18728		gb:Human nonspecific crossreacting antig	15.75	0.03	upregulate stage
65	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	16.3	0.04	upregulate stage
	407242	M18728		gb:Human nonspecific crossreacting antig	12.58	0.03	upregulate stage
	407347	AA829847	Hs.167347	ESTs, Weakly similar to ALU8_HUMAN ALU S	12.91	0.06	upregulate stage
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	14.2	0.06	upregulate stage
	408243	Y00787	Hs.624	interleukin 8	18.52	0.02	upregulate stage
70	408380	AF123050	Hs.44532	diubiquitin	16	0.03	upregulate stage
	408618	AK000637	Hs.46624	HSPC043 protein	12.6	0.06	upregulate stage
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.5	0.03	upregulate stage
	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.55	0.04	upregulate stage
	410315	AI638871	Hs.17625	ESTs	14	0.05	upregulate stage
75	410324	AW292539	Hs.30177	ESTs	15.65	0.05	upregulate stage
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	12.6	0.05	upregulate stage
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	16.45	0.03	upregulate stage
	413281	AA861271	Hs.34396	ESTs	12.95	0.04	upregulate stage
	414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYK1 pr	15.25	0.04	upregulate stage
	414161	AA136106	Hs.184852	KIAA1553 protein	13.25	0.06	upregulate stage
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	12.5	0.05	upregulate stage

	414219	W20010	Hs.75823	ALL 1-fused gene from chromosome 1q	12.71	0.05	upregulate stage
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	13.05	0.05	upregulate stage
	414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	30.45	0.02	upregulate stage
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	29	0.02	upregulate stage
5	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	13.2	0.05	upregulate stage
	416114	AI695549	Hs.183868	glucuronidase, beta	14.7	0.04	upregulate stage
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	13	0.06	upregulate stage
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	13.3	0.04	upregulate stage
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	15.55	0.04	upregulate stage
10	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	23.85	0.03	upregulate stage
	417258	N58885	Hs.294040	ESTs	15.05	0.06	upregulate stage
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	23.05	0.04	upregulate stage
	417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	13	0.05	upregulate stage
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	19.45	0.04	upregulate stage
15	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	12.45	0.03	upregulate stage
	417777	AI823763	Hs.7055	ESTs	12.6	0.06	upregulate stage
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.8	0.04	upregulate stage
	417928	AA209344	Hs.282973	ESTs	14.65	0.05	upregulate stage
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	13	0.05	upregulate stage
20	418791	AA935633	Hs.194628	ESTs	12.95	0.06	upregulate stage
	419145	N99638		gb2a39g11.1 r1 Soares fetal liver spleen	13.2	0.05	upregulate stage
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	12.6	0.05	upregulate stage
	422150	AI857118	Hs.2953	ribosomal protein S15a	13.55	0.05	upregulate stage
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	15.7	0.05	upregulate stage
25	424673	AA345051	Hs.294092	ESTs	16.9	0.04	upregulate stage
	424848	AI263231	Hs.145607	ESTs	15.2	0.05	upregulate stage
	424865	AF011333	Hs.153563	lymphocyte antigen 75	12.85	0.04	upregulate stage
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	13.25	0.06	upregulate stage
	425787	AA363867	Hs.155029	ESTs	17.55	0.05	upregulate stage
30	426252	BE176980	Hs.28917	ESTs	12.95	0.05	upregulate stage
	426329	AL389551	Hs.271623	nucleoporin 50kD	13.8	0.05	upregulate stage
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	13.85	0.05	upregulate stage
	427351	AW402593	Hs.123253	Homo sapiens cDNA: FLJ22009 fis, clone H	12.8	0.06	upregulate stage
	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	16.95	0.05	upregulate stage
35	428044	AA093322	Hs.182225	RNA binding motif protein 3	14.65	0.05	upregulate stage
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xa	17.15	0.05	upregulate stage
	428840	M15590	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	16.8	0.05	upregulate stage
	430191	AI149880	Hs.188809	ESTs	14.5	0.05	upregulate stage
40	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	14.9	0.05	upregulate stage
	430853	AI734179	Hs.105676	ESTs	13.55	0.06	upregulate stage
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	16.2	0.04	upregulate stage
	431211	M86849	Hs.5566	gap junction protein, beta 2, 25kD (conn	27	0.01	upregulate stage
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	13.45	0.06	upregulate stage
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	21.2	0.03	upregulate stage
45	431770	BE221880	Hs.268555	5'-3' exonuclease 2	13.05	0.06	upregulate stage
	431863	AA188185	Hs.271871	spindlin	15.6	0.05	upregulate stage
	434263	N34895	Hs.44648	ESTs	14.25	0.05	upregulate stage
	434651	BE616902	Hs.285313	core promoter element binding protein	17.95	0.05	upregulate stage
50	436286	AA804442	Hs.3459	Homo sapiens cDNA: FLJ22003 fis, clone H	14.95	0.05	upregulate stage
	436385	BE551618	Hs.144097	ESTs	13.85	0.06	upregulate stage
	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	12.75	0.06	upregulate stage
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.3	0.04	upregulate stage
	439941	AI392640	Hs.18272	ESTs	17.42	0.05	upregulate stage
55	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	12.59	0.05	upregulate stage
	440116	AI798851	Hs.9403	ESTs	14.5	0.05	upregulate stage
	441020	W79283	Hs.35962	ESTs	12.4	0.04	upregulate stage
	441633	AW958544	Hs.112242	ESTs	15.85	0.03	upregulate stage
	441980	AK001441	Hs.8055	hypothetical protein FLJ10579	13.6	0.05	upregulate stage
60	442043	BE567620	Hs.99210	ESTs	12.5	0.06	upregulate stage
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	12.65	0.06	upregulate stage
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	15.15	0.05	upregulate stage
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	13.4	0.05	upregulate stage
	445033	AV652402	Hs.155145	ESTs	13.3	0.05	upregulate stage
65	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	30.5	0.02	upregulate stage
	446847	T51454	Hs.82845	Human clone Z3815 mRNA sequence	13.8	0.04	upregulate stage
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	15.15	0.04	upregulate stage
	448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L	13.2	0.05	upregulate stage
	448772	AW390822	Hs.24639	ESTs	12.75	0.06	upregulate stage
	448926	AI798164	Hs.140903	ESTs, Moderately similar to neuronal thr	13.35	0.06	upregulate stage
70	449962	AA004879	Hs.187820	ESTs	12.79	0.05	upregulate stage
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	14.76	0.06	upregulate stage
	451035	AU076785	Hs.430	plastin 1 (I isoform)	17.65	0.04	upregulate stage
	451334	AI122691	Hs.13268	ESTs	14.7	0.05	upregulate stage
	452567	D87120	Hs.29882	predicted osteoblast protein	12.45	0.06	upregulate stage
75	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	13.4	0.05	upregulate stage
	453331	AI240655	Hs.8895	ESTs	12.6	0.05	upregulate stage
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.2	0.17	upregulate stage

401256				2	0.16	upregulate stage
402075				1	0.1	upregulate stage
403029				1.75	0.16	upregulate stage
403047				3.3	0.1	upregulate stage
403426				1.7	0.18	upregulate stage
403754				2.8	0.12	upregulate stage
403822				1.2	0.14	upregulate stage
407835	AK002081	Hs.40337	hypothetical protein	1.9	0.15	upregulate stage
407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	1.35	0.1	upregulate stage
408081	AW451597	Hs.167409	ESTs	2.3	0.18	upregulate stage
408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	1.65	0.12	upregulate stage
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	1	0.2	upregulate stage
409810	AW500895		gb:U1-HF-BPOp-air-a-02-Q-U1.r1 NIH_MGC_5	2.25	0.2	upregulate stage
410094	BE147897	Hs.58593	general transcription factor IIF, polype	4.05	0.12	upregulate stage
410603	AA086219	Hs.58714	ESTs	1.9	0.18	upregulate stage
410763	AF279145	Hs.8966	tumor endothelial marker 8	4.15	0.13	upregulate stage
411418	BE241870		gb:TCAAP2E0047 Pediatric acute myelogeno	1.6	0.22	upregulate stage
411691	AW857199		gb:RC2-CT0304-080100-011-106 CT0304 Homo	1.45	0.24	upregulate stage
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.2	0.2	upregulate stage
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.75	0.06	upregulate stage
412102	H56435	Hs.75935	KIAA0077 protein	1.7	0.2	upregulate stage
412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	1	0.17	upregulate stage
412312	AW936686		gb:PM2-DT0023-080300-004-g01 DT0023 Homo	3.4	0.16	upregulate stage
412598	AI681997	Hs.107057	ESTs	2.25	0.2	upregulate stage
413383	AA128978	Hs.154706	Homo sapiens cDNA FLJ13594 fis, clone PL	2.3	0.17	upregulate stage
413406	AW452823	Hs.135268	ESTs	3.52	0.14	upregulate stage
413618	BE154078		gb:PMO-HT0339-200400-010-F04 HT0339 Homo	1	0.18	upregulate stage
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.05	0.12	upregulate stage
417708	N74392	Hs.50495	ESTs	2	0.16	upregulate stage
417974	AA210765		gb:zr90c06.r1 NCI_CGAP_GCB1 Homo sapiens	1.7	0.18	upregulate stage
418604	AA225632	Hs.190016	ESTs	3.75	0.13	upregulate stage
418631	AA225921	Hs.115105	ESTs	1.75	0.2	upregulate stage
418830	BE513731	Hs.88959	Human DNA sequence from clone 967N21 on	3.8	0.09	upregulate stage
418893	N32264	Hs.44330	ESTs	2.35	0.14	upregulate stage
418950	T78517	Hs.13941	ESTs	2.15	0.19	upregulate stage
419044	AI799135	Hs.87164	Homo sapiens cDNA FLJ14001 fis, clone Y7	1.85	0.15	upregulate stage
420082	N43741	Hs.203148	ESTs	3.8	0.14	upregulate stage
420653	AI224532	Hs.88550	ESTs	2.05	0.16	upregulate stage
421112	AW243875	Hs.265427	ESTs	3.3	0.13	upregulate stage
421683	AI147535	Hs.143769	ESTs	2	0.14	upregulate stage
421799	AW972292	Hs.292998	ESTs	2.35	0.15	upregulate stage
422177	AA720878	Hs.201375	ESTs	3.3	0.14	upregulate stage
422429	AA310527		gb:EST181333 Jurkat T-cells V Homo saple	3.45	0.12	upregulate stage
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	2.15	0.11	upregulate stage
424026	AI798295	Hs.123218	ESTs	3.8	0.14	upregulate stage
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1	0.09	upregulate stage
425761	AW664214	Hs.196729	ESTs	2	0.19	upregulate stage
426427	M86699	Hs.169840	TTK protein kinase	2.1	0.16	upregulate stage
427558	D49493	Hs.2171	growth differentiation factor 10	2.15	0.14	upregulate stage
427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.9	0.11	upregulate stage
428766	AA477989	Hs.98800	ESTs	3.8	0.12	upregulate stage
429761	AI276780	Hs.135173	ESTs	1.9	0.17	upregulate stage
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	5.05	0.11	upregulate stage
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.55	0.15	upregulate stage
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.5	0.14	upregulate stage
431187	AW971146	Hs.293187	ESTs	3.95	0.13	upregulate stage
431364	AW971382	Hs.294016	ESTs, Weakly similar to alpha-1(XVII) c	1.8	0.15	upregulate stage
431401	AA504626	Hs.105735	ESTs	1.65	0.22	upregulate stage
431419	AL041844	Hs.277522	ESTs, Weakly similar to FYVE finger-cont	1.45	0.16	upregulate stage
432361	AI378582	Hs.159585	ESTs	2.15	0.14	upregulate stage
432810	AA863400	Hs.23054	ESTs	3.7	0.08	upregulate stage
432926	AA570416	Hs.32271	hypothetical protein FLJ10846	2	0.2	upregulate stage
433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	2.35	0.14	upregulate stage
434153	AF118072	Hs.283916	Homo sapiens PRO1716 mRNA, complete cds	1	0.14	upregulate stage
435202	AI971313	Hs.170204	KIAA0551 protein	1.25	0.16	upregulate stage
435313	AI769400	Hs.189729	ESTs	2	0.18	upregulate stage
435359	T60843	Hs.189679	ESTs	3.6	0.11	upregulate stage
435488	H57954	Hs.34394	ESTs	2.2	0.22	upregulate stage
436583	AW293909	Hs.156935	ESTs	1.4	0.19	upregulate stage
436862	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	3.2	0.12	upregulate stage
437485	AI149570	Hs.127363	ESTs	2.05	0.22	upregulate stage
437854	AL119723		gb:DKFZp761A2124_r1 761 (synonym: hamy2)	2.75	0.15	upregulate stage
438316	AA789249		gb:aj27g08.s1 Soares_testis_NHT Homo sap	2.45	0.13	upregulate stage
438390	AI422017		gb:tf45f12.x1 NCI_CGAP_Bm23 Homo sapien	3.1	0.13	upregulate stage
438915	AA280174	Hs.23282	ESTs	1.35	0.12	upregulate stage
439983	AA858394	Hs.117955	ESTs	4	0.13	upregulate stage
442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	5.55	0.09	upregulate stage

	442369	AI565071	Hs.159983	ESTs	3.85	0.14	upregulate stage
	442748	AI016713	Hs.135787	ESTs	2.35	0.23	upregulate stage
	443717	BE163884	Hs.282331	ESTs	2.5	0.18	upregulate stage
	445935	AA287537	Hs.167585	ESTs	1	0.2	upregulate stage
5	446078	AI339982	Hs.156051	ESTs	2.25	0.24	upregulate stage
	446139	H77395	Hs.39749	ESTs	2.15	0.18	upregulate stage
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (tr	3.45	0.14	upregulate stage
	448253	H25899	Hs.201591	ESTs	1.65	0.18	upregulate stage
	448956	AK001674	Hs.22630	cofactor required for Spl transcription	2.2	0.14	upregulate stage
10	449199	AI990122	Hs.196988	ESTs	1.25	0.23	upregulate stage
	449558	AA001765	Hs.157079	KIAA1227 protein	1	0.16	upregulate stage
	449576	AW014631	Hs.225068	ESTs	2.3	0.19	upregulate stage
	449859	T98077	Hs.18214	ESTs	6.3	0.07	upregulate stage
15	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	1.65	0.22	upregulate stage
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	1.35	0.19	upregulate stage
	451337	AI400209	Hs.60787	ESTs	1.6	0.16	upregulate stage
	451686	AA059246	Hs.110293	ESTs	3.4	0.14	upregulate stage
	452079	AA830908	Hs.15825	ESTs	1.9	0.23	upregulate stage
	452220	BE158006	Hs.212296	ESTs	3.1	0.17	upregulate stage
20	453918	AW005123	Hs.231975	ESTs	1	0.21	upregulate stage
	455350	AW901809		gb:QVO-NN1020-170400-195-h02 NN1020 Homo	2	0.2	upregulate stage
	456511	AA282330	Hs.145668	ESTs	1.15	0.12	upregulate stage
	456986	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	1.65	0.18	upregulate stage
	457427	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	2.35	0.16	upregulate stage
25	460296	AA305827	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1	0.27	upregulate stage
	460409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	2.33	0.2	upregulate stage
	460471				7.45	0.09	upregulate stage
	460641				0.71	0.31	upregulate stage
	460749				7.25	0.1	upregulate stage
30	460751				5.35	0.09	upregulate stage
	460761				5.9	0.1	upregulate stage
	460843				5.85	0.07	upregulate stage
	461045				2.42	0.17	upregulate stage
	461049				1.2	0.19	upregulate stage
35	461192				2.47	0.3	upregulate stage
	461203				6.73	0.08	upregulate stage
	461205				6.63	0.1	upregulate stage
	461276				6.95	0.1	upregulate stage
	461561				2.2	0.13	upregulate stage
40	461604				1	0.19	upregulate stage
	462245				7.65	0.09	upregulate stage
	462296				1	0.33	upregulate stage
	462530				5.1	0.13	upregulate stage
	462812				1.65	0.17	upregulate stage
45	462820				1	0.34	upregulate stage
	462892				1	1	upregulate stage
	463344				6.5	0.08	upregulate stage
	464156				3.7	0.11	upregulate stage
	464290				4.45	0.09	upregulate stage
50	464538				8.38	0.09	upregulate stage
	464676				8.3	0.09	upregulate stage
	464977				0.9	0.35	upregulate stage
	465033				1.52	0.31	upregulate stage
55	465109	N47812	Hs.81360	CGI-35 protein	6.2	0.1	upregulate stage
	465654				1.95	0.06	upregulate stage
	466081				3	0.07	upregulate stage
	466270				6.09	0.13	upregulate stage
	466399				1.55	0.41	upregulate stage
60	466475				6.2	0.12	upregulate stage
	466485				1	0.48	upregulate stage
	466741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	5.4	0.07	upregulate stage
	466867	AA157857	Hs.182265	keratin 19	2.26	0.37	upregulate stage
	467173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.35	0.11	upregulate stage
65	467230	AA157857	Hs.182265	keratin 19	2.15	0.38	upregulate stage
	467266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	2.1	0.09	upregulate stage
	467783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.25	0.11	upregulate stage
	467825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.25	0.08	upregulate stage
	467870	AB032990	Hs.40719	hypothetical protein KIAA1164	4.5	0.12	upregulate stage
	467877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	3.3	0.15	upregulate stage
70	467968	NM_004863	Hs.59403	serine palmitoyltransferase, long chain	7.35	0.1	upregulate stage
	468162	AA993833	Hs.118527	ESTs	6.2	0.09	upregulate stage
	468363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	5.35	0.14	upregulate stage
	468576	NM_003542	Hs.46423	H4 histone family, member G	7.28	0.1	upregulate stage
	468673	BE208517	Hs.184109	ribosomal protein L37a	2.53	0.24	upregulate stage
75	468684	R61377	Hs.12727	hypothetical protein FLJ21610	1	0.3	upregulate stage
	469361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	7.7	0.06	upregulate stage
	469592	BE280951	Hs.55058	EH-domain containing 4	3.95	0.1	upregulate stage

	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	1.55	0.16	upregulate stage
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	4.1	0.18	upregulate stage
	410232	AW372451	Hs.61184	CGI-79 protein	3.65	0.14	upregulate stage
5	410269	AW613597		gb:hh79g12.x1 NCI_CGAP_GU1 Homo sapiens	7.55	0.09	upregulate stage
	410297	AA148710	Hs.159441	ESTs	3.8	0.1	upregulate stage
	410337	M83822	Hs.62354	cell division cycle 4-like	4.35	0.19	upregulate stage
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.42	0.4	upregulate stage
	410541	AA065003	Hs.64179	hypothetical protein	1.61	0.48	upregulate stage
10	410724	AW799269		gb:RC0-UM0051-210300-012-01 UM0051 Homo	6.65	0.12	upregulate stage
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	1.4	0.16	upregulate stage
	410968	AA199907	Hs.67397	homeo box A1	3.05	0.1	upregulate stage
	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2	0.23	upregulate stage
	411173	R81571		gb:yj02h10.r1 Soares placenta Nb2HP Homo	7.2	0.1	upregulate stage
	411243	AB039886	Hs.69319	CA11	0.36	0.93	upregulate stage
15	411407	R00903		gb:ye87a07.r1 Soares fetal liver spleen	8	0.09	upregulate stage
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	1.75	0.22	upregulate stage
	412121	AB033061	Hs.73287	KIAA1235 protein	5.3	0.11	upregulate stage
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	6.9	0.1	upregulate stage
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	0.27	1.06	upregulate stage
20	412354	AW939148		gb:QV1-DT0069-110200-067-d06 DT0069 Homo	6.9	0.11	upregulate stage
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.88	0.21	upregulate stage
	412700	BE222433	Hs.201262	ESTs	2.85	0.15	upregulate stage
	412706	R97106	Hs.167546	ESTs	3.75	0.16	upregulate stage
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	7	0.09	upregulate stage
25	413402	T24065		gb:seq2245 HMSWMYK Homo sapiens cDNA clo	6.3	0.12	upregulate stage
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.45	0.11	upregulate stage
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	3.9	0.13	upregulate stage
	413587	AA156164	Hs.271833	Homo sapiens cDNA FLJ13473 fis, clone PL	7.63	0.09	upregulate stage
	413800	AI129238	Hs.192235	ESTs	3.2	0.18	upregulate stage
30	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	2.54	0.33	upregulate stage
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	1.75	0.21	upregulate stage
	413991	H44725	Hs.71300	ESTs	1.3	0.21	upregulate stage
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	8.1	0.07	upregulate stage
35	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens c	1.45	0.14	upregulate stage
	414343	AL036166	Hs.75914	coated vesicle membrane protein	1	0.23	upregulate stage
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	1	0.36	upregulate stage
	414987	AA524394	Hs.165544	ESTs	1.51	0.51	upregulate stage
	414993	AW819403	Hs.77724	KIAA0586 gene product	2.72	0.23	upregulate stage
40	415276	U88665	Hs.78353	SFRS protein kinase 2	6.95	0.1	upregulate stage
	415303	R11813		gb:yf53a04.r1 Soares infant brain 1NIB H	8.1	0.09	upregulate stage
	415392	Z44067		gb:HSC1RF051 normalized infant brain cDN	5.56	0.11	upregulate stage
	415572	F12294		gb:HSC38B051 normalized infant brain cDN	5.7	0.11	upregulate stage
	415773	R21651		gb:yh19g02.r1 Soares placenta Nb2HP Homo	5.3	0.11	upregulate stage
45	416012	AF061959	Hs.78861	protein phosphatase 1, regulatory (inhib	2.19	0.28	upregulate stage
	416074	R40174	Hs.21209	ESTs	7.61	0.11	upregulate stage
	416182	NM_004354	Hs.79069	cyclin G2	1	0.39	upregulate stage
	416518	H60730	Hs.18917	ESTs	6.6	0.1	upregulate stage
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	3.9	0.17	upregulate stage
50	416987	D86957	Hs.80712	KIAA0202 protein	2.54	0.31	upregulate stage
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.26	0.12	upregulate stage
	417275	X63578	Hs.81849	parvalbumin	1	0.12	upregulate stage
	417395	BE564245	Hs.82084	Integrin beta 3 binding protein (beta3-e	8.4	0.08	upregulate stage
	417683	AW566008	Hs.239154	Homo sapiens cDNA FLJ12814 fis, clone NT	2.2	0.17	upregulate stage
55	417759	R13567	Hs.12548	ESTs	8.18	0.09	upregulate stage
	417848	AA206581	Hs.39457	ESTs	8.6	0.08	upregulate stage
	417985	AA187545	Hs.83114	crystallin, zeta (quinone reductase)	7	0.11	upregulate stage
	418073	R39789	Hs.119714	EST	6.3	0.11	upregulate stage
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	1.63	0.46	upregulate stage
60	418406	X73501	Hs.84905	cytokeratin 20	3.5	0.02	upregulate stage
	418555	AA172115	Hs.87159	Homo sapiens cDNA FLJ12577 fis, clone NT	6.75	0.06	upregulate stage
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	4.1	0.11	upregulate stage
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	7.5	0.08	upregulate stage
	418827	BE327311	Hs.47166	HT021	5.6	0.13	upregulate stage
65	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	1.5	0.22	upregulate stage
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.44	0.29	upregulate stage
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	8.08	0.1	upregulate stage
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport reg	1.64	0.48	upregulate stage
	419712	AA360838	Hs.179909	Homo sapiens cDNA: FLJ22995 fis, clone K	5.4	0.11	upregulate stage
70	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	7.9	0.06	upregulate stage
	419720	AA249131	Hs.143607	hypothetical protein FLJ11068	2.95	0.15	upregulate stage
	419791	AI579909	Hs.105104	ESTs	2.45	0.2	upregulate stage
	419872	AI422951	Hs.146162	ESTs	4.25	0.17	upregulate stage
	419903	T16938	Hs.87902	ESTs	2.5	0.22	upregulate stage
75	419932	AA281594		gb:z03a01.r1 NCI_CGAP_GCB1 Homo sapiens	6.1	0.12	upregulate stage
	420026	AI831190	Hs.166676	ESTs	3.4	0.14	upregulate stage
	420187	AK001714	Hs.95744	hypothetical protein similar to ankyrin	4.03	0.18	upregulate stage
	420193	AI460080	Hs.202869	ESTs	1	0.28	upregulate stage

5	420281	AI623693	Hs.191533	ESTs	6.6	0.11	upregulate stage
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	6	0.09	upregulate stage
	420370	Y13645	Hs.97234	uroplakin 2	1.2	0.45	upregulate stage
	420383	T55154	Hs.144880	ESTs	3.8	0.12	upregulate stage
	420450	AW968989	Hs.177726	ESTs	2.75	0.14	upregulate stage
10	420588	AF000982	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	8.1	0.09	upregulate stage
	420763	AA419392	Hs.178354	ESTs	8	0.09	upregulate stage
	420838	AW118210	Hs.5244	ESTs	8.65	0.07	upregulate stage
	420981	L40904	Hs.100724	peroxisome proliferative activated recep	1.98	0.32	upregulate stage
	421013	M62397	Hs.1345	mutated in colorectal cancers	1	0.29	upregulate stage
15	421072	AJ215069	Hs.89113	ESTs	5.8	0.12	upregulate stage
	421110	AJ250717	Hs.1355	cathepsin E	5.45	0.03	upregulate stage
	421141	AW117261	Hs.125914	ESTs	2.75	0.16	upregulate stage
	421338	AA287443	Hs.105115	gbz552c10.r1 NCL CGAP_GCB1 Homo sapiens	7.45	0.09	upregulate stage
	421508	NM_004833	Hs.105115	absent in melanoma 2	4.21	0.19	upregulate stage
20	421634	AA437414	Hs.105283	hypothetical protein FLJ10262	7.79	0.08	upregulate stage
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	7.5	0.1	upregulate stage
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	8.45	0.08	upregulate stage
	421855	F06504	Hs.27384	ESTs	2.9	0.16	upregulate stage
	421898	AA259011	Hs.109268	hypothetical protein FLJ12552	7.05	0.11	upregulate stage
25	422156	N34524	Hs.300893	ESTs, Weakly similar to envelope protein	3.75	0.16	upregulate stage
	422225	BE245652	Hs.118281	zinc finger protein 266	2.95	0.17	upregulate stage
	422243	AW803733	Hs.250655	prothymosin, alpha (gene sequence 28)	8.15	0.08	upregulate stage
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	2.21	0.17	upregulate stage
	422634	NM_016010	Hs.118821	CGI-62 protein	1.3	0.29	upregulate stage
30	422988	AW673847	Hs.97321	ESTs	4.15	0.11	upregulate stage
	423081	AF262992	Hs.123159	sperm associated antigen 4	2.82	0.3	upregulate stage
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.75	0.19	upregulate stage
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.95	0.13	upregulate stage
	423979	AF229181	Hs.136844	CS box-containing WD protein	7.12	0.11	upregulate stage
35	424005	AB033041	Hs.137507	KIAA1215 protein	1.71	0.37	upregulate stage
	424014	AA333653	Hs.24790	KIAA1573 protein	4.85	0.12	upregulate stage
	424028	AF065084	Hs.153692	KIAA0686 protein	8.5	0.07	upregulate stage
	424194	BE245833	Hs.169854	hypothetical protein SP192	6.1	0.1	upregulate stage
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.59	0.11	upregulate stage
40	424550	AI650541	Hs.115298	ESTs	3.25	0.12	upregulate stage
	424631	AA688021	Hs.179808	ESTs	5.45	0.11	upregulate stage
	424659	AW891298	Hs.301877	ESTs, Weakly similar to hSIAH2 [H.sapien	3.55	0.15	upregulate stage
	424704	AI263293	Hs.152096	cytochrome P450, subfamily 1J (arachido	8.45	0.06	upregulate stage
	424775	AB014540	Hs.153026	SWAP-70 protein	6.65	0.11	upregulate stage
45	424800	AL035588	Hs.153203	MyoD family inhibitor	1.94	0.3	upregulate stage
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	2.85	0.19	upregulate stage
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (tr	5.2	0.1	upregulate stage
	425277	NM_001241	Hs.155478	cyclin T2	6	0.13	upregulate stage
	425508	AA991551	Hs.97013	ESTs	5.67	0.1	upregulate stage
50	425689	W16480	Hs.24283	ESTs	4.55	0.13	upregulate stage
	425721	AC002115	Hs.159309	uroplakin 1A	0.71	0.8	upregulate stage
	426069	H10807	Hs.30998	ESTs	3.4	0.17	upregulate stage
	426088	AF038007	Hs.165196	ATPase, Class I, type 8B, member 1	6.84	0.09	upregulate stage
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	6.7	0.1	upregulate stage
55	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	3.05	0.14	upregulate stage
	426603	AA382291	Hs.171731	gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.8	0.26	upregulate stage
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.96	0.36	upregulate stage
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	1.32	0.49	upregulate stage
	426902	AI125334	Hs.97408	ESTs	5.05	0.07	upregulate stage
60	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.95	0.12	upregulate stage
	427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	4.9	0.13	upregulate stage
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	0.57	0.86	upregulate stage
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	1.86	0.31	upregulate stage
	427399	NM_014883	Hs.177664	KIAA0914 gene product	5	0.13	upregulate stage
65	427450	AB014526	Hs.178121	KIAA0626 gene product	5.3	0.09	upregulate stage
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	6.37	0.13	upregulate stage
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME	5.7	0.11	upregulate stage
	428042	AA419529	Hs.183752	gb:zv03d12.r1 Soares_NhHMPu_S1 Homo sapi	1.65	0.14	upregulate stage
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.37	0.05	upregulate stage
70	428337	AA644508	Hs.183752	gb:af73c01.r1 Soares_NhHMPu_S1 Homo sapi	3.4	0.13	upregulate stage
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	1	0.17	upregulate stage
	428471	X57348	Hs.184510	stratifin	1.81	0.39	upregulate stage
	428583	AA430589	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	7.55	0.11	upregulate stage
	428670	AA431682	Hs.134832	ESTs	8.05	0.1	upregulate stage
75	428785	AI015953	Hs.125265	ESTs	1.65	0.15	upregulate stage
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.64	0.26	upregulate stage
	429343	AK000785	Hs.199480	epsin 3	3.15	0.27	upregulate stage
	429556	AW139399	Hs.98988	ESTs	1.87	0.31	upregulate stage
	429663	M68874	Hs.211587	phosphatase A2, group IVA (cytosolic,	0.61	1.02	upregulate stage
	429824	AA286363	Hs.121520	Human BAC clone GS1-99H8	2.03	0.39	upregulate stage
	429966	BE081342	Hs.226799	HSPC039 protein	7.85	0.08	upregulate stage

5	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1	0.61	upregulate stage
	430042	AB023170	Hs.227850	KIAA0953 protein	2.5	0.17	upregulate stage
	430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113.1 promi	1.98	0.4	upregulate stage
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	6.7	0.09	upregulate stage
	430399	AI916284	Hs.199671	ESTs	8.09	0.08	upregulate stage
10	430763	AA485468	Hs.105658	ESTs	3.18	0.24	upregulate stage
	431474	AL133990	Hs.190642	ESTs	0.37	0.51	upregulate stage
	431567	N51357	Hs.260855	Homo sapiens mRNA; cDNA DKFZp761G2311 (f	1.74	0.39	upregulate stage
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.55	0.15	upregulate stage
	431683	AK001749	Hs.267604	hypothetical protein FLJ10450	8.55	0.08	upregulate stage
15	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	7.95	0.1	upregulate stage
	431846	BE019924	Hs.271580	uroplakin 1B	1.33	0.5	upregulate stage
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	4.15	0.12	upregulate stage
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	3.7	0.13	upregulate stage
	432520	AI075978	Hs.188007	ESTs	2.05	0.22	upregulate stage
20	432524	AI458020	Hs.293287	ESTs	5.15	0.14	upregulate stage
	432540	AI821517	Hs.105866	ESTs	5.5	0.11	upregulate stage
	432623	AA557351	Hs.152448	ESTs, Moderately similar to PUR6_HUMAN M	8.43	0.09	upregulate stage
	432632	AW973801	Hs.134656	ESTs	2.45	0.16	upregulate stage
	432820	AI554067	Hs.152477	ESTs	8.29	0.09	upregulate stage
25	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	3.22	0.23	upregulate stage
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.15	0.39	upregulate stage
	433037	NM_014158	Hs.279938	HSPC067 protein	5.1	0.11	upregulate stage
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.9	0.1	upregulate stage
	433171	AA579425		gb:nt37c08.s1 NCL_CGAP_Pr2 Homo sapiens	3.54	0.14	upregulate stage
30	433311	AA588149		gb:mv16h12.s1 NCL_CGAP_Pr22 Homo sapiens	6.6	0.08	upregulate stage
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	2.45	0.21	upregulate stage
	433409	AI278802	Hs.25661	ESTs	4.75	0.1	upregulate stage
	433650	AA603472	Hs.28456	ESTs	1.6	0.18	upregulate stage
	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	3.88	0.17	upregulate stage
35	434328	BE564937	Hs.15984	pp21 homolog	3	0.15	upregulate stage
	434476	AW358520	Hs.271825	ESTs	4.6	0.1	upregulate stage
	434683	AW298724	Hs.202639	ESTs	2.1	0.19	upregulate stage
	434726	AF062719	Hs.139053	ESTs	1.76	0.34	upregulate stage
	435124	AA725362	Hs.120456	ESTs	7.7	0.09	upregulate stage
40	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	5.8	0.09	upregulate stage
	435899	W89093	Hs.189914	ESTs	1.32	0.42	upregulate stage
	436026	AI349764	Hs.217081	ESTs	1	0.22	upregulate stage
	436154	AA764950	Hs.119898	ESTs	8.4	0.05	upregulate stage
	436293	AI601188	Hs.120910	ESTs	2.42	0.2	upregulate stage
45	436361	AA825814	Hs.149065	ESTs	6.95	0.09	upregulate stage
	436455	AI027959	Hs.132300	ESTs	3.25	0.15	upregulate stage
	436577	W84774	Hs.17643	ESTs	6.3	0.06	upregulate stage
	436684	AW976319	Hs.94806	KIAA1062 protein	4.75	0.12	upregulate stage
	437036	AI571514	Hs.133022	ESTs	1.4	0.13	upregulate stage
50	437146	AA730977		gb:rw55f05.s1 NCL_CGAP_Ew1 Homo sapiens	1	0.37	upregulate stage
	437262	BE250537	Hs.174838	Homo sapiens cDNA FLJ14192 fis, clone NT	3.25	0.17	upregulate stage
	437277	AA748016	Hs.123370	ESTs	6.75	0.09	upregulate stage
	437882	AI243203	Hs.131572	ESTs	8.12	0.09	upregulate stage
	438392	AA806395	Hs.123205	ESTs	1	0.34	upregulate stage
55	438416	N76398	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	8.1	0.1	upregulate stage
	438739	AA815391		gb:at61c02.s1 Soares_tastis_NHT Homo sap	4.69	0.12	upregulate stage
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	6.65	0.11	upregulate stage
	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 P	3.19	0.11	upregulate stage
	439544	W26354	Hs.28891	hypothetical protein FLJ11360	2.3	0.34	upregulate stage
60	439569	AW602166	Hs.222399	CEP1 protein	0.73	0.51	upregulate stage
	439586	AA922936	Hs.110039	ESTs	4.3	0.1	upregulate stage
	439706	AW872527	Hs.59761	ESTs	1	0.14	upregulate stage
	439897	NM_015310	Hs.6763	KIAA0942 protein	8.4	0.08	upregulate stage
	439898	AW505514	Hs.209561	ESTs, Weakly similar to C05E11.1 gene pr	7.35	0.1	upregulate stage
65	439949	AW979197	Hs.292073	ESTs	8.55	0.08	upregulate stage
	440035	BE561589	Hs.285122	hypothetical protein FLJ21839	6	0.11	upregulate stage
	440519	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	7.95	0.07	upregulate stage
	440635	AW610331		gb:RC4-ST0316-190100-011-c08 ST0316 Homo	5.95	0.11	upregulate stage
	440787	AW292043	Hs.209433	ESTs	5.05	0.12	upregulate stage
70	441233	AA972965	Hs.135568	ESTs	1.7	0.12	upregulate stage
	441528	AI003797	Hs.130815	hypothetical protein FLJ21870	7.2	0.09	upregulate stage
	441670	AW874090	Hs.127392	ESTs, Moderately similar to p33ING1 [H.s	2.45	0.19	upregulate stage
	441683	BE564214	Hs.102946	ESTs	5.9	0.13	upregulate stage
	441847	AI215564	Hs.220972	ESTs	6.95	0.11	upregulate stage
75	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3	0.19	upregulate stage
	442299	AW467791	Hs.155561	ESTs	5.05	0.13	upregulate stage
	442315	AA173992	Hs.7956	ESTs	3.97	0.17	upregulate stage
	442528	AF150317	Hs.134217	ESTs	1.4	0.34	upregulate stage
	442571	C06338	Hs.165464	ESTs	8	0.08	upregulate stage
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	6.7	0.1	upregulate stage
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	7.15	0.11	upregulate stage

5	442947	R40800	Hs.21303	ESTs	8.5	0.08	upregulate stage
	442993	BE018682	Hs.44343	ESTs	1.91	0.34	upregulate stage
	443015	R33261	Hs.6614	ESTs	8.5	0.09	upregulate stage
	443085	AI032660	Hs.164711	ESTs	4	0.13	upregulate stage
	443228	W24781	Hs.293798	ESTs	1.61	0.47	upregulate stage
10	443367	AW071349	Hs.215937	ESTs	1.75	0.29	upregulate stage
	443371	AI792888	Hs.145489	ESTs	5.85	0.11	upregulate stage
	443564	AI921685	Hs.199713	ESTs	1.4	0.18	upregulate stage
	443638	AW028696	Hs.145679	ESTs	3.25	0.15	upregulate stage
	443677	AV646096	Hs.293776	ESTs, Weakly similar to 1207289A reverse	6.45	0.11	upregulate stage
15	443861	AW449462	Hs.134743	ESTs	6.72	0.09	upregulate stage
	444097	AW517412	Hs.150757	ESTs	4.25	0.11	upregulate stage
	444171	AB018249	Hs.10458	small inducible cytokine subfamily A (Cy	8.45	0.09	upregulate stage
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	8.1	0.1	upregulate stage
	444385	BE278964	Hs.11085	CGI-111 protein	8.6	0.09	upregulate stage
20	444624	AV650476	Hs.282936	ESTs	7.52	0.1	upregulate stage
	444631	AW995395	Hs.84520	ESTs	1.25	0.21	upregulate stage
	444707	AI188613	Hs.143866	ESTs	2.1	0.21	upregulate stage
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	6.8	0.1	upregulate stage
	444779	AI192105	Hs.147170	ESTs	0.94	0.6	upregulate stage
25	444823	BE262989	Hs.12045	putative protein	8.09	0.1	upregulate stage
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein	4.6	0.09	upregulate stage
	444875	AI200759	Hs.44737	ESTs	6.85	0.11	upregulate stage
	444888	AI651039	Hs.148559	ESTs	3.15	0.18	upregulate stage
	445076	AI206888	Hs.154131	ESTs	7.81	0.09	upregulate stage
30	445182	AW189787	Hs.147474	ESTs	2	0.07	upregulate stage
	445189	AI936450	Hs.147482	ESTs	2.65	0.12	upregulate stage
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	1.47	0.46	upregulate stage
	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.2	0.07	upregulate stage
	445674	BE410347	Hs.13063	transcription factor CA150	3.8	0.15	upregulate stage
35	445817	NM_003642	Hs.13340	histone acetyltransferase 1	5.6	0.1	upregulate stage
	445871	AI702901	Hs.145582	ESTs	2.3	0.33	upregulate stage
	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone H	2.15	0.18	upregulate stage
	446553	AB021179	Hs.15299	HMBa-inducible	2.55	0.18	upregulate stage
	446651	AA393907	Hs.97179	ESTs	8.05	0.07	upregulate stage
40	447086	AI421397	Hs.161321	ESTs	6.9	0.1	upregulate stage
	447290	AI476732	Hs.263912	ESTs	2.35	0.18	upregulate stage
	447379	AI554946	Hs.158794	ESTs	6.3	0.09	upregulate stage
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	7.25	0.08	upregulate stage
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	1	0.24	upregulate stage
45	447548	N53388	Hs.7222	ESTs	8.6	0.07	upregulate stage
	447731	AA373527	Hs.19385	CGI-58 protein	7.3	0.08	upregulate stage
	447853	AI434204	Hs.164285	ESTs, Weakly similar to Afp1p [S.cerevis	6.75	0.11	upregulate stage
	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	2.2	0.24	upregulate stage
	447965	AW292577	Hs.94445	ESTs	3.6	0.13	upregulate stage
50	448072	AI459306	Hs.24908	ESTs	5.8	0.11	upregulate stage
	448474	AI792014	Hs.13809	ESTs	2.72	0.28	upregulate stage
	448513	AA344741	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	4.8	0.12	upregulate stage
	448601	R61656	Hs.293690	ESTs	2.65	0.2	upregulate stage
	448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone H	1.68	0.44	upregulate stage
55	448735	AW473830	Hs.171442	ESTs	2.95	0.19	upregulate stage
	448807	AI571940	Hs.7549	ESTs	2.3	0.14	upregulate stage
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	8.6	0.08	upregulate stage
	449448	D60730	Hs.57471	ESTs	1	0.13	upregulate stage
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	6.4	0.11	upregulate stage
60	449585	AI655321	Hs.197693	ESTs	1	0.16	upregulate stage
	449619	AI655992	Hs.300647	ESTs	8.35	0.09	upregulate stage
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	6.65	0.11	upregulate stage
	449689	AF228421	Hs.301039	Human DNA sequence from clone RP1-132F21	8.35	0.06	upregulate stage
	449901	AI674072	Hs.273193	gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	5.8	0.1	upregulate stage
65	449964	AW001741	Hs.32775	hypothetical protein FLJ10706	8.7	0.09	upregulate stage
	450170	AI685366	Hs.224623	ESTs	6.77	0.12	upregulate stage
	450193	AI916071	Hs.224623	ESTs	5.73	0.1	upregulate stage
	450336	AA046814	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone H	8.2	0.08	upregulate stage
	450341	N90956	Hs.17230	hypothetical protein FLJ22087	4.2	0.19	upregulate stage
70	450353	AI244661	Hs.103296	ESTs	4.71	0.15	upregulate stage
	450737	AW007152	Hs.203330	ESTs	2.14	0.25	upregulate stage
	450795	AW173371	Hs.60435	ESTs	6	0.1	upregulate stage
	450928	AI744417	Hs.25999	gb:tr10h12x1 NCI_CGAP_Ov23 Homo sapiens	1.75	0.18	upregulate stage
	451134	AA318315	Hs.26090	hypothetical protein FLJ22195	4.3	0.1	upregulate stage
75	451230	BE546208	Hs.26706	hypothetical protein FLJ20272	4.75	0.16	upregulate stage
	451593	AF151879	Hs.26764	CGI-121 protein	5.8	0.11	upregulate stage
	451618	AA115639	Hs.26764	KIAA0546 protein	5.8	0.13	upregulate stage
	451668	Z43948	Hs.26789	hypothetical protein FLJ10320	0.73	0.26	upregulate stage
	451790	AA927403	Hs.43897	ESTs, Weakly similar to P2CA_HUMAN PROTE	3.2	0.25	upregulate stage
	452001	AI827675	Hs.297735	Homo sapiens cDNA: FLJ22094 fis, clone H	3.7	0.13	upregulate stage
	452039	AI922988	Hs.172510	ESTs	1	0.65	upregulate stage

5	452046	AB018345	Hs.27657	KIAA0802 protein	1.13	0.39	upregulate stage
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.2	0.15	upregulate stage
	452278	AL037715	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586F0219 (f	8.25	0.07	upregulate stage
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.34	upregulate stage
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	4.97	0.13	upregulate stage
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	7.6	0.09	upregulate stage
	453078	AF053551	Hs.31584	metaxin 2	5.3	0.09	upregulate stage
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation	3.78	0.13	upregulate stage
10	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	3.95	0.11	upregulate stage
	453972	AW137224	Hs.245869	ESTs	6	0.09	upregulate stage
	454044	AW022393		gb:df37h12.y1 Morton Fetal Cochlea Homo	1.15	0.18	upregulate stage
	454289	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	7.05	0.1	upregulate stage
	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	1	0.37	upregulate stage
15	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	2.7	0.13	upregulate stage
	454775	BE160229		gb:QV1-HT0413-090200-062-a12 HT0413 Homo	8.5	0.09	upregulate stage
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	1.15	0.14	upregulate stage
	454792	AW820794	Hs.252405	hypothetical protein FLJ12296 similar to	3.65	0.12	upregulate stage
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	5.7	0.07	upregulate stage
20	455511	BE144752		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	1	0.25	upregulate stage
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22255 fis, clone H	8.35	0.09	upregulate stage
	456258	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 fis, clone C	4.85	0.14	upregulate stage
	456279	AW006783	Hs.6686	ESTs	7.25	0.1	upregulate stage
	457518	AA825350	Hs.143805	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.84	0.11	upregulate stage
25	457570	AA579426	Hs.190226	ESTs	2.6	0.2	upregulate stage
	457982	AW856093	Hs.183617	ESTs	1	0.25	upregulate stage
	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo	2.05	0.27	upregulate stage
	458340	AI457102	Hs.121583	Human glucose transporter pseudogene	2.25	0.18	upregulate stage
	458440	AI095468	Hs.135254	ESTs, Weakly similar to thrombospondin 1	2.35	0.13	upregulate stage
30	458771	AW295151	Hs.163612	ESTs	1	0.19	upregulate stage
	459092	AA722012	Hs.255757	ESTs, Weakly similar to KIAA0611 protein	6.95	0.1	upregulate stage

TABLE 1B

35
 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT	Accessions
	407774	101538_1	AA084958 AA214034 AA044587 AA130152 AA130116 D81924
	407939	1027688_1	W05608 AW118352 AW196215
	407980	103087_1	AA046309 AI263500 AA046397
45	408224	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	408241	1048867_1	AW176546 AW178965 BE141057
	408268	104987_1	AL138247 AA053529 BE173313
	408277	1050131_1	AW177959 AW177960 AW178056 AW178022
	408306	1050863_1	BE141991 AW178855 BE141990 BE141993 BE141994 BE062405 BE062404 AW178850
	409281	111502_1	AA069998 AA075659 AA075660 AA069828
50	409408	1128045_1	AW387837 AW387874 AW387826 AW387758 AW387864 AW809268 AW387754
	409566	114012_1	AA078899 AA078782 AA075788
	409760	115373_1	AA302840 T93016 T92950 AA077551
	409794	1154785_1	AW885691 BE185989 BE185940 AW500322 H10282
	409810	1155339_1	AW500895 AW937549
55	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	410071	1174764_1	AW582568 AW818656 AW818647 AW818655 AW818637 AW818234
	410128	117773_1	AW904599 AA325920 AW964919 AA081785 T05150
	410269	1189983_1	AW613597 BE080235 BE080168
60	410475	1204788_1	AW749927 AW749938 AW749986 AW749966 R87124 AW860547
	410495	1205826_1	N95428 W24040 AW751366 H81987
	410520	1205965_1	AW752710 BE180336 BE180186
	410534	1207247_1	AW905138 AW753008 R13818 Z43519
	410537	1207336_1	AW753108 AW852909 N36993 AW894327 AW903629
	410560	1208311_1	N29220 AW754225 AW754224
65	410562	1208415_1	AW858528 AW754362 H74000
	410724	1218202_1	AW799269 AW799385 AW799501 AW799386 AW799270 AW799467
	410751	121964_1	AA357918 AA089516 AA357917
	410754	1219733_1	T63840 AW801569 AW801568
70	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
	410844	1223878_1	AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
			AW807195 AW807271
	410910	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
	410973	1228236_1	AW812278 AW812286 AW812274
	410997	1228736_1	AW812877 AW812878 AW812952 AW812880
75	411110	1232598_1	H93000 AW818022 AW818044
	411112	1232692_1	AW818158 AW865743 AW865702 AW865698
	411132	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190

		AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
	411137	1233775_1 AW819455 AW819711 AW819553
	411157	1234099_1 AW819867 AW819956 AW820159
5	411159	1234102_1 AW820178 AW820183 AW819870 AW819937 AW835709 AW820184 AW820157 AW819945 AW820096
	411162	1234161_1 AW819944 AW820182 AW820168 AW819959 AW819953
	411170	1234379_1 AW820503 AW820306 AW820429 BE174741 AW820244 BE174738
	411173	123446_1 R81571 AW962014 AA324277
	411193	1235254_1 AW821484 AW821461 AW821490 AW821525 AW821526 AW821519
10	411242	1236393_1 BE146808 BE146949 AW833828 BE147002 BE147066 AW833422 AW833475 AW833485 AW833414 AW833406 AW833395 AW833640
		AW833835 AW833421 BE146805 AW833465 BE146753 BE147004 AW833473 AW833573 BE147068 AW833466 AW833680 BE147063 BE147058
		BE146807 AW833830 AW833694 AW833596 AW833601
	411245	1236412_1 AW833441 AW833552 AW833700 AW833610 AW833673 AW833675
	411282	1237660_1 AW995011 AW880630 AW995662 AW880195 AW860455 AW995379 AW880634 AW938253 AW880580 AW938263 AW880584 AW860454
15		AW880603 AW880026 AW938265 AW880592 AW852203 AW880588 AW880680 AW995392 AW880598 AW860603 AW880590 AW880175
		AW846534 AW880098 AW880108 AW860453 AW938051 AW995191 AW880532 AW880542 AW938197 AW994929 AW880635 AW835438
		AW938057 AW938054
	411327	1238874_1 AW836922 AW876719 AW876688 AW836919 AW836997 AW836908 AW836912 AW836993
	411336	1239216_1 AW837675 AW837356 AW837581 AW837348 AW837681
20	411339	1239387_1 BE164598 AW837578 AW837582
	411407	1244071_1 R00903 R20424 AW844169
	411418	124518_1 BE241870 A1752584 Z19223 AA307961 AA181165 AA093272 AW368570
	411425	1245503_1 AW846012 AW846007 AW845996 AW845975
	411461	1246730_1 AW847937 AW847672 AW847809 AW847923 AW847808 AW847616
25	411474	1247047_2 AW848427 AW848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162
	411526	1248748_1 AW850327 AW850350 AW850348 AW850375
	411560	1249443_1 AW851186 AW969667 BE143456
	411568	1249777_1 BE144593 AW851632 AW968149 AW968144 W21059
30	411691	1254166_1 AW857199 BE066018 BE065982 BE066082 BE065949 BE066019 BE066081 BE065954 BE066084
	411727	1255052_1 AW858443 AW858436 AW861923 AW858551 AW861872 AW858474 AW861904 AW858398
	411741	1255976_1 AW859650 BE071806 AW859655
	411771	1257335_1 AW933247 AW861464
	411787	1258789_1 AW863568 BE161696 BE161629 BE161824
	411788	125879_1 AW897793 R20054 H23321
35	411826	1260006_1 AW947946 AW947986 AW947977 AW865187 AW865246 AW865182 AW865376 AW865392 AW865184
	411840	1260678_1 AW866330 AW866410 AW866332 AW866411 AW866327 AW866326 AW866335 AW866334 AW866331 AW866333 AW866328 AW866329
	411860	126168_1 T89420 N87510 AA095932
	411880	1263110_1 AW872477 BE088101 T05990
	411932	1266125_1 AW876548 AW876577 AW876528 AW876623 AW876519 AW876540 AW876569 AW876534 AW876563 AW876545 AW876574
40	412134	1279147_1 AW895560 AW895557 AW895314 AW895537 AW895287 AW895411
	412178	1281471_1 AW898526 AW898525 Z19700
	412296	1288043_1 AW936233 AW936272
	412303	1288130_1 AW936336 AW936339
	412305	1288141_1 AW936369 AW936377 AW936355 AW936410 AW936460
45	412312	1288349_1 AW936686 AW936656 AW936608 AW936635 AW936652 AW936679 AW936726 AW936602 AW936733
	412327	1288935_1 AW937355 AW937450 BE162340 BE162397
	412354	1290342_1 AW939148 AW939200 BE161819
	412357	1290611_1 AW939537 AW939584 W92705
50	412359	129085_1 AW837985 AW837938 AA101955 AW837913 AW837935
	412367	1291505_1 AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016
		AW946039 AW946045 AW946028 AW946036
	412389	1292588_1 AW947655 AW984020
	412547	1305813_1 W27161 AW961828
55	412559	1306011_1 T31474 T31123 Z45146 AW962040
	412671	1319959_1 AW977734 H62048
	412744	1324622_1 N31101 N46491 AW994084
	412838	1331178_1 D61870 D61866 BE002674
	413119	1349658_1 BE065941 BE066098 BE066070 BE065997 BE066003
	413141	1350477_1 BE166323 BE067045
60	413266	1356260_1 BE300352 BE299274 BE075351 BE297444
	413294	1359149_1 BE144034 N72932 BE080176
	413342	136279_1 AA128535 AW973587 AA553822
	413402	1366932_1 T24065 BE092527 BE092528 BE092204 BE092271 BE092516 BE092202 BE092280 BE092065 BE091991 BE092284 BE092514
		BE091995 BE092063 BE092068 BE091994 BE092283 BE092447
65	413445	1370833_1 BE141022 BE141513 BE141532 BE141488 BE141481 BE141526 BE141516 BE141471 BE141478 BE141476 BE141475 BE141021
		BE141533 BE141484 BE141490 BE141472 BE141480
	413485	1372953_1 N52628 BE143639 BE143706
	413508	1374273_1 BE145364 BE145429 BE145418
	413618	1380384_1 BE154078 BE154006 BE153891 BE153523 BE153983
70	413707	1384137_1 BE158679 BE158714
	413743	1385884_1 BE161004 BE162497 BE161135 BE160999 BE162492
	413782	1389068_1 BE546104 BE165710 BE382801
	413792	1389912_1 BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
	413804	1390710_1 T64682 BE168190 BE168256
75	414091	141621_1 T83742 AW672882 AA135378
	414203	1425510_2 BE262170 BE382553 BE261026 BE273627
	414220	1426940_1 BE298094 BE267860
	414276	1432115_1 BE297862

	414366	1438636_1	BE549143 BE390613 BE277344
	414833	1496271_1	T07114 BE543688
	414985	1511215_1	C17372 D63180 D78908 D63262
5	415027	1515978_1	D31010 D30991 D31168 D31166 D31465
	415104	1522849_1	D60076 D60259 D61037
	415114	1523035_1	D60468 D60950 D61218 N98936
	415178	1527354_1	D80503 D81739 N95691
	415296	1533528_1	F05066 F05091 R17158
10	415303	153360_1	R11813 AA164376 T56632
	415352	1534744_1	F06565 Z43466 R18417 F06477 F06476 F07098
	415364	1535008_1	F06771 H04895 Z42778
	415371	1535066_1	R15239 Z45189 F06836
	415392	1535746_1	Z44067 F07617 R34555
15	415569	1539911_1	Z43930 F12170 H10881 T65261
	415572	1539951_1	F12294 F12213 T66272 T66261
	415600	1540373_1	F12664 T74312 N80318 Z20039
	415626	1540758_1	Z43847 F13068 T75331
	415635	1540853_1	F13168 R21289 T77628
20	415750	155215_1	AA167712 AW936024 AW364438 AW364446
	415773	1554447_1	R21651 H00542
	415822	155791_1	D59243 D63202 AA169716
	415948	156264_1	AA262226 A1984175 AA171807
	416173	1574973_1	R52782 R17313 H24192 R19876
25	416343	1589633_1	H49213 W90725 H49398 W90726
	416395	1592777_1	R94576 T99886 H52989
	416624	1604694_1	H69044 T47567 H75691 T50292
	417304	166556_1	H15635 H16691 AA195506
	417396	1674485_1	T98987 T96744 N78306
30	417742	1696282_1	R64719 Z44580 R12451
	417974	171237_1	AA210765 T95700 H94407
	418297	1736343_1	R91254 T97156 R58711
	418454	175699_1	AA315308 AA223392 BE538098 BE087173
	418498	1762961_1	T78248 T88763 R93361
35	418546	176677_1	AA224827 T59708 T59843 BE156903
	418573	176907_1	AA225188 AL157508 AL157509 AA225189
	418636	177402_1	AW749855 AA225995 AW750208 AW750206
	418712	1784125_1	Z42183 T31621 T97478
40	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	419059	1816038_1	T86216 T86117 T83316
	419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
	419472	185148_1	AW978038 AA804204 AA243400
	419477	185172_1	AA826279 AA243426 AW971614 AW957805 AW971605
	419716	187390_1	AA953770 AA249091
45	419805	188248_1	AW966945 AA250984 H91733 AW966941
	419807	188252_1	R77402 AA262462 AA250988 R06794
	419834	188386_1	AA251139 AW967485 AA251204
	419932	189159_1	AA281594 AI365043 AA251996
	419998	189768_1	AA252691 AW298356 AA688063
50	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420270	192170_1	AA257990 AW816460 AI416981 AW500873
	420643	195293_1	W87731 AA279004 AA279001
	420928	197723_1	AA281809 H89487 N46537
	421280	200885_1	AA811804 AA809404 AA286907 AW977624
55	421338	201378_1	AA287443 AA419385 BE084078 AI478347
	421381	201903_1	AA361752 AW963276 AA288017
	421418	202288_1	AA806639 AA291008 AA836274 AW978806
	421708	205732_1	AW754341 AW858420 AW858475 AW861969 AW861925 AW858554 AW858616 AW858450 AW858545
	421813	207654_1	BE048255 AA313083 AA298419
60	422204	213258_1	AA339015 AW962948 AA306188
	422342	215498_1	AA309272 AA309312 AW961837
	422429	216469_1	AA310527 AW962295 Z44865 H06641
	422504	217160_1	AA311407 AW958321 N23583 R70050
	422588	218192_1	AA312730 AW953285 W28250 W27318
65	422760	221034_1	BE409561 BE162756 AW732798
	422834	221906_1	AA318334 AW961457 AA317752
	423100	224988_1	AA323114 AA321992 BE161391 BE161392
	423121	225175_1	AW864848 AA322213 AA322209 AW961624
	423368	227560_1	AA364195 AA325029 AW962050
70	423632	230430_1	AA328824 AW961410 AW958096
	423644	230585_1	AA329048 AW962484 T83628
	423818	232362_1	AA332439 AA332579 AA331470 AW962539
	423837	232478_1	AW937053 AW937056 AW937062 AW937059 AW937057 AA331599 AW937061 AW937093 AW937094 AW937058 AW851327 BE082872
			AW752885 AW937055 AW937054
75	423912	233241_1	BE091233 BE080904 BE079414 BE075356 AA332482
	424353	238398_1	AA339646 AA339189 AW966286
	424589	241202_1	AW854298 AA343691 H50917 H50907 H50938
	424951	245273_1	AW964082 AA348838 AA348839

	424993	245782_1	F07625 R35115 AW953115 F06102 H13351 AA349497 F11152 AA707254
	425360	250631_1	BE547704 AA355909
	425362	250655_1	AA355936 A1741379
5	425672	254716_1	AA361483 A1557239
	426355	265381_1	BE536836 AA376153
	426475	267785_1	AL134728 AA379975 AA379440 AW963931
	426561	269158_1	AA381437 AA628833 AW407275
	426603	269825_1	AA382291 AA994657
10	427259	276594_1	AA400096 AA400167
	427566	280401_1	A1743515 AA405617 AW276706
	427980	285225_1	AA418305 A1264351
	428042	286282_1	AA419529 H97089 H96977
	428192	288021_1	AA424051 AW104616
15	428337	289967_1	AA644508 AA479489 AA426174
	428436	291472_1	BE080180 AW827313 AW231970 AA955028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
			AA528743 AA552874 AA564758 AW063245 A1267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311
			AA429538
20	429236	301580_1	AA448407 AA448404 AA448424 AA448426
	429917	31049_1	H80572 AL109691 H80520
	429979	311517_1	AA463338 M86137 M85945 A1040226
	430076	312952_1	AA465115 AW967750 AW869525
	430350	316401_1	BE169639 AA476976
	430661	319932_1	BE065227 BE065366 BE065182 BE065184 AA481239
25	430640	321094_1	AA482636 R16336 R16343 R60706 R53647
	430795	323756_1	AW971398 AA507162 AA486494
	431319	331474_1	AA873350 T82429 T82428
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	431670	336353_1	AW971287 AA524976 AA513479
	431828	338201_1	AA572994 AA516249 AA702595
30	432093	341283_1	H28383 AW972670 H28359 AA525808
	432222	343347_1	A1204995 AW827539 AW969908 AW440776 AA528756
	432724	35330_1	X98266 N41124
	433005	357346_1	AW939074 AW939073 BE160476 AW939338 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
35	433108	35896_1	AB002446 T03146
	433129	359479_1	AA577814 N68543 N68478 H79613 A1910764
	433171	360292_1	AA579425 AW969965 AA579102
	433311	362908_1	AA688149 AW975336 R82513 R79237
	433371	364430_1	T25451 AA585296 AA585305
40	433440	36629_1	AF052127
	433586	370470_1	T85301 AW517087 AA601054 BE073959
	433782	37414_1	AF090945 AW995754 A1064870
	434006	37855_1	AF113688 A1114617
	434092	379978_1	AA625155 BE502124
45	434138	380572_1	AA625804 AW418787 AW074833 A1675642 A1393368
	434280	382816_1	BE005398 AA628622 AA994155
	435382	405265_1	N54493 AA679039 N76605
	436023	413582_1	T81819 AW393709 AA703541 AW370185
	436359	41847_1	Z83806 A132091 A132090
50	436383	41888_1	BE065178 A1227879
	436740	426095_1	AW975133 AA729943 AA805813
	436884	428731_1	BE046657 AA736610 AW827495
	437087	432797_1	AA745563 AA745334 AA744168 AA744044 AA744034 AA744056 AA745569 AA744397
	437145	43371_1	AA730977 A1261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920
55	437214	434730_1	AA167612 A1239729 A1251752 AA485791 BE568425 AW962958
	437240	435139_1	BE092336 BE092259 BE092497 BE092051 AA746882 A1336378
	437251	435242_1	AA747537 BE089068 BE089070
	437274	435465_1	AW976082 AW976085 AA747803 AA747680
60	437324	43609_1	AA747965 A1248281 A1752458
	437471	43747_1	AL162077 AW023677
	437798	443128_1	AL390169 AW277196 AW131001
	437854	44418_1	AW811767 AA831890 AW977539 AA768655
65	437938	44573_2	AL119723 AL119874 A1909018 U50537
			A1950087 N70208 R97040 N36809 A1308119 AW967677 N35320 A1251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
			AA251875 A1820501 A1820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE326517 A1219788 AA884444 N92578
			F13493 AA927794 A1560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 A1890387 A1950344 A1741346
			A1689062 AA282915 AW102898 A1872193 A1763273 AW173588 AW150329 A1653832 A1762688 AA988777 AA488892 A1356394 AW103813
			A1539642 AA642789 AA856975 AW505512 A1981530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009
			AA337499 AW961101 AA251669 AA251874 A1819225 AW205862 A1683339 A1858509 AW276905 A1633006 AA972584 AA908741 AW072629
70			AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 A1022058 AA780419 AA551005 W80701 AW613456 A1373032
			A1564269 F00531 H83488 W37181 W78802 R66056 A1002839 R67840 AA300207 AW959581 T63226 F04005
	438316	454745_1	AA789249 AA904217 AA904142
	438366	456119_1	AA805760 BE000856
	438390	45662_1	A1422017 A1422945 A1363249 A1423113 A1925592 A1420795 A1208187 A1423279 A1423645 A1424090 A1359637 AL044732 D17003
	438739	464193_1	AA815391 AW573185
75	438990	46760_1	AF085890 H29949 H29856
	439183	46956_1	AW970600 AA503323 H89218 AF086031 H89112
	439330	47119_1	AF086147 W20068 N91464

	439550	473671_1	H10438 AA837479 H16299 AW978825
	439780	47673_1	AL109688 R23655 R26578
	440012	483290_1	AA861072 H02819 R25946
5	440635	498968_1	AW610331 AW610338 AA897379
	442048	531432_1	AA974603 AI984319 AW340495
	442518	544159_1	AF150226 AI240137
	444163	593658_1	AI126098 AI184746 AI148521
	444282	599268_1	AI138955 BE149059 BE149027
10	444584	611496_1	AI168422 D80113 T59074
	444646	613548_1	AI184565 AL037304 AW793549
	445396	638138_1	BE181792 AI222266 BE181789 BE181837
	445832	651925_1	AI261545 N59134 AW875371 AW875247
	446119	662531_1	D29527 AI275850
	446312	671114_1	BE087853 AI285184
15	446922	69865_1	BE175605 Z43529 F06610 BE175602 AV661027
	447258	71439_1	BE047911 AA984167 BE617316
	447376	719483_1	AI376747
	447522	724922_1	BE143888 AI382949 T06429
20	448632	77303_1	BE614269
	448643	773566_1	AI557531
	448778	7800_1	AF074913 AW505435 U62539
	448871	78566_2	BE616709 BE616712
	449213	80240_1	BE616861
	449231	80303_1	BE410360 AA442408 AA315540
25	449344	805184_1	AI640355 BE464385 AW197679
	449666	81249_1	AA002047 N72537 H54142 H81580
	449901	818599_1	AI674072 BE268487
	450257	830121_1	AW820313 BE065936 BE065948 BE155658 AI689473 AW862275 AW820265 AW820438 AW820331
	450573	83907_1	AW964334 AW967230 T08913 R11895 F11463 AA010271
30	450625	84032_1	AW970107 AA513951 AA010406
	450870	84994_1	AA011471 AA700636
	450928	851593_1	AI744417 R91614 H77365
	451283	86479_1	H83979 R84433 AA017024
	451359	86711_1	H85334 AA017286 H86654
35	451365	867325_1	AI791783
	451373	867533_1	AI792030 AW386116 AW875146
	451487	87131_1	AA018072 N46370 R84847
	451495	87182_1	H86887 H86898 H86906 AA019519 AA018127 AA056306 AA053726
40	451535	87353_1	AW970577 AA861861 AA418358 AA018329 AA501885
	451724	882130_1	AI903765 AI811194 BE007147 AW130760
	451844	888230_1	T61430 AI820546 AI821336
	452163	902067_1	AI863140 W80703 R43474
	452453	918300_1	AI902519 AI902518 AI902516
45	452457	918409_1	AW062499 AW062495 AW062500 AW062492 AW062494 AW062493 AW062496 AW062498 AI902650 AI902649
	452519	920292_1	BE006701 BE006709 BE006704 AI904981
	452530	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
	452536	921149_1	BE063380 BE063346 AI906097
	452550	92188_1	AA026735 BE264405 AL040323 AA323099
50	452560	922216_1	BE077084 AW139953 AW863127 AW806209 AW806204 AW806205 AW806206 AW806211 AW806212 AW806207 AW806208 AW806210
	452738	929698_1	AI907497
	452825	933090_1	AL133800 AI916209
	453472	968371_1	AI921523 AW903707 AW903687
	453677	977149_1	AL037925 AL037931 AL037957
55	453725	978760_1	AL079389 AL079390
	453846	983043_1	W28543 AL119531
	454044	996486_1	AL157586 AL157590
	454049	996858_1	AW022393 AW022578
	454099	1007650_1	AW022885 AW023064
60	454314	1108161_1	AW062974 AW859625 BE081366
	454327	1114097_1	AW364844 AW364847 AW937534 AW937593 AW937659
	454331	1115278_1	BE064097 BE064124 BE064087 AW371617
	454380	1152648_1	AW372937 AW378043 AW377970 BE145850 AW377858 AW377964 AW378040
	454471	1213795_1	AW858722
65	454524	1221640_1	AW902125 AW792853 AW837703 AW837710
	454554	1223842_1	AW857191 AW857192 AW804060
	454592	1226050_1	AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806998 BE061436 BE061430 BE142460 BE146499 AW806994
	454622	1226951_1	AW809156 AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504
	454637	1227707_1	BE142458 BE061431 BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459
70	454648	1227976_1	BE142462 AW854330 AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440
	454687	1229077_1	AW806997 AW806998 BE061745 BE061753
	454692	1229118_1	AW810112 AW810114 AW810032 AW809631 AW810183 AW810178
			U70071 AW883715 AW810701
			AW811613 AW811611 AW811610
			AW811960 AW811957 AW811959
			AW814473 AW816157 AW816064 AW813298 AW813315 AW816100 AW813389 AW813338 AW813342 AW816108 AW813318 AW816105
			AW816160 AW816163 AW814480 AW813392 AW816063 AW813399
			AW813350 AW816082 AW813476 AW813383

5	454702	1229722_1	BE145915 BE145893 AW892892 BE145806 BE145901 AW814144
	454729	1231926_1	AW817003 AW816997 AW817126 AW817331 AW817120 BE158378 AW817121
	454750	1233434_1	AW866285 AW819000 AW819153 AW819014 AW866541
	454775	1234106_1	BE160229 AW819879 AW820179 AW819882 AW819876 AW820169 BE153201 AW993736 BE152911
	454789	1234742_1	BE156314 BE156316 AW820750
	454790	1234752_1	AW820852 AW820773 AW821088
	454797	1235093_1	BE161168 BE162466 AW821260
	454851	1237414_1	AW835127 BE071463 AW991660 BE071473 BE071461 BE071469 BE071472
10	454863	1237794_1	AW835610 AW835806
	454893	1239472_1	AW837753 AW837754 AW837700
	454898	1239633_1	AW838125 AW838205
	454951	1246612_1	AW847464 AW847462 BE063767 BE063755
	454956	1246711_1	AW847725 AW847599 AW847600 AW847705 AW847854 AW847595 AW847850 AW847795 AW847798
	455040	1250028_1	AW852286 AW851934 AW852096 AW852274
15	455047	1250536_1	AW852530 AW852527 AW852526
	455073	1252361_1	AW854829 AW854805 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826
	455128	1254554_1	AW861555 AW857776 AW861556 AW861567 AW857799 AW857768
	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
20	455207	1260400_1	AW994394 AW865900 AW865905 AW865891 AW866014 AW865898
	455225	1262318_1	AW996689 AW996380 AW996453 BE085650 AW868687 BE085595
	455235	1265634_1	AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
	455267	1269025_1	AW880861 AW880883 AW881117 AW881012
	455331	1280616_1	AW897292 AW897251 AW897298 AW897248 AW897250 AW897246 AW897242
25	455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
	455351	1284023_1	AW901942 AW901937 AW902016 AW901947
	455380	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	455414	1288605_1	AW936959 AW936920 AW936975 AW936906
30	455428	1289639_1	AW938204 AW938195 AW938205 AW938206 AW938193 AW938199 AW938200 AW938190 AW938201 AW938198 AW938203 AW938202
	455511	1321229_1	BE144762 AW979091
	455573	1332529_1	BE004988 BE004574
	455586	1334857_1	BE070794 BE070791 BE070792 BE070795 BE070789 BE070788 BE070786 BE070787 BE070790
35	455595	1335422_1	BE008343 BE008321 BE008326 BE008314 BE008345 BE008330 BE008344 BE008327
	455610	1337549_1	BE011703 BE011692 BE011697 BE011624 BE011673 BE011644
	455647	1348563_1	BE064415 BE064430 BE064448
	455650	1348720_1	BE064655 BE153953
	455657	1349078_1	BE065209 BE065364 BE065110 BE065111
40	455669	1349554_1	BE065803 BE065826
	455678	1349716_1	BE066007 BE066017 BE066074
	455761	1359566_1	BE080895 BE080906
	455831	1373969_1	BE144956 BE144957 BE144958
	455874	1379514_1	BE152283 BE152260 BE152297 BE152292 BE152259 BE152250
45	455880	1380022_1	BE153208 BE153146 BE152981
	455903	1381603_1	BE155185 BE155264 BE155186
	455938	1384537_1	BE159432 BE159313 BE159295 BE159242
	455950	1385884_1	BE161004 BE162497 BE161135 BE160999 BE162492
	455951	1385886_1	BE161001 BE162494 BE162470 BE161172
	455965	1389984_1	BE167014 BE167058 BE167062
50	455981	1396805_1	BE177000 BE177003 BE176816 BE176952
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	456122	153360_1	BE011368 BE011362 BE011215 BE011365 BE011363
55	456212	1655565_1	R11813 AA164376 T56632
	456235	168686_1	N51636 T51874 T51829
	456493	193331_1	AA203637 AA832266 H67452
	456592	202684_1	AA261830 AW967855 H26953 AA262478
	456800	233842_1	R91600 T87079 AA291455
60	457340	322100_1	AL118754 AA333202 H38001
	457427	336353_1	AA492071 AA484229 AW969850
	457437	337879_1	AW971287 AA524976 AA513479
	457474	341077_1	AW969732 AW970974 AA515741
	457625	373012_1	AW972935 AA525272 N28227
65	457892	432926_1	T10073 H14872 AA604786
	458080	471050_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
	458172	497769_1	BE142728 AA834047 AW937124
	458781	743159_1	BE007237 BE007496 BE007263 W19919 BE546311 AA984819
	458841	784186_1	AA444821 W26012
70	458880	80785_1	W28985 W28971
	459028	868710_1	AA046742 AA551269 AA001505
	459128	918011_1	AI940577 AI940580 AI940568 AI940578 AI940569 AI795858 AI795867 AI940572
	459182	922744_1	AI902169 AI902173 AI902323 AI902174 AI902347
			BE178517 AI908132 BE142437

TABLE 1C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

5				
	Pkey	Ref	Strand	Nt_position
10	400471	9931670	Minus	105629-105760
	400495	9714773	Minus	61902-62137
	400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
	400577	7960401	Plus	101535-101881
	400608	9887666	Minus	96756-97558
	400641	8117693	Plus	4786-4992
15	400644	8117693	Plus	27682-27840
	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9283
	400750	8119067	Plus	198991-199168,199316-199548
	400751	7331445	Minus	35395-35533
20	400761	8131609	Minus	114220-115164
	400762	8131616	Plus	7235-7605
	400773	8131629	Minus	44116-44238,48208-48321
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
25	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	400860	9757499	Minus	151830-152104,152649-152744
	400880	9931121	Plus	29235-29336,36363-36580
	400887	9958187	Plus	119239-121542
30	400888	9958187	Minus	199600-199875
	400937	7652890	Minus	89519-89905
	400977	8072510	Plus	73950-74364
	401002	8117251	Minus	77898-78050
	401024	8117489	Plus	60551-60802
35	401045	8117619	Plus	90044-90184,91111-91345
	401048	7232177	Plus	132430-132761
	401049	7232177	Plus	149157-150692
	401086	9957912	Plus	84561-84884
40	401093	8516137	Minus	22335-23166
	401101	8568122	Plus	77081-77226
	401192	9719502	Minus	69559-70101
	401197	9719705	Plus	176341-176452
	401203	9743387	Minus	172981-173056,173868-173928
45	401205	9743388	Plus	167373-167433,167938-168031
	401256	9796573	Minus	45482-45620
	401262	9796963	Plus	35662-35799
	401271	9797373	Minus	61292-61911
	401276	8954274	Minus	15919-16096
50	401279	9800062	Minus	13535-13669
	401342	9908882	Plus	3096-3242
	401365	9796180	Minus	119572-119672
	401395	7327842	Minus	11502-11771,46357-46489,58720-58916
	401420	7452889	Minus	141362-141502
55	401439	8246737	Plus	92993-94026
	401451	6634068	Minus	119926-121272
	401508	7534110	Minus	110779-110983
	401519	6649315	Plus	157315-157950
	401537	7960358	Minus	185786-187029,190607-190779,198218-198348
60	401561	8224660	Minus	10652-10838,19815-20018
	401566	8469090	Minus	96277-96420,96979-97160
	401604	7689963	Minus	119835-120185
	401619	8516761	Minus	141309-143576
	401669	9801805	Plus	25414-26310
	401691	3582311	Plus	162333-162715
65	401694	3540172	Minus	64056-64168
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401759	9929699	Plus	59811-60665
70	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401866	8018106	Plus	73126-73623
	401905	8671966	Plus	153955-154441,156599-156819
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
75	402076	8117410	Plus	128316-128627
	402089	7249154	Plus	101610-101819
	402110	8131678	Minus	173889-174062

	402176	7543687	Minus	10-750
	402230	9966312	Minus	29782-29932
	402245	7690231	Minus	88253-88417
	402296	6598824	Plus	22587-23723
5	402325	7636348	Minus	60658-60738,61677-61803
	402407	3962498	Minus	115812-116187
	402408	9796239	Minus	110326-110491
	402430	9796372	Minus	62382-62552
	402435	9796462	Plus	114593-115588
10	402472	9797116	Plus	53716-54470
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402480	9797375	Plus	59708-59999
	402490	9797648	Plus	149982-150929
	402522	9798493	Plus	20605-20731
15	402530	7630937	Minus	1524-2003
	402546	7637348	Plus	24673-25170
	402553	9863566	Plus	48292-48398,49564-49944
	402604	9909420	Plus	20393-20767
	402716	8969253	Minus	84065-84242
20	402727	9211324	Plus	54596-54777
	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402846	9408716	Minus	5726-5850
	402889	9931133	Plus	89392-89498,90358-90571
25	402892	8086844	Minus	194384-194645
	402901	8894222	Minus	175426-175667
	402922	8216969	Minus	19036-19401,19589-19849,19951-20102
	402938	8953442	Plus	22365-22473
	402995	2996643	Minus	5962-6216
30	403005	5791501	Minus	16945-17053,20018-20403
	403020	6984114	Minus	96644-97021,97462-97868
	403029	7768593	Minus	44558-44766
	403047	3540153	Minus	59793-59968
	403073	8954241	Plus	142964-143260
35	403085	8954241	Plus	165035-165334,165420-165713
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403106	7331404	Plus	77162-77350,81338-81511
	403172	7464784	Minus	64007-64275
	403212	7630897	Minus	156037-156210
40	403214	7630945	Minus	76723-77027,79317-79484
	403277	8072597	Minus	27494-27642
	403331	8567936	Plus	169793-169966
	403344	8569726	Plus	70823-70990
	403362	8571772	Plus	64099-64260
45	403381	9438267	Minus	26009-26178
	403426	9719529	Minus	157156-158183
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403567	8101141	Plus	35349-35614
	403588	8101227	Minus	197672-197944
50	403590	8101229	Plus	405-1296
	403615	8567964	Plus	107671-107866
	403687	7387384	Plus	9009-9534
	403754	7229815	Minus	163899-164726
	403776	7770611	Minus	1414-1513,1624-1756
55	403822	9369510	Minus	142803-142922
	403851	7708872	Plus	22733-23007
	403860	7708960	Minus	95755-96045
	403894	7381715	Minus	1442-2224
	403903	7710671	Minus	101165-102597
60	403959	8224399	Minus	175363-177474
	404015	8655948	Minus	587821-588222
	404059	3548785	Plus	104326-106788
	404113	9588571	Minus	13446-13646
65	404148	9863703	Plus	78218-78418,79571-79709
	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404156	9886577	Plus	127319-127754
	404229	7159766	Plus	16607-16841
	404232	8218045	Minus	71800-71956
	404268	9711362	Plus	33239-33463
70	404274	9885189	Plus	104127-104318
	404288	2769644	Plus	3512-3691
	404290	2769644	Plus	36651-36813
	404336	9838028	Plus	157951-158129
	404403	7272157	Minus	72053-72238
75	404440	7528051	Plus	80430-81581
	404488	8113286	Minus	64835-64994
	404498	8151654	Plus	13292-13497

	404507	8151803	Plus	146359-146739
	404516	8151967	Plus	114153-114322
	404538	8247909	Minus	192748-192945
5	404594	9958262	Minus	15310-15510
	404639	9796778	Plus	5779-14387
	404653	9796999	Plus	164997-165230
	404676	9797204	Minus	56167-56342,58056-58189,58891-59048,60452-60628
	404684	9797403	Minus	110881-111020
10	404685	9797437	Minus	153217-153315,154043-154124,159185-159353,161290-161420,163544-163669,166127-166207,167654-167734
	404704	9800728	Minus	88841-89018
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
	404860	8979555	Plus	65852-65081
15	404874	9650523	Minus	96066-96192
	404881	5931510	Minus	36360-36608
	404894	6850447	Plus	102822-103127
	404939	6862697	Plus	175318-175476
	404977	3738341	Minus	43081-43229
20	405033	7107731	Minus	142358-142546
	405059	7656683	Plus	349-822
	405064	7658416	Plus	81207-81416
	405071	7708797	Minus	11115-11652
	405102	8076881	Minus	120922-121296
25	405167	9966316	Plus	43796-43981,48245-48427,54141-54317
	405170	9966524	Plus	37047-37198
	405177	7139696	Minus	118465-118663
	405186	7229793	Plus	161475-161581,162930-163067
	405258	7329310	Plus	129930-130076
30	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405308	3638954	Plus	40778-41034,41383-41573
	405349	2914717	Minus	85552-85806
	405379	6513908	Minus	22332-22473,24333-24439
35	405390	6606064	Minus	94007-94177
	405411	3451356	Minus	17503-17778,18021-18290
	405463	7715530	Minus	123097-123260
	405494	8050952	Minus	70284-70518
	405520	9454643	Plus	60849-60981
40	405526	9558556	Minus	132704-133277
	405580	4512267	Plus	169232-169547
	405600	5923640	Plus	26662-27225
	405654	4895155	Minus	53624-53759
	405720	9797144	Plus	13409-13861
45	405725	9838299	Minus	106417-106521
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
	405809	5304920	Minus	6655-6883,6687-8859
	405838	5686575	Plus	3460-3717
50	405863	7657810	Plus	49410-49620
	405867	6758731	Minus	74553-75173
	405906	7705124	Minus	10835-11059
	405920	6758795	Plus	120621-120971
	405968	8247789	Plus	14893-15148
55	406017	8272661	Minus	46271-46874
	406036	6758919	Plus	17942-18163
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406187	7289992	Plus	8044-8877
60	406243	7417725	Plus	38899-39369
	406270	7534217	Plus	13136-13591
	406320	9211754	Minus	20170-20511
	406322	9212102	Minus	130230-130418
	406360	9256107	Minus	7513-7673
65	406367	9256126	Minus	58313-58489
	406397	9256243	Minus	127317-127454
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
70	406471	9795566	Plus	87383-87589
	406475	9797684	Plus	125417-125563,128052-128180
	406485	7711305	Plus	125036-125422
	406511	7711412	Plus	177277-177384
	406588	8189273	Minus	135629-135848

TABLE 2A: 485 GENES UP-REGULATED IN BLADDER CANCER

5	Pkey:	Unique Eos probe/est identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of mRNA expression in bladder tumors compared to normal bladder			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	3.473
	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	2.279
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	3.052
15	435136	R27299	Hs.10172	ESTs	4.717
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	0.003
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	188.231
	421318	U63973	Hs.103501	rhodopsin kinase	1.381
20	421359	AK001589	Hs.103816	hypothetical protein FLJ10727	1.000
	459462	AA481396	Hs.105167	ESTs	1.000
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.000
	433227	AB040923	Hs.106808	kelch (Drosophila)-like 1	1.000
	421742	AW970004	Hs.107528	androgen induced protein	1.514
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.782
25	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	20.064
	451686	AA059246	Hs.110293	ESTs	0.033
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	56.751
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.512
	422119	AI277829	Hs.111862	KIAA0590 gene product	2.634
30	422170	AJ791949	Hs.112432	anti-Mullerian hormone	0.055
	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	0.008
	445958	BE326257	Hs.114536	ESTs	0.002
	434288	AW189075	Hs.116265	fibrillin3	11.401
	435347	AW014873	Hs.116963	ESTs	0.003
35	453134	AA032211	Hs.118493	ESTs	262.962
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	5.336
	436154	AA764950	Hs.119898	ESTs	103.154
	436246	AW450963	Hs.119991	ESTs	0.071
	436293	AJ601188	Hs.120910	ESTs	29.129
40	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	274.769
	438181	AW978608	Hs.122121	ESTs, Weakly similar to I38022 hypotheti	0.024
	449399	AA760881	Hs.122408	ESTs	1.000
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	4.314
	457465	AW301344	Hs.122908	DNA replication factor	0.264
45	409757	NM_001898	Hs.123114	cystatin SN	1.390
	439907	AA853978	Hs.124577	ESTs	0.010
	437181	AJ305615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.344
	440304	BE159984	Hs.125395	ESTs	0.025
50	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	0.014
	441495	AW294603	Hs.127039	ESTs	0.198
	435376	AW770956	Hs.127280	ESTs	0.008
	427685	AJ751124	Hs.127311	ESTs	3.244
	423349	AF010258	Hs.127428	homeo box A9	0.134
	445457	AF168793	Hs.12743	camitine O-octanoyltransferase	7.255
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.000
	441875	AI435973	Hs.128056	ESTs	0.013
	441940	AW298115	Hs.128152	ESTs	6.075
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	0.137
	429983	W92620	Hs.128656	ESTs	162.590
60	445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	0.959
	437553	AJ829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	9.163
	459204	AW194601	Hs.13219	ESTs	1.000
	439842	AJ910896	Hs.132413	ESTs	1.000
	443113	AJ040686	Hs.132908	ESTs	0.069
65	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.100
	420792	AA280321	Hs.13392	tethering factor SEC34	16.103
	427719	AJ393122	Hs.134726	ESTs	0.667
	443861	AW449462	Hs.134743	ESTs	5.100
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	1.691
70	445550	AI242754	Hs.137306	ESTs	0.006
	454284	AW297935	Hs.138493	ESTs, Moderately similar to ALU7_HUMAN A	0.003
	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	0.042
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.347
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.186
75	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	47.949
	426900	AW163564	Hs.142375	ESTs	0.404
	439337	AA448718	Hs.142505	ESTs	0.012

	427961	AW293165	Hs.143134	ESTs	0.073
	419888	AI243493	Hs.144049	ESTs	11.958
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	77.269
5	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	183.782
	445911	AI985587	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.362
	424395	AA165082	Hs.146388	microtubule-associated protein 7	203.038
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.808
	444517	AI939339	Hs.146883	ESTs	0.004
10	445020	AI205655	Hs.147221	ESTs	0.307
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.000
	445352	AI221087	Hs.147761	ESTs	0.015
	444444	AI149332	Hs.14855	ESTs	140.859
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	2.037
	446248	AI283014	Hs.149638	ESTs	0.018
15	433159	AB035898	Hs.150587	kinesin-like protein 2	0.110
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.179
	456840	H03754	Hs.152213	wingless-type MMTV integration site fami	0.005
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	1.111
20	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	257.949
	446082	AI274139	Hs.156452	ESTs	0.779
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	1.919
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	0.417
	447073	AW204821	Hs.157726	ESTs	10.349
25	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.839
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.691
	447475	AI380797	Hs.158992	ESTs	44.641
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	0.340
	418343	AA216372	Hs.159501	ESTs	0.023
30	441143	AI027604	Hs.159650	ESTs	0.280
	440917	AA909651	Hs.160025	ESTs	1.000
	418365	AW014345	Hs.161690	ESTs	0.066
	431839	AW020280	Hs.162025	ESTs	0.005
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	0.606
35	438817	AI023799	Hs.163242	ESTs	2.202
	432441	AW292425	Hs.163484	ESTs	2.305
	442577	AA292998	Hs.163900	ESTs	688.038
	435212	AW300100	Hs.164185	ESTs	0.002
	425048	H05468	Hs.164502	ESTs	0.083
40	442083	R50192	Hs.165062	ESTs	3.844
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	0.157
	418678	NM_001327	Hs.167379	cancer/testis antigen	269.487
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	0.208
	456967	AW004056	Hs.168357	T-box 2	160.397
45	447979	AI457197	Hs.170348	ESTs	0.016
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	1.036
	446312	BE087853	Hs.171802	ESTs, Weakly similar to T08729 RING zinc	1.334
	428783	Z19084	Hs.172210	MUF1 protein	1.654
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	154.064
50	409092	AI735283	Hs.172608	ESTs	0.007
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	0.009
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	0.002
	407581	R48402	Hs.173508	P3ECSL	0.866
	427239	BE270447	Hs.174070	ubiquitin carrier protein	15.708
55	427268	X78520	Hs.174139	chloride channel 3	207.938
	436577	W84774	Hs.17643	ESTs	62.333
	420876	AA918425	Hs.177744	ESTs	32.959
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	1.171
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.000
60	427747	AW411425	Hs.180655	serine/threonine kinase 12	12.446
	429813	AW139678	Hs.180791	ESTs	0.013
	439806	AA846824	Hs.180908	ESTs	0.561
	427878	C05766	Hs.181022	CGI-07 protein	0.002
	440284	AA912032	Hs.181059	ESTs, Weakly similar to Z108276A ssDNA-b	0.030
65	427922	AK001934	Hs.181112	HSPC126 protein	0.039
	427972	AA864870	Hs.181304	putative gene product	0.004
	428071	AF212848	Hs.182339	ets homologous factor	4.321
	428336	AA503115	Hs.183752	microseminoprotein, beta-	145.128
	428450	NM_014791	Hs.184339	KIAA0175 gene product	0.370
70	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	0.632
	438746	AI885815	Hs.184727	ESTs	0.339
	420557	AA960844	Hs.186579	Homo sapiens, clone IMAGE:4081483, mRNA	0.006
	431014	W67730	Hs.187573	ESTs	0.344
	428651	AF196478	Hs.188401	annexin A10	1.459
75	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.502
	432497	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	2.499
	431474	AL133990	Hs.190642	ESTs	0.044
	427742	AA411880	Hs.190888	ESTs	0.158

	428058	AI821625	Hs.191602	ESTs	0.006
	431245	AA496933	Hs.191687	ESTs	0.006
	453204	R10799	Hs.191990	ESTs	1.734
5	436608	AA626980	Hs.192371	down syndrome critical region protein DS	115.500
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	0.152
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	60.103
	449121	AI915858	Hs.194980	ESTs	0.003
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor I	305.974
10	438401	AL046321	Hs.197484	ESTs, Weakly similar to JC4295 ring finger	0.002
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.011
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3)	9.390
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	178.436
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	0.729
15	449818	AW594365	Hs.199365	ESTs	1.000
	429345	R11141	Hs.199695	hypothetical protein	7.339
	443564	AI921685	Hs.199713	ESTs	0.001
	449847	AW204447	Hs.199750	organic anion transporter polypeptide-re	1.000
	449351	AW016537	Hs.200760	ESTs	0.005
20	426322	J05058	Hs.2012	transcobalamin I (vitamin B12 binding pr	381.474
	434411	AA632649	Hs.201372	ESTs	0.039
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.337
	446555	AV659046	Hs.201847	ESTs	0.024
	450411	D61167	Hs.202156	ESTs	0.004
25	442282	AW451086	Hs.202390	ESTs	1.000
	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	228.705
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	0.133
	426682	AV660038	Hs.2055	UDP glycosyltransferase 1 family, polype	2.070
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotid	0.528
30	448275	BE514434	Hs.20830	kinesin-like 2	19.718
	459058	H85939	Hs.209605	EST	0.005
	441795	N58115	Hs.21137	AD024 protein	1.000
	451592	AI805416	Hs.213897	ESTs	0.012
	443357	AW071349	Hs.215937	ESTs	0.003
35	415949	H10582	Hs.21691	ESTs	0.072
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	213.962
	432548	AW973399	Hs.22133	hypothetical protein FLJ20121	0.250
	427857	NM_005073	Hs.2217	solute carrier family 15 (oligopeptide t	0.010
	453123	AI953718	Hs.221849	ESTs	0.566
40	439569	AW602166	Hs.222399	CEGP1 protein	10.625
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	27.603
	435956	AF269255	Hs.22604	lysosomal apyrase-like protein 1	127.564
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcription	2.216
	431253	R06428	Hs.226351	ESTs	0.023
45	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.103
	430034	X60155	Hs.227767	zinc finger protein 41	1.000
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	0.024
	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	1.635
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	120.167
50	452956	AW003578	Hs.231872	ESTs	1.000
	446009	AI989885	Hs.231926	ESTs	4.000
	430499	AW969408	Hs.231991	ESTs	0.014
	448560	BE613183	Hs.23213	ESTs	285.090
	441508	AW015203	Hs.232237	ESTs	0.261
55	453228	AW628325	Hs.232327	ESTs	1.000
	442167	H18740	Hs.23248	hypothetical protein from EUROIMAGE 2005	0.240
	453321	AI984381	Hs.232521	ESTs	0.609
	449207	AL044222	Hs.23255	nucleoporin 155kD	0.551
	430152	AB001325	Hs.234642	aquaporin 3	1.040
60	439239	AI031540	Hs.235331	ESTs	0.598
	435087	AW975241	Hs.23567	ESTs	0.007
	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 (Hsa	0.012
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.280
	431011	AA490631	Hs.23783	ESTs	0.016
65	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	284.526
	444371	BE540274	Hs.239	forkhead box M1	3.691
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.255
	449722	BE280074	Hs.23960	cyclin B1	0.467
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	13.419
70	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.192
	452292	AW139588	Hs.244369	ESTs	1.000
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.500
	456682	AW500321	Hs.246766	Homo sapiens cDNA FLJ12350 fis, clone MA	0.014
75	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	0.233
	430978	U53583	Hs.248182	olfactory receptor, family 1, subfamily	1.000
	431020	AF097874	Hs.248226	caspase 14, apoptosis-related cysteine p	5.666
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.838
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	0.004

	454170	AW177225	Hs.250158	ESTs	0.243
	439223	AW238299	Hs.250618	UL16 binding protein 2	0.516
	438081	H49546	Hs.251391	claudin 16	0.080
5	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	843.974
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	5.928
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.000
	413094	H24184	Hs.25413	TOLLIP protein	268.885
	450796	NM_001988	Hs.25482	envoplakin	1.643
10	408827	AW275730	Hs.254825	ESTs	0.008
	444129	AW294292	Hs.256212	ESTs	0.002
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.240
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	0.679
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	260.231
15	453459	BE047032	Hs.257789	ESTs	2.133
	456535	AW135986	Hs.257859	ESTs	98.795
	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	1.882
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	0.012
	430634	AI860651	Hs.26685	calyphosine	9.561
20	435562	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	0.957
	417964	R71449	Hs.268760	ESTs	0.004
	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	1.324
	431846	BE019924	Hs.271580	uropolakin 18	303.679
	453074	AA031813	Hs.271880	ESTs	0.004
25	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.828
	435182	AA669386	Hs.272035	ESTs, Weakly similar to gonadotropin ind	0.013
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	8.978
	432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	0.316
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	0.014
30	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	26.348
	423031	AI278955	Hs.27457	ESTs	53.288
	455612	BE042896	Hs.274848	ESTs	21.013
	452046	AB018345	Hs.27657	KIAA0802 protein	129.013
	436567	AI492860	Hs.276904	ESTs	0.007
35	459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	0.031
	430157	BE348706	Hs.278543	ESTs	99.244
	452012	AA307703	Hs.279766	kinesin family member 4A	0.408
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.721
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	38.231
40	450020	AI680684	Hs.282219	ESTs	0.003
	435858	AF254260	Hs.283009	tufellin 1	1.516
	430733	AW975920	Hs.283361	ESTs	1.000
	446024	AB040946	Hs.284227	KIAA1513 protein	9.424
	433967	AF113018	Hs.284302	PRO1621 protein	0.008
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	0.030
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.058
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	273.013
	432097	X51730	Hs.2905	progesterone receptor	0.002
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	4.010
50	457733	AW974812	Hs.291971	ESTs	1.000
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	1.000
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	0.006
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	0.003
	433365	AF026944	Hs.293797	ESTs	0.049
55	417151	AA194055	Hs.293858	ESTs	6.593
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	1.656
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	17.094
	422424	AI186431	Hs.296638	prostate differentiation factor	2.646
	432410	X68561	Hs.2982	Sp4 transcription factor	0.007
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.005
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	0.488
	452142	AB028947	Hs.301654	KIAA1024 protein	0.009
	449773	R76294	Hs.302383	ESTs	0.001
	438366	AA805760	Hs.303567	ESTs	1.000
65	452724	R84810	Hs.30464	cyclin E2	1.000
	429343	AK000785	Hs.307036	Homo sapiens, Similar to epsin 3, clone	0.494
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	0.022
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H29H_HUMAN HISTO	16.744
	432789	D26361	Hs.3104	KIAA0042 gene product	0.302
70	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	0.001
	453028	AB006532	Hs.31442	RecQ protein-like 4	13.392
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.766
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	553.782
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp568G0321 (f	84.115
75	443247	BE614387	Hs.333893	c-Myc target JPO1	79.385
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	337.474
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	0.842
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	402.500

	433958	AW043909	Hs.334707	aminoacylase 1	191.179
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	313.462
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	21.744
5	451359	H85334	Hs.336623	ESTs	0.038
	440249	AI246590	Hs.337275	ESTs	0.432
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	1.102
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	0.483
	447519	U46258	Hs.339655	ESTs	1.032
10	434192	AW387314	Hs.34371	ESTs	0.003
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	0.056
	441020	W79283	Hs.35982	ESTs	75.141
	453884	AA355925	Hs.36232	KIAA0186 gene product	0.138
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	0.008
15	453945	NM_005171	Hs.36908	activating transcription factor 1	0.044
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	0.002
	407626	U39196	Hs.37169	potassium inwardly-rectifying channel, s	0.009
	423620	N71320	Hs.39938	ESTs	1.000
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	0.042
20	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	1.810
	443133	AI033878	Hs.41379	ESTs	0.534
	434534	H90477	Hs.41407	ESTs	0.013
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.679
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.885
25	432237	AK001926	Hs.44143	polybromo 1	0.010
	420900	AL045633	Hs.44269	ESTs	10.436
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	3.393
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	386.256
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	0.922
30	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.003
	435647	AI853240	Hs.49823	ESTs	175.910
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.584
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	0.610
	455506	AA703584	Hs.5105	hypothetical protein FLJ10569	0.008
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.089
	409287	AL080213	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	16.910
	435047	AA454985	Hs.54973	cadherin-like protein VR20	0.612
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.938
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	1.000
40	439482	W70045	Hs.58089	ESTs	0.118
	439606	W79123	Hs.58561	G protein-coupled receptor 87	0.095
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.055
	452240	AI591147	Hs.61232	ESTs	0.221
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	2.595
45	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.677
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	7.587
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	0.046
	438779	NM_003787	Hs.6414	nucleolar protein 4	0.030
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.016
50	440126	AA975145	Hs.66194	ESTs	0.008
	451291	R39288	Hs.6702	ESTs	0.012
	439953	AW247529	Hs.6793	platelet-activating factor acetylhydrola	1.653
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	8.628
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	140.908
55	418107	R41726	Hs.7284	ESTs	0.146
	436326	BE085236	Hs.75313	aldo-keto reductase family 1, member B1	0.649
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	0.237
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.242
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	0.202
60	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	2.318
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.622
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	245.564
	451575	AA767622	Hs.78893	KIAA0244 protein	1.000
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.552
65	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	5.128
	458921	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	0.246
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	7.249
	440371	BE268550	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.792
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	360.782
70	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	60.590
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	9.988
	417312	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (402.705
	417389	BE260954	Hs.82045	midkine (neurite growth-promoting factor	10.806
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	1.051
75	438315	R56795	Hs.82419	ESTs	0.226
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	26.260
	417933	X02308	Hs.82962	thymidylate synthetase	221.090
	418067	AI127958	Hs.83393	cystatin E/M	2.396

	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.000
	418205	L21715	Hs.83760	troponin I, skeletal, fast	0.159
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.490
5	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.527
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.077
	458027	L49054	Hs.85195	myeloid leukemia factor 1	0.008
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.813
	418583	AA604379	Hs.86211	hypothetical protein	125.769
10	441801	AW242799	Hs.86366	ESTs	55.026
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	8.139
	407246	S70348	Hs.87149	integrin, beta 3 (platelet glycoprotein	0.020
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	313.141
	445060	AA830811	Hs.88808	ESTs	1.000
15	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	137.718
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	0.006
	401464	AF039241	Hs.9028	histone deacetylase 5	6.846
	443162	T49951	Hs.9029	DKFZP434G032 protein	14.057
	431024	AA713666	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.507
20	419559	Y07828	Hs.91096	ring finger protein	0.025
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	684.577
	443426	AF088158	Hs.9329	chromosome 20 open reading frame 1	0.363
	424457	AI249036	Hs.94292	hypothetical protein FLJ23311	175.667
	410348	AW182663	Hs.95469	ESTs	0.011
25	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	428.231
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	0.005
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	1.168
	426902	AI126334	Hs.97408	ESTs	37.457
	444874	AI218496	Hs.97515	BRCA1-Interacting protein 1; BRCA1-assoc	0.067
30	427356	AW023482	Hs.97849	ESTs	1.000
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	0.812
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	0.342
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	19.785
	421934	AA300625		gb:EST13476 Testis tumor Homo sapiens cD	103.769
35	413322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.258
	424040	AA334400		gb:EST38610 Embryo, 9 week Homo sapiens	0.011
	433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	0.023
	458829	AI557388		gb:PT2.1_6_G03.r.tumor2 Homo sapiens cDN	1.000
	459169	AI905517		gb:RC-BT091-210199-105 BT091 Homo sapien	0.773
40	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	468.462
	440012	AA861072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	0.002
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	0.010
	412964	BE019688		gb:bb28g08.x1 NIH_MGC_5 Homo sapiens cDN	0.003
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	0.005
45	414969	C16195		gb:C16195 Clontech human aorta polyA mRN	0.023
	413158	BE068098		gb:CM1-BT0368-061299-060-c09 BT0368 Homo	0.007
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.994
	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	0.004
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	0.037
50	415204	T27434		gb:hbc2294 Human pancreatic islet Homo s	76.500
	434572	AF147340		gb:Homo sapiens full length Insert cDNA	0.030
	438990	AF085890		gb:Homo sapiens full length Insert cDNA	1.000
	439780	AL109688		gb:Homo sapiens mRNA full length Insert	0.256
	413671	Z43712		gb:HSC1JA121 normalized infant brain cDN	0.009
55	406974	M57293		gb:Human parathyroid hormone-related pep	0.004
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.616
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	0.413
	432189	AA527941		gb:bnh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	0.015
	443309	AI821874		gb:nl58f10.x5 NCI_CGAP_Pr3 Homo sapiens	0.007
60	437240	AA747537		gb:rx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	0.006
	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	0.059
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	394.282
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	0.757
	454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.000
65	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	0.013
	455380	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	0.249
	455650	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1.000
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1.000
	413100	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314 Homo	271.372
70	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	0.002
	455831	BE144956		gb:RC6-HT0187-201099-031-c04 HT0187 Homo	0.011
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	293.654
	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.807
	409488	AW402825		gb:UI-HF-BK0-aaq-d-08-0-UI.r1 NIH_MGC_36	0.965
75	437938	AI950087		gb:wxq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.952
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	7.341
	449325	AA001162		gb:ze48b06.r1 Soares retina N2b4HR Homo	0.004
	413316	W91931		gb:zh47c01.r1 Soares_fetal_liver_spleen_	0.004

	401016	0.342
	401335	0.256
	401555	1.000
5	401760	301.372
	401781	247.141
	401961	1.722
	402239	5.180
	402305	0.917
10	402424	551.141
	402777	153.231
	402778	0.006
	402837	0.367
	402948	154.103
	402952	17.038
15	403142	0.196
	403297	12.744
	403637	0.304
	403657	0.032
20	404136	0.008
	404249	0.065
	404875	1.105
	404917	69.590
	404983	1.000
	405238	1.000
25	405364	294.141
	405531	1.747
	405601	145.551
	405621	0.224
30	405932	1.968
	406117	0.333
	406354	1.000
	406548	0.002
	406599	0.010
35	459702 AI204995	0.449

TABLE 2B

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
45	409488	1134791_1 AW402825 BE544338
	412799	132817_1 AI267606 AA121045 AA126521
	412964	1339278_1 BE019688 BE144460
	413100	1349119_1 BE065208 BE065224 BE065168 BE065313
	413158	1351251_1 BE068098 BE068119 BE068083 BE068088 BE068120 BE068155 BE068111
	413316	1360169_1 W91931 W94979 BE081744
50	413671	1382504_1 Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
	414221	142696_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	414969	1510393_1 BE011368 BE011362 BE011215 BE011365 BE011363
	415204	1529407_1 C16195 C16230 C16211 C16164 C16251
55	421934	209339_1 T27434 Z25288 F00323 D82802 R85077
	424040	234659_1 AA300625 R16859 R16860 AW898335 W24337
	428436	291472_1 AA334400 AA334257 AW966124
	431322	331543_1 BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743
60	432189	342819_1 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
	433005	357346_1 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	433108	35898_1 AA527941 AI810608 AI620190 AA635266
	434414	38585_1 AW939074 AW939073 BE160476 AW939938 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
	434572	38911_1 AB002446 T03146
65	436383	41888_1 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
	437240	435139_1 AW875541 AW814172 H66214 AW814388 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
	437938	44573_2 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
		AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
		AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
		AW817705 AW817703 AW817659 BE081531 H59570
70	437938	44573_2 AF147340 T51948 T52029
		BE065178 AJ227879
		AA747537 BE089068 BE089070
		AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
75		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI695062
		AA282915 AI102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103913 AI539642
		AA642789 AA856975 AW505512 AI961530 AW529970 BE612881 AW276997 AW513501 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205882 AI683338 AI858509 AW276905 AI633005 AA972584 AA908741 AW072629 AW513995

		AA293273 AA969759 N75628 N22388 HB4729 H50052 T92487 AJ022058 AA780419 AA551005 W80701 AW613456 AJ373032 AI564269 F00531 HB3488 W37181 W78802 R66056 AJ002839 R67840 AA300207 AW959581 T63226 F04005
5	438990	45760_1 AF085890 H29949 H29856
	439780	47673_1 AL109688 R23665 R26578
	440012	483290_1 AA861072 H02819 R25946
	443309	56604_1 AI821874 AI821868 AA630932 AA653897 AA650103 AI821131 AI821124
	444163	593658_1 AI126098 AI184746 AI148521
	449325	80480_1 AA001162 AA018950 AA017505 R84446
10	451385	85787_1 AA017656 AA017374 AA019761
	453823	982526_1 AL137967 BE064160 BE064186
	453846	983043_1 AL157586 AL157590
	454789	1234742_1 BE156314 BE156316 AW820750
	455170	1256906_1 AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455189	1259271_1 AW864176 AW864133 AW864185 AW864137
15	455380	1287679_1 BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	455650	1348720_1 BE064655 BE153953
	455797	1366826_1 BE091833 BE091874 BE091871
	455807	1370914_1 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
20	455831	1373969_1 BE144966 BE144957 BE144958
	458829	773443_1 AI557388 BE158936
	459169	920641_1 AI905517 AI905455 AI905452

TABLE 2C

25	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
30	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
35	401016	8117441	Plus	126234-126359,128050-128236
	401335	9884881	Plus	15736-16352
	401555	8099284	Minus	162520-162657
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
40	401961	4581193	Minus	124054-124209
	402239	7690131	Plus	38175-38304,42133-42266
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
45	402837	9369121	Minus	2013-2186,9570-9758,11138-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
	402948	9368458	Minus	143456-143626,143808-143935
	402952	9408724	Minus	119452-119619
	403142	9444521	Plus	89286-90131
50	403297	8096824	Minus	16584-17264
	403637	8671936	Minus	142647-142771,145531-145762
	403657	8843996	Minus	158223-156370
	404136	6981900	Minus	42538-46428
	404249	8655533	Plus	64270-64633
55	404875	9801324	Plus	96588-96732,97722-97831
	404917	7341851	Plus	49330-49498
	404983	4432779	Minus	51178-51374,52000-52173
	405238	7249119	Minus	51728-51836
	405364	2281075	Minus	48325-48491,49136-49252
	405531	9665194	Plus	35602-35803
60	405601	5815493	Minus	147835-147935,149220-149299
	405621	5523811	Plus	59362-59607
	405932	7767812	Minus	123525-123713
	406117	9142932	Plus	54304-54584
65	406354	9256049	Minus	2095-2377
	406548	7711514	Minus	25138-26762
	406599	8248616	Plus	10933-11086

Table 3A: Preferred therapeutic targets for bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of bladder tumor Als divided by the 90th percentile of normal bladder sample Als			
10	R2:	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	421948	L42583	Hs.334309	keratin 6A	14.20 1.20
	439926	AW014875	Hs.137007	ESTs	11.31 21.34
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15 45.75
	421110	AJ250717	Hs.1355	cathepsin E	9.07 45.35
20	417308	H60720	Hs.81892	KIAA0101 gene product	8.50 1.99
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	8.39 1.28
	418406	X73501	Hs.84905	cytokeratin 20	8.10 40.50
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98 1.38
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67 2.12
25	408243	Y00787	Hs.624	interleukin 8	7.56 4.85
	417715	AW969587	Hs.85366	ESTs	7.45 4.70
	417720	AA205625	Hs.208067	ESTs	7.34 9.18
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	7.30 26.07
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12 35.60
30	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	6.95 4.96
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42 0.89
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.08 3.49
	407242	M18728		gb:Human nonspecific crossreacting anti	5.96 0.96
	405033			C1002652*:gij544327[sp]Q04799JFMO5_RABIT	5.84 16.22
35	448230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.82 2.28
	406685	M18728		gb:Human nonspecific crossreacting anti	5.80 0.89
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	5.77 28.85
	415511	AI732617	Hs.182362	ESTs	5.65 28.25
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60 6.51
40	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.59 2.33
	428651	AF196478	Hs.188401	annexin A10	5.55 27.75
	400843			NM_003105*:Homo sapiens sortilin-related	5.51 4.92
	402230			Target Exon	5.36 21.44
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.33 2.80
45	415065	BE267931	Hs.78996	proliferating cell nuclear antigen	5.17 1.98
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.90 2.63
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.77 2.35
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	4.77 3.71
	418663	AK001100	Hs.41690	desmocollin 3	4.74 1.48
50	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.74 2.92
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68 1.61
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65 11.63
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.63 2.06
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55 3.35
55	401780			NM_005557*:Homo sapiens keratin 16 (foca	4.49 1.62
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43 2.39
	401093			C12000586*:gij6330167[dbj]BAAB8477.1) (A	4.40 12.94
	417933	X02308	Hs.82962	thymidylate synthetase	4.35 2.29
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.32 2.82
60	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklins	4.24 8.15
	401781			Target Exon	4.15 1.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	4.14 7.39
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.12 2.51
	408380	AF123050	Hs.44532	diubiquitin	4.11 3.26
65	449722	BE280074	Hs.23960	cyclin B1	4.09 3.72
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07 2.50
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00 7.14
	404977			Insulin-like growth factor 2 (somatomedi	3.89 5.17
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.88 7.29
70	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87 1.61
	444371	BE540274	Hs.239	forkhead box M1	3.87 2.75
	443171	BE281128	Hs.9030	TONDU	3.83 9.48
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	3.82 2.98
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.77 3.83
75	407137	T97307		gbye53h05.s1 Soares fetal liver spleen	3.73 4.91
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68 7.08
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.68 2.29
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67 3.06
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67 1.18
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.67 3.65
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.66 3.21

	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.66	3.57
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	3.62	2.73
	441495	AW294603	Hs.127039	ESTs	3.60	2.71
5	422282	AF019225	Hs.114309	apolipoprotein L	3.57	3.92
	417079	U85590	Hs.81134	interleukin 1 receptor antagonist	3.55	0.80
	417275	X63578	Hs.295449	parvalbumin	3.54	4.60
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.52	2.59
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.61
10	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	17.50
	404875			NM_022819:Homo sapiens phospholipase A2	3.46	3.24
	420005	AW271106	Hs.133294	ESTs	3.40	2.22
	409757	NM_001898	Hs.123114	cystatin SN	3.39	2.93
	427719	AJ393122	Hs.134726	ESTs	3.31	2.51
15	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.28	0.42
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.28	2.62
	406081			Target Exon	3.25	13.54
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.25	2.46
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.23	2.88
20	429983	W92620	Hs.260855	ESTs	3.20	2.84
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.18	1.54
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	3.17	5.44
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	3.13	15.65
	415752	BE314524	Hs.78776	putative transmembrane protein	3.11	2.46
25	408633	AW963372	Hs.46677	PRO2000 protein	3.11	3.30
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.09	1.52
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.08	2.22
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.05	12.49
	437931	AI249468	Hs.124434	ESTs	3.01	3.70
30	421451	AA291377	Hs.50831	ESTs	2.99	14.95
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.97	2.10
	402239			Target Exon	2.97	3.37
	429345	R11141	Hs.199695	hypothetical protein	2.96	2.61
35	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.93	2.13
	423961	D13666	Hs.136348	periostin (OSF-2os)	2.93	1.44
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.92	0.95
	436608	AA628980	Hs.236894	down syndrome critical region protein DS	2.92	4.86
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.88	2.93
	439223	AW238299	Hs.250618	UL16 binding protein 2	2.88	2.15
40	401747			Homo sapiens keratin 17 (KRT17)	2.88	3.44
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.86	14.30
	444444	AI149332	Hs.14855	ESTs	2.85	2.68
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	2.84	2.46
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.78	2.26
45	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.77	2.34
	442994	AI026718	Hs.16954	ESTs	2.75	2.82
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.74	2.44
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.72	3.37
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.69	2.70
50	404440			NM_021048:Homo sapiens melanoma antigen,	2.69	13.45
	400844			NM_003105:Homo sapiens soritin-related	2.69	13.45
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.69	1.36
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.69	12.08
	403381			ENSP00000231844:Ecotropic virus integra	2.68	13.40
55	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.68	2.43
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.67	2.68
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.67	1.79
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	2.65	0.73
	413281	AA861271	Hs.222024	transcription factor BMAL2	2.65	2.23
60	446082	AI274139	Hs.156452	ESTs	2.65	2.65
	422424	AI186431	Hs.296538	prostate differentiation factor	2.64	2.68
	407839	AA045144	Hs.161566	ESTs	2.64	1.08
	432441	AW292425	Hs.163484	ESTs	2.64	6.14
	417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (2.64	1.31
65	430157	BE348706	Hs.278543	ESTs	2.63	2.58
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.61	1.93
	418686	Z36830	Hs.87268	annexin A8	2.60	1.62
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.59	2.87
70	429276	AF055085	Hs.198612	G protein-coupled receptor 51	2.57	3.89
	439738	BE246502	Hs.9598	sema domain, Immunoglobulin domain (Ig),	2.57	2.49
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	2.56	1.43
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.54	3.10
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.51	3.60
75	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.50	2.91
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.49	1.78
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.49	1.80
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.49	3.46
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.48	2.36

5	418941	AA452970	Hs.239527	E18-55kDa-associated protein 5	2.46	2.33
	414807	AI738816	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.44	2.49
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.43	1.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.41	2.05
	449019	AI949095	Hs.57776	ESTs, Weakly similar to T22341 hypotheti	2.40	1.90
10	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.40	0.49
	420370	Y13645	Hs.97234	uroplakin 2	2.39	3.81
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	2.38	1.45
	406399			NM_003122*:Homo sapiens serine protease	2.36	4.20
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.31	4.05
15	442117	AW654964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.31	1.17
	436246	AW450963	Hs.119991	ESTs	2.30	11.50
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.30	2.40
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.29	1.89
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.28	2.14
20	432829	W60377	Hs.57772	ESTs	2.28	4.85
	415025	AW207091	Hs.72307	ESTs	2.28	11.40
	436293	AI601188	Hs.120910	ESTs	2.27	3.80
	415989	AI267700		ESTs	2.27	11.35
	418067	AI127958	Hs.83393	cystatin EM	2.25	1.54
25	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.25	2.45
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.25	1.55
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	2.22	11.10
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.21	1.32
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.21	1.52
30	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	2.20	1.55
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.19	1.99
	423271	W47225	Hs.126256	interleukin 1, beta	2.19	2.01
	420305			C19000735*:gi4508027[ref]NP_003414.1] z	2.19	2.54
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.19	2.16
35	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.18	1.80
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.17	10.85
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	2.17	2.14
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	2.16	1.37
	407581	R48402	Hs.173508	P3EC5L	2.15	1.95
40	400845			NM_003105*:Homo sapiens sortilin-related	2.15	2.23
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.14	1.70
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.13	1.83
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.13	3.49
	453459	BE047032	Hs.257789	ESTs	2.13	2.30
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	2.12	10.60
	436251	BE515065	Hs.295585	nucleolar protein (KKE/D repeat)	2.11	1.89
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.11	2.57
	420876	AA918425	Hs.177744	ESTs	2.09	2.30
	438817	AJ023799	Hs.163242	ESTs	2.09	10.45
50	434293	NM_004445	Hs.3796	EphB6	2.08	2.42
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.08	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	2.08	4.62
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	2.08	10.40
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	2.05	5.39
55	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	1.20
	400773			NM_003105*:Homo sapiens sortilin-related	2.05	1.78
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.04	2.06
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.04	1.70
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.03	2.26
60	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	2.02	1.73
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.02	2.93
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	2.02	1.55
	441801	AW242799	Hs.86366	ESTs	2.01	10.05
	439780	AL109588		gb:Homo sapiens mRNA full length insert	2.00	10.00
65	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.00	1.53
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.00	1.91
	430152	AB001325	Hs.234642	aquaporin 3	1.99	1.74
	453134	AA032211	Hs.118493	ESTs	1.99	3.16
	412719	AW016610	Hs.816	ESTs	1.99	0.34
70	442577	AA292998	Hs.163900	ESTs	1.99	3.09
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.98	1.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.97	1.84
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.95	1.42
	447334	AA515032	Hs.91109	ESTs	1.95	2.53
75	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (I	1.94	9.70
	429002	AW248439	Hs.2340	junction plakoglobin	1.94	1.57
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.94	2.02
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.93	0.56
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	1.92	1.01
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.92	1.47
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.92	1.59

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.92	2.77
	424522	AL134847	Hs.149957	ribosomal protein S6 kinase, 90kD, polyp	1.92	1.21
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.92	1.72
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.91	1.41
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	1.90	1.61
10	400846			sortilin-related receptor, L(DLR class)	1.90	1.93
	417409	BE272506	Hs.82109	syndecan 1	1.89	1.75
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.88	1.16
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.88	3.09
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.88	1.18
15	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.87	2.01
	431347	AI133461	Hs.251664	Insulin-like growth factor 2 (somatomedi	1.86	1.87
	430168	AW968343	Hs.24255	DKFZP4341735 protein	1.86	2.11
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.86	1.77
	402901			NM_025206: Homo sapiens hypothetical pro	1.85	2.35
20	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.85	1.59
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.84	1.90
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.84	1.03
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.84	1.54
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.83	1.74
25	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.82	1.84
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.82	1.83
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.82	1.74
	402424			NM_024901: Homo sapiens hypothetical prot	1.81	1.61
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	1.81	3.67
30	431846	BE019924	Hs.271580	uroplakin 1B	1.80	4.11
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.80	9.00
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.80	1.02
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.80	2.26
	451541	BE279383	Hs.26557	plakophilin 3	1.79	1.16
35	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	1.79	5.59
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.79	8.95
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.79	2.08
	437852	BE001836	Hs.256897	ESTs, Weakly similar to DJ365012.1 [H.s.	1.77	2.96
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	1.76	1.43
40	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.76	8.80
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.76	0.57
	430890	X54232	Hs.2699	glypican 1	1.73	1.39
	452862	AW378065	Hs.8687	ESTs	1.73	1.99
	427335	AA448542	Hs.251677	G antigen 7B	1.73	8.65
45	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.72	2.07
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.72	1.65
	426484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	1.72	1.03
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.71	1.66
	448993	AJ471630	Hs.8127	KIAA0144 gene product	1.71	1.52
50	422406	AF025441	Hs.116206	Opa-interacting protein 5	1.71	5.52
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.71	8.55
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.71	8.55
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.71	8.55
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.71	13.98
55	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.70	1.84
	414053	BE391635	Hs.75725	transgelin 2	1.69	1.51
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.69	8.45
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	1.69	1.60
	448262	AW880830	Hs.186273	ESTs	1.67	2.07
60	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.66	0.70
	452240	AI591147	Hs.61232	ESTs	1.66	1.23
	417151	AA194055	Hs.293858	ESTs	1.65	2.08
	452461	N78223	Hs.108106	transcription factor	1.65	8.25
	418462	BE001596	Hs.85266	Integrin, beta 4	1.65	1.78
65	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.64	1.59
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	1.64	1.13
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.63	1.81
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	1.62	1.51
	402777			C1002652: gij544327spjQ04799jFMO5_RABIT	1.62	2.33
70	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	1.62	2.18
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.62	1.27
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	1.61	2.05
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.60	1.78
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.60	1.63
75	437016	AU076916	Hs.5398	guanine monophosphate synthetase	1.59	1.50
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	1.58	1.92
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.57	1.79
	408908	BE296227	Hs.250822	serine/threonine kinase 15	1.56	7.80
	433159	AB035898	Hs.150587	kinesin-like protein 2	1.56	7.80
	443211	AI128388	Hs.143655	ESTs	1.56	7.80
	408893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.55	1.44

	426900	AW163564	Hs.142375	ESTs	1.54	1.93
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mito	1.54	1.71
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	1.53	1.55
5	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.53	1.59
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), aci	1.52	7.60
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	1.49	0.52
	418543	NM_005329	Hs.85952	hyaluronan synthase 3	1.48	1.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.48	1.39
10	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.47	1.48
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	1.47	7.35
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.47	1.37
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.46	1.80
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.45	1.58
15	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.45	1.58
	445182	AW189787		ESTs	1.43	7.15
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.43	1.53
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.43	1.34
	406467			Target Exon	1.42	7.10
20	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.42	1.32
	422094	AF129535	Hs.272027	F-box only protein 5	1.41	4.55
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.39	10.36
	401760			Target Exon	1.37	1.16
25	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.36	1.39
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.33	1.49
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.31	1.44
	422119	AI277829	Hs.111862	KIAA0590 gene product	1.31	1.22
	418729	AB028449	Hs.87889	helicase-mol	1.30	0.84
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.30	1.32
30	453028	AB006532	Hs.31442	RecQ protein-like 4	1.29	1.42
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.29	0.61
	453321	AI984381	Hs.232521	ESTs	1.27	6.35
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.26	6.30
	425726	AF085808	Hs.159330	uropodkin 3	1.26	2.26
35	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.26	1.11
	429413	NM_014058	Hs.201877	DESC1 protein	1.25	1.01
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.23	1.17
	41840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.22	1.59
	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	1.20	1.38
40	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.19	1.23
	403903			C5001632:gil10645308[gb]AAG21430.1 AC00	1.19	1.98
	425721	AC002115	Hs.159309	uropodkin 1A	1.17	2.30
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	1.17	5.85
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.17	1.39
45	443859	NM_013409	Hs.9914	folistatin	1.17	1.17
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.13	2.83
	422330	D30783	Hs.115263	epiregulin	1.13	5.65
	420281	AI623693	Hs.323494	Predicted cation efflux pump	1.11	5.55
	424717	H03754	Hs.152213	wingless-type MMTV Integration site fami	1.08	5.40
50	440304	BE159984	Hs.125395	ESTs	1.06	5.30
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.06	1.55
	417599	AA204688	Hs.62954	ESTs	1.05	1.02
	411874	AA096106	Hs.20403	ESTs	1.04	7.20
	449961	AW265634	Hs.133100	ESTs	1.03	0.65
55	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.03	0.92
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	1.02	5.10
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.02	0.60
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1.00	0.05
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.00	0.25
60	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	1.00	0.25
	439239	AI031540	Hs.235331	ESTs	1.00	0.27
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	0.45
	425650	NM_001944	Hs.1925	desmoglein 3 (pamphigus vulgaris antigen	1.00	0.72
	404403			Target Exon	1.00	1.00
65	406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00	1.00
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
	426320	W47595	Hs.169300	transforming growth factor, beta 2	1.00	1.00
70	426958	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	1.00	1.00
	432097	X51730	Hs.2905	progesterone receptor	1.00	1.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	1.00
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	1.25
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	1.00	1.35
75	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.75
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.80
	415178	D80503	Hs.322850	ESTs	1.00	2.20

5	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	2.25
	425048	H05468	Hs.164502	ESTs	1.00	2.25
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	1.00	2.60
	449448	D60730	Hs.57471	ESTs	1.00	2.70
	417791	AW965339	Hs.111471	ESTs	1.00	2.95
	421373	AA808229	Hs.167771	ESTs	1.00	3.00
	427366	AW023482	Hs.97849	ESTs	1.00	3.15
	421070	AA283185	Hs.19327	ESTs	1.00	3.25
10	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00	3.35
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	1.00	3.55
	402075			ENSP00000251056*:Plasma membrane calcium	1.00	3.95
	419559	Y07828	Hs.91096	ring finger protein	1.00	4.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.00	4.00
	418738	AW388633	Hs.6582	solute carrier family 7, (cationic amino	1.00	4.35
15	412723	AA648459	Hs.335951	hypothetical protein AF301222	1.00	4.40
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	4.45
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	4.45
	403047			NM_005656*:Homo sapiens transmembrane pr	1.00	4.50
	406434			NM_030579*:Homo sapiens cytochrome b5 ou	1.00	4.65
20	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	1.00	4.65
	433365	AF026944	Hs.293797	ESTs	1.00	10.05
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	0.99	0.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.99	1.00
	431474	AL133990	Hs.190642	CEGP1 protein	0.94	9.14
25	411880	AW872477		gb:hm3003.x1 NCI_CGAP_Thy4 Homo sapiens	0.93	21.15
	414221	AW450979		gb:UL-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.91	2.60
	444649	AW207523	Hs.197628	ESTs	0.89	11.15
	456034	AW450979		gb:UL-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.89	5.13
30	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	0.84	0.85
	439569	AW602166	Hs.222399	CEGP1 protein	0.84	2.42
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.81	6.75
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.80	0.57
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	0.77	1.40
35	431089	BE041395		ESTs, Weakly similar to unknown protein	0.76	14.88
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.74	11.03
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.56	0.80
	406964	M21305		gb:Human alpha satellite and satellite 3	0.53	11.16
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.48	3.01
40	400288	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	0.40	0.70
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.40	0.61

TABLE 3B

45	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
50	Pkey	CAT Number
	411880	1263110_1
	413804	1390710_1
	414221	142696_1
55	415989	156454_1
	431089	327825_1
	431322	331543_1
	432222	343347_1
	435608	42361_3
60	439780	47673_1
	444163	593658_1
	445182	632151_1
	451844	888230_1
65	456034	142696_1
		Accession
		AW872477 BE088101 T05990
		T64682 BE168190 BE168266
		AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
		BE011368 BE011362 BE011215 BE011365 BE011363
		AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
		BE041395 AA491825 AA621946 AA715980 AA666102
		AW970622 AA503009 AA502998 AA502989 AA502805 T92188
		AI204395 AW827539 AW969908 AW440776 AA528756
		AA528980 AI126603 BE504035
		AL109688 R23665 R26578
		AI126098 AI184746 AI148521
		AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010
		T61430 AI820546 AI821336
		AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
		BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 3C

70	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.
75	Pkey	Ref
	400773	8131629
		Strand
		Minus
		Nt_position
		44116-44238,48208-48321

5	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	401093	8516137	Minus	22335-23166
10	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
15	402230	9966312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
	402260	3399665	Minus	113765-113910,115653-115765,116808-116940
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
20	402777	9588235	Plus	126786-126948
	402901	8894222	Minus	175426-175667
	403047	3540153	Minus	59793-59968
	403381	9438267	Minus	26009-26178
	403903	7710671	Minus	101165-102597
25	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404875	9801324	Plus	96588-96732,97722-97831
	404877	1519284	Plus	1095-2107
	404977	3738341	Minus	43081-43229
30	405033	7107731	Minus	142358-142546
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958

TABLE 4A: Preferred diagnostics for bladder cancer

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigenelD:	Unigene number					
	Unigene Title:	Unigene gene title					
	R1:	80th percentile of muscle-invasive bladder tumor (stage T2-T4) Als divided by the 80th percentile of exophytic non-invasive carcinoma (stage Ta) Als					
	R2:	90th percentile of bladder tumor Als minus background divided by 90th percentile of normal body sample Als minus background, where background equals the 15th percentile of all sample Als					
10	R3:	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als					
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
15	423961	D13666	Hs.136348	perlestin (OSF-2os)	11.22	1.40	1.44
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40	1.31	1.38
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	7.88	2.06	2.44
	408243	Y00787	Hs.624	interleukin 8	7.54	2.86	4.85
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14	1.18	1.18
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32	1.34	1.36
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27	0.61	0.57
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17	7.47	35.60
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30	1.75	1.54
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29	1.35	1.60
25	413324	V00571	Hs.75294	corticotropin releasing hormone	4.20	6.27	45.75
	412429	AV650262	Hs.75765	GRO2 oncogene	4.00	0.94	0.93
	406636	L12054		gb:Homo sapiens (clone WR4.12VL) anti-th	3.66	1.25	1.25
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58	2.07	2.26
	406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41	4.37	3.37
30	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	3.09	0.39	0.40
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	2.96	0.44	0.45
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.90	1.94	3.46
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	2.80	1.67	3.10
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.77	5.62	26.07
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.71	2.26	2.91
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	2.40	0.47	0.37
	417849	AW291587	Hs.82733	nidogen 2	2.34	0.88	0.86
	400419	AF084545		Target	2.33	1.54	2.12
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag	2.10	1.01	1.01
40	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	1.99	3.19	17.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.94	2.49	1.84
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	1.94	2.02	5.39
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.84	1.99	8.55
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	1.76	0.33	0.31
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	1.76	1.13	1.16
	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.75	1.33	1.27
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.58	2.42	1.39
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.57	2.02	8.55
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	1.55	1.57	1.55
50	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	1.41	0.79	0.67
	429344	R94038	Hs.199538	Inhibin, beta C	1.36	1.39	1.34
	402727			NM_025065:Homo sapiens hypothetical prot	1.34	1.34	1.56
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.31	1.63	2.22
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.27	2.00	1.67
55	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	1.25	0.16	0.30
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.23	1.70	4.34
	424479	AF064238	Hs.149098	smoothelin	1.19	0.27	0.47
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.17	1.59	2.93
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	1.16	0.82	0.80
60	421634	AA437414	Hs.106283	hypothetical protein FLJ10262	1.16	1.05	1.05
	439569	AW602166	Hs.222399	CEGP1 protein	1.15	2.01	2.42
	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.10	1.64	1.52
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	1.10	0.31	0.31
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	1.03	1.51	1.42
65	422424	AJ186431	Hs.296638	prostate differentiation factor	1.02	2.77	2.68
	458781	AJ444821	Hs.63085	ESTs, Weakly similar to MPP3_HUMAN MAGUK	1.00	1.64	5.45
	445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.51	5.20
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	1.00	1.55	4.30
	403106			C8000084*:gij10432393[emb]CAC10283.1[(A	1.00	1.48	4.24
70	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.67	3.95
	404860			C1003394*:gij12314272[emb]CAC00591.1[(A	1.00	1.40	3.90
	434037	AF116601		WW domain-containing oxidoreductase	1.00	1.58	3.70
	405738			CX000390*:gij16014646[gb]AAAF01438.1[AF187	1.00	1.36	2.95
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.00	1.45	1.60
75	439898	AW505514	Hs.203561	KIAA1715 protein	1.00	1.28	1.59
	452567	D87120	Hs.29882	predicted osteoblast protein	1.00	1.10	1.31
	401271			C9000559*:gij12314195[emb]CAB99338.1[(A	1.00	2.12	1.00
	411339	BE164598	Hs.274251	hypothetical protein FLJ20375; KIAA1797	1.00	2.05	1.00

	403005		C21000027*:gij1817556[dbj]BAA13672.1] (D	1.00	1.89	1.00
	431146	Z83850	Human DNA sequence from PAC 82J11 and co	1.00	1.89	1.00
	434939	AF161422	Hs.305567 Homo sapiens HSPC304 mRNA, partial cds	1.00	1.86	1.00
	431753	X76029	Hs.2841 neuromedin U	1.00	1.82	1.00
5	419121	AA374372	Hs.89626 parathyroid hormone-like hormone	1.00	1.69	1.00
	435505	AF200492	Hs.211238 interleukin-1 homolog 1	1.00	1.67	1.00
	452401	NM_007115	Hs.29352 tumor necrosis factor, alpha-induced pro	1.00	1.67	1.00
	406397		C16001447*:gij12053709[emb]CAC20419.1] (1.00	1.66	1.00
	404488		NM_030958*:Homo sapiens organic anion tr	1.00	1.56	1.00
10	441206	BE552314	Hs.131823 ESTs, Weakly similar to TERA HUMAN [H.sa	1.00	1.49	1.00
	407853	AA336797	Hs.40499 dickkopf (Xenopus laevis) homolog 1	1.00	1.47	1.00
	446119	D29527	Hs.290931 ESTs	1.00	1.47	1.00
	406471		Target Exon	1.00	1.44	1.00
	402110		C18000178:gij11990779[emb]CAC19649.1] (A	1.00	1.42	1.00
15	407911	AF104922	Hs.41565 growth differentiation factor 8	1.00	1.40	1.00
	404829		C1002937*:gij7499208[pir]T20993 hypothe	1.00	1.37	1.00
	421925	S80310	Hs.109620 acidic epididymal glycoprotein-like 1	1.00	1.26	1.00
	406076	AL390179	Hs.13755 Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1.00	1.19	1.00
20	458622	AA972412	Hs.13755 f-box and WD-40 domain protein 2	1.00	1.09	1.00
	416018	AW138239	Hs.78977 proprotein convertase subtilisin/kexin t	1.00	1.04	1.00
	409357	M73628	Hs.54415 casein, kappa	1.00	1.03	1.00
	436684	AW976319	Hs.94806 ATP-binding cassette, sub-family A (ABC1	1.00	0.84	0.84
	436178	BE152396	Hs.21590 hypothetical protein DKFZp564O0523	1.00	0.91	0.80
25	402522		C1000568*:gij12697965[dbj]BAB21801.1] (A	1.00	0.80	0.67
	405735		ENSP00000252164*:KIAA1578 protein (Fragm	1.00	0.86	0.56
	401905		ENSP00000252232*:Sterol regulatory eleme	1.00	0.65	0.52
	404152		C6000931*:gij9558454[dbj]BAB03398.1] (AB	1.00	0.58	0.51
	418693	AI750878	Hs.87409 thrombospondin 1	1.00	0.85	0.51
30	451375	AI792066	Hs.283902 Homo sapiens BAC clone RP11-481J13 from	1.00	0.46	0.38
	430132	AA204686	Hs.234149 hypothetical protein FLJ20647	1.00	0.84	0.33
	456983	AI081687	Hs.11355 thymopoietin	1.00	0.61	0.29
	439681	AW384815	Hs.149208 KIAA1555 protein	1.00	0.60	0.28
	409038	T97490	Hs.50002 small inducible cytokine subfamily A (Cy	1.00	0.39	0.19
35	409196	NM_001874	Hs.334873 carboxypeptidase M	1.00	0.43	0.13
	410023	AB017169	Hs.57929 slit (Drosophila) homolog 3	1.00	0.30	0.12
	420674	NM_000055	Hs.1327 butyrylcholinesterase	1.00	0.30	0.08
	415165	AW887604	Hs.78065 complement component 7	1.00	0.08	0.06
	425545	N98529	Hs.158295 Homo sapiens, clone MGC:12401, mRNA, com	1.00	0.10	0.01
40	448256	BE614149	Hs.20814 CGI-27 protein	0.96	1.32	1.55
	417389	BE260964	Hs.82045 midkine (neurite growth-promoting factor	0.95	3.15	2.34
	403214		NM_016232*:Homo sapiens interleukin 1 re	0.94	1.63	2.51
	414799	AI752416	Hs.77326 insulin-like growth factor binding prote	0.92	1.87	1.60
	406665	U22961	Hs.184411 albumin	0.92	1.09	1.03
45	401519		C15000476*:gij12737279[ra]XP_012163.1] (0.88	1.46	3.44
	417501	AL041219	Hs.82222 sema domain, immunoglobulin domain (Ig),	0.87	0.41	0.50
	409632	W74001	Hs.55279 serine (or cysteine) proteinase inhibito	0.85	1.38	1.43
	405494		C2001837*:gij12697903[dbj]BAB21770.1] (A	0.83	1.46	4.65
	444171	AB018249	Hs.10458 small inducible cytokine subfamily A (Cy	0.80	0.91	0.91
50	439706	AW872527	Hs.59761 ESTs, Weakly similar to DAPI_HUMAN DEATH	0.79	0.58	0.43
	436396	AI683487	Hs.152213 wingless-type MMTV integration site fami	0.77	1.47	2.37
	426716	NM_006379	Hs.171921 sema domain, immunoglobulin domain (Ig),	0.75	1.13	1.18
	431347	AI133461	Hs.251664 insulin-like growth factor 2 (somatomedi	0.68	2.61	1.87
	413753	U17760	Hs.75517 laminin, beta 3 (nicein (125kD), kalinin	0.68	2.70	4.96
55	426322	J05058	Hs.2012 transcobalamin I (vitamin B12 binding pr	0.67	1.50	1.36
	426514	BE616633	Hs.170195 bone morphogenetic protein 7 (osteogenic	0.56	2.05	2.46
	422282	AF019225	Hs.114309 apolipoprotein L	0.55	3.91	3.92
	409757	NM_001898	Hs.123114 cystatin SN	0.53	2.72	2.93
	427450	AB014526	Hs.178121 KIAA0526 gene product	0.52	1.34	1.97
60	414555	N98569	Hs.76422 phospholipase A2, group IIA (platelets,	0.50	1.04	1.05
	423774	L39064	Hs.1702 interleukin 9 receptor	0.49	2.81	6.46
	404977		Insulin-like growth factor 2 (somatomedi	0.28	5.78	5.17
	428336	AA503115	Hs.183752 microseminoprotein, beta-	0.21	1.47	1.56
	451668	Z43948	Hs.326444 cartilage acidic protein 1	0.18	4.05	3.60
65	428651	AF196478	Hs.188401 annexin A10	0.17	5.14	27.75
	421110	AJ250717	Hs.1355 cathepsin E	0.12	5.49	45.35

TABLE 4B

70 Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75 Key: CAT Number Accession
 431146 32854_1 Z83850 AA459717 AW965384 AA333635
 434037 37918_1 AF116601 AI110691 AF063566

TABLE 4C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
10	Pkey	Ref	Strand	NL_position
	401271	9797373	Minus	61292-61911
15	401519	6649315	Plus	157315-157950
	401905	8671966	Plus	153965-154441,156599-156819
20	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402110	8131678	Minus	173889-174062
25	402522	9798493	Plus	20605-20731
	402727	9211324	Plus	54596-54777
30	403005	5791501	Minus	16945-17053,20018-20403
	403106	7331404	Plus	77162-77350,81338-81511
	403214	7630945	Minus	76723-77027,79317-79484
	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404488	8113286	Minus	64835-64994
	404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
	404860	8979555	Plus	65852-66081
	404977	3738341	Minus	43081-43229
	405494	8050952	Minus	70284-70518
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
	406076	9123123	Plus	89972-90319
	406397	9256243	Minus	127317-127454
	406471	9795566	Plus	87383-87589

TABLE 5A: Genes upregulated in bladder cancer

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
5	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	459702	AI204995		gb:an03c03x1 Stratagene schizo brain S1	11.03
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	10.40
	404917			Target Exon	9.65
	401066			C11000517*:gij7293105jgb AAF48490.1 (AE	9.00
15	447475	AI380797	Hs.158992	ESTs	8.92
	427335	AA448542	Hs.251677	G antigen 7B	8.65
	450061	AI797034	Hs.346238	ESTs	8.35
	401335			Target Exon	7.95
20	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.35
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	7.20
	436608	AA628980		down syndrome critical region protein DS	4.86
	451950	AW292317	Hs.213307	ESTs	4.45
	406542			C19000728*:gij12585552 sp Q9Y2Q1 Z257_HU	3.73
25	437931	AI249468	Hs.124434	ESTs	3.70
	443133	AI033878	Hs.41379	ESTs	3.60
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	3.37
	402239			Target Exon	3.37
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.21
30	403383			Target Exon	3.13
	438315	R56795	Hs.82419	ESTs	3.04
	452827	AI571835	Hs.55468	ESTs	3.01
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 fertilin	3.01
	402948			NM_025206:Homo sapiens hypothetical prot	2.91
35	429983	W92620	Hs.260855	ESTs	2.84
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.78
	444371	BE540274	Hs.239	forkhead box M1	2.75
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.70
	414906	AA157911	Hs.72200	ESTs	2.70
40	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.68
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.62
	429345	R11141	Hs.199695	hypothetical protein	2.61
	414221	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_Su	2.60
	402305			C19000735*:gij4508027 ref NP_003414.1 z	2.54
45	432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.51
	427719	AI393122	Hs.134726	ESTs	2.51
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.50
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15(N	2.49
	456967	AW004056	Hs.168357	T-box 2	2.49
	406387			Target Exon	2.48
50	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	2.48
	415752	BE314524	Hs.78776	putative transmembrane protein	2.46
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.43
	434293	NM_004445	Hs.3796	EphB6	2.42
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.40
55	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	2.38
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.35
	452012	AA307703	Hs.279766	kinesin family member 4A	2.34
	445600	AF034803	Hs.12953	PTPRF Interacting protein, binding prote	2.33
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.33
60	454609	AW810204		gb:MR4-ST0125-021199-017-008 ST0125 Homo	2.28
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.26
	420005	AW271106	Hs.133294	ESTs	2.22
	439826	NM_014965	Hs.6705	KIAA1042 protein	2.22
	405531			Target Exon	2.21
65	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	2.18
	404394			ENSP00000241075:TRRAP PROTEIN.	2.17
	427479	BE410092	Hs.178471	KIAA0798 gene product	2.17
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.13
70	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	2.12
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.10
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
	451385	AA017656		gb:z839h01.r1 Soares retina N2b4HR Homo	2.09
	403477			C3002160*:gij7662420 ref NP_055738.1 KI	2.09
	417151	AA194055	Hs.293858	ESTs	2.08
75	448262	AW880830	Hs.186273	ESTs	2.07
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	2.04
	402994			NM_002463*:Homo sapiens myxovirus (influ	2.04

	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.02
	423271	W47225	Hs.126256	interleukin 1, beta	2.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.99
	407581	R48402	Hs.173508	P3ECSE	1.95
5	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.95
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	1.93
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.93
	435251	BE515055	Hs.296585	nucleolar protein (KKE/D repeat)	1.89
	401961			NM_021626:Homo sapiens serine carboxypep	1.86
10	434042	AI589941	Hs.8254	Homo sapiens, Similar to tumor different	1.85
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.84
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	1.83
	429512	AF062649	Hs.252587	pituitary tumor-transforming 1	1.80
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.80
15	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.79
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.78
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.77
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.75
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.74
20	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.74
	459198	AI086347	Hs.151138	ESTs	1.74
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.71
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.70
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	1.70
25	417324	AW265494		ESTs	1.67
	453883	AI538516	Hs.347524	cofactor required for Sp1 transcriptiona	1.66
	428000	R35145	Hs.291904	accessory proteins BAP31/BAP29	1.65
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.63
30	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	1.62
	415440	D83782	Hs.78442	SREBP CLEAVAGE-ACTIVATING PROTEIN	1.62
	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	1.62
	426783	Z19084	Hs.172210	MUF1 protein	1.62
	445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.61
	445462	AA378776	Hs.288549	hypothetical protein MGC3077	1.60
35	400965			C11002190*:gij12737279;refXP_012163.1)	1.59
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	1.59
	429578	AI969028	Hs.99389	ESTs	1.59
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.59
40	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.59
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.59
	429002	AW248439	Hs.2340	junction plakoglobin	1.57
	442410	AW996503	Hs.197680	ESTs	1.56
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.55
45	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.54
	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain transcript	1.54
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.54
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.53
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.52
50	414053	BE391635	Hs.75725	transgelin 2	1.51
	433562	W07162	Hs.150826	CATX-8 protein	1.50
	432562	BE531048	Hs.278422	DKFZP586G1122 protein	1.50
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.48
	426127	L36983	Hs.167013	dynamitin 2	1.48
55	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	1.48
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.47
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mob	1.46
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.46
	432344	AI476474	Hs.248156	ESTs	1.46
60	453449	W15752	Hs.32981	sema domain, immunoglobulin domain (Ig),	1.46
	450690	AA296696	Hs.333418	FXRD domain-containing ion transport reg	1.46
	441940	AW298115	Hs.128152	ESTs	1.45
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.44
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.42
65	422565	BE259035	Hs.118400	slinged (Drosophila)-like (sea urchin fas	1.41
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial	1.41
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10195 fis, clone HE	1.39
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	1.37
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.35
70	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.32
	432636	AA340864	Hs.278562	claudin 7	1.32
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.32
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.31
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.28
75	430056	X97548	Hs.228059	KRAB-associated protein 1	1.24
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	1.20
	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.19

451541	BE279383	Hs.26557	plakophilin 3	1.16
406906	Z25424		gb:H.sapiens protein-serine/threonine k	1.11
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.00
414002	NM_006732	Hs.75978	FBJ murine osteosarcoma viral oncogene h	0.86
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor {	0.61

TABLE 5B

10 Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011382 BE011215 BE011365 BE011363
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
436608	42361_3	AA628980 AI126603 BE504035
451385	86787_1	AA017656 AA017374 AA019761
454609	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
455797	1366826_1	BE091833 BE091874 BE091871

TABLE 5C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400965	7770576	Minus	173043-173564
401066	8217436	Plus	71448-71574
401335	9884881	Plus	15736-16352
401961	4581193	Minus	124054-124209
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402305	7328724	Plus	40832-41362
402948	9368458	Minus	143456-143626,143808-143935
402994	2996643	Minus	4727-4969
403383	9438267	Minus	119837-121197
403477	9958251	Plus	111834-112008
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404917	7341851	Plus	49330-49498
405531	9665194	Plus	35602-35803
406387	9256180	Plus	116229-116371,117512-117651
406542	7711499	Plus	117335-118473

TABLE 6A: Genes upregulated in bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy AIs			
10	R2	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy and normal bladder AIs			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	439928	AW014875	Hs.137007	ESTs	11.31 11.31
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15 9.15
	421110	AJ250717	Hs.1355	cathepsin E	9.07 9.07
15	417308	H60720	Hs.81892	KIAA0101 gene product	8.50 8.50
	418406	X73501	Hs.84905	cytokeratin 20	8.10 8.10
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, clone HQ0310 PRO0310p1	7.98 7.98
	433001	AF217513	Hs.279905	interleukin 8	7.67 7.67
	408243	Y00787	Hs.624	proliferating cell nuclear antigen	7.56 7.56
20	416065	BE267931	Hs.78996	topoisomerase (DNA) II alpha (170kD)	7.17 5.17
	425397	J04088	Hs.156346	ESTs	7.17 8.24
	414183	AW957446	Hs.301711	matrix metalloproteinase 1 (interstitial	7.14 4.62
	418007	M13509	Hs.83169	FAT tumor suppressor (Drosophila) homolog	7.12 7.12
	426125	X87241	Hs.166994	Fc fragment of IgG, low affinity IIb, r	6.90 3.38
25	427337	Z46223	Hs.176663	normal mucosa of esophagus specific 1	6.85 4.98
	441633	AW958544	Hs.112242	nuclear receptor subfamily 1, group I, m	6.42 6.42
	438091	AW373062	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein	6.32 6.32
	413063	AL035737	Hs.75823	ALL 1-fused gene from chromosome 1q	6.09 3.67
	414219	W20010	Hs.75823	C1002652* ^g [544327]s[Q04799]FMO5_RABIT	5.93 4.68
30	405033			protein kinase (cAMP-dependent, catalytic	5.84 5.84
	413132	NM_006823	Hs.75209	microseminoprotein, beta-	5.79 5.68
	428336	AA503115	Hs.183752	melanoma cell adhesion molecule	5.78 4.57
	449230	BE613348	Hs.215179	matrix metalloproteinase 12 (macrophage	5.69 5.82
	423673	BE003054	Hs.1636	ESTs	5.69 7.30
35	415511	AJ732617	Hs.182362	a disintegrin and metalloproteinase domain	5.65 5.65
	426028	NM_001110	Hs.172028	keratin 6A	5.60 5.60
	421948	L42583	Hs.334309	annexin A10	5.59 14.20
	428651	AF196478	Hs.188401	putative chemokine receptor; GTP-binding	5.55 5.55
	424008	R02740	Hs.137555	matrix metalloproteinase 11 (stromelysin	5.38 5.59
40	406687	M31126		thyroid hormone receptor interactor 13	5.36 5.34
	439453	BE284974	Hs.6566	mitochondrial ribosomal protein L13	5.35 5.35
	408246	N55669	Hs.333823	mitochondrial ribosomal protein S16	5.20 3.50
	427678	BE267756	Hs.180312	v-erb-b2 avian erythroblastic leukemia v	5.13 4.10
	426158	NM_001982	Hs.199067	ESTs, Moderately similar to ZN91_HUMAN Z	4.97 3.71
45	442315	AA173992	Hs.7956	cyclin-dependent kinase inhibitor 3 (CDK	4.90 4.90
	418322	AA284166	Hs.84113	ESTs	4.90 4.77
	417720	AA205625	Hs.208067	CS box-containing WD protein	4.84 7.34
	423979	AF229181	Hs.136644	peroxisome proliferative activated recep	4.81 4.81
	420981	L40904	Hs.100724	transmembrane 4 superfamily member 1	4.81 4.43
50	433470	AW960564		NS1-binding protein	4.72 4.72
	429138	AB020657	Hs.197298	calcineurin-binding protein calsarcin-1	4.71 4.71
	408063	BE086548	Hs.42346	hypothetical protein KIAA1165	4.71 4.71
	452714	AW770994	Hs.30340	hypothetical protein FLJ23468	4.69 4.69
	442432	BE093589	Hs.38178	Homo sapiens cDNA FLJ10570 fis, clone NT	4.68 4.68
55	424834	AK001432	Hs.153408	small inducible cytokine subfamily A (Cy	4.65 4.65
	446921	AB012113	Hs.16530	mitogen-activated protein kinase 13	4.64 4.64
	427490	Z95152	Hs.178695	Homo sapiens cDNA: FLJ22528 fis, clone H	4.63 5.12
	412490	AW803564	Hs.288850	neuromedin B	4.61 4.61
	418030	BE207573	Hs.83321	Target Exon	4.60 4.60
60	401192			Homo sapiens mRNA; cDNA DKFZp586I2022 (I	4.60 4.29
	426761	AI015709	Hs.172089	Ig superfamily receptor LNIR	4.59 3.51
	452747	BE153855	Hs.61460	KIAA1272 protein	4.58 5.33
	446618	AJ076459	Hs.15978	hypothetical protein LOC57822	4.58 4.58
	423725	AJ403108	Hs.132127	gamma-glutamyl hydrolase (conjugase, fol	4.55 4.55
65	415701	NM_003878	Hs.78619	putative G-protein coupled receptor	4.52 4.70
	446742	AA232119	Hs.16085	hypothetical protein FLJ23182	4.49 4.11
	419433	AA814807	Hs.7395	small inducible cytokine A3 (homologous	4.48 4.48
	412326	R07566	Hs.73817	minichromosome maintenance deficient (S.	4.47 4.47
	427528	AU077143	Hs.179565	forkhead box M1	4.45 4.45
70	444371	BE540274	Hs.239	type I transmembrane protein Fn14	4.44 3.87
	444006	BE395085	Hs.10086	minichromosome maintenance deficient (S.	4.43 3.63
	424308	AW975531	Hs.154443	C12000586* ^g [6330167]dt[BA88477.1] (A	4.43 4.43
	401093			Homo sapiens cDNA FLJ14934 fis, clone PL	4.40 4.40
	447644	AW861622	Hs.108646	thymidylate synthetase	4.39 4.39
75	417933	X02308	Hs.82962	N-myc (and STAT) interactor	4.38 4.35
	409461	AA382169	Hs.54483	NM_004496*:Homo sapiens hepatocyte nucle	4.36 3.68
	401451			general transcription factor II, I	4.35 4.35
	450746	D82673	Hs.278589		4.35 3.36

5	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.34	4.74
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.31	4.31
	417615	BE548541	Hs.82314	hypoxanthine phosphoribosyltransferase 1	4.30	4.30
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.30	4.30
	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	4.29	4.29
10	417715	AW969587	Hs.86366	ESTs	4.27	7.45
	409757	NM_001898	Hs.123114	cystatin SN	4.24	3.39
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	4.24
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.21	4.12
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	4.20	4.20
15	436856	AI469355	Hs.127310	ESTs	4.19	4.19
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.16	4.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.14	4.14
	409231	AA446544	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.14	5.99
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	4.12	4.12
20	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	4.12	3.43
	400843			NM_003105*:Homo sapiens sortilin-related	4.11	5.51
	449722	BE280074	Hs.23960	cyclin B1	4.09	4.09
	405506			Target Exon	4.09	3.75
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07	4.07
25	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	4.05	4.80
	456525	AIW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.03	7.64
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.02	4.02
	413794	AF234532	Hs.61638	myosin X	4.02	4.02
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.02	4.72
30	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.01	3.99
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.01	4.01
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	4.00
	400277			Eos Control	4.00	3.47
	415791	H09366	Hs.78853	uracil-DNA glycosylase	3.99	3.37
35	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.98	4.77
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.98	3.95
	413753	U17760	Hs.75517	laminin, beta 3 (nlcn (125kD), kalinin	3.96	6.95
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.92	5.04
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.91	3.88
40	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.90	3.90
	411678	AI907114	Hs.71465	squalene epoxidase	3.89	3.89
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	3.87
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	3.87	3.87
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.85	4.50
45	429083	Y09397	Hs.227817	BCL2-related protein A1	3.85	3.85
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.82	3.77
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.82	3.82
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.81	3.81
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.81	3.62
50	430259	BE550182	Hs.127826	RatGEF-like protein 3, mouse homolog	3.80	3.80
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.77	3.77
	404875			NM_022819*:Homo sapiens phosphatase A2	3.77	3.46
	411299	BE409857	Hs.69499	hypothetical protein	3.76	3.76
	418827	BE327311	Hs.47166	HT021	3.76	3.76
55	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.75	3.75
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	3.73
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.71	3.71
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	3.70	3.45
	409518	BE384836	Hs.3454	KIAA1821 protein	3.69	3.69
60	430024	AI808780	Hs.227730	integrin, alpha 6	3.69	3.69
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	3.68
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.68	3.66
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.67
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	3.67	3.41
65	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.67	3.88
	434263	N34895	Hs.44648	ESTs	3.65	3.65
	438280	AW015534	Hs.217493	annexin A2	3.63	3.36
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.63	3.68
	408989	AW361656	Hs.49500	KIAA0746 protein	3.61	3.66
70	416640	BE262478	Hs.79404	neuron-specific protein	3.60	4.22
	416926	H03109	Hs.108920	HT018 protein	3.59	3.59
	414368	W70171	Hs.75939	uridine monophosphate kinase	3.59	3.53
	402727			NM_025065:Homo sapiens hypothetical prot	3.58	3.58
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.56	3.77
75	416114	AI695549	Hs.183868	glucuronidase, beta	3.55	3.55
	424941	AA128376	Hs.153884	ATP binding protein associated with cell	3.55	3.55
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.54	4.63
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	3.53	3.92
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	3.51	5.77
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	3.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.50

5	415220	AA431880	Hs.181174	ESTs, Weakly similar to T19201 hypotheti	3.50	3.50
	428371	AB012193	Hs.183874	cullin 4A	3.46	3.46
	418663	AK001100	Hs.41690	desmocollin 3	3.45	4.74
	404977			Insulin-like growth factor 2 (somatomedi	3.45	3.89
	422663	AW500087	Hs.119014	zinc finger protein 175	3.44	3.44
	434061	AW024973	Hs.283675	NP0009 protein	3.41	5.64
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.41	4.32
	431689	AA305688	Hs.287695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.40	3.40
10	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	3.39	4.27
	420005	AW271106	Hs.133294	ESTs	3.38	3.40
	453450	AW797627	Hs.347459	ADP-ribosylation factor 6	3.38	3.87
	410315	AJ638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	3.36	3.36
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.35	3.35
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	3.35	3.35
15	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.34	3.34
	428157	AJ738719	Hs.198427	hexokinase 2	3.33	3.73
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.33	3.33
	400750			Target Exon	3.33	3.33
20	450139	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.33	3.33
	412636	NM_004415		desmoplakin (DPI, DPL)	3.30	4.81
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28cdc	3.27	3.38
	430315	NM_004293	Hs.239147	guanine deaminase	3.26	4.30
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	3.26	3.41
25	443030	R68048	Hs.9238	hypothetical protein FLJ23515	3.19	3.34
	436911	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.17	3.40
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.06	3.52
	443171	BE281128	Hs.9030	TONDU	3.05	3.83
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	3.01	3.53
30	408380	AF123050	Hs.44532	diubiquitin	2.99	4.11
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.99	3.67
	439750	AL359053	Hs.57654	Homo sapiens mRNA full length insert cDN	2.97	4.55
	452046	AB018345	Hs.27657	KIAA0802 protein	2.95	3.39
	451940	AJ735759	Hs.52620	integrin, beta 8	2.93	3.58
35	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	2.90	3.68
	422282	AF019225	Hs.114309	apolipoprotein L	2.89	3.57
	402230			Target Exon	2.88	5.36
	406685	M18728		gb:Human nonspecific crossreacting antig	2.80	5.80
40	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.79	3.89
	447957	NM_014821	Hs.20126	KIAA0317 gene product	2.75	3.45
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.75	3.46
	417275	X63578	Hs.295449	parvalbumin	2.73	3.54
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.72	8.39
	401781			Target Exon	2.62	4.15
45	407242	M18728		gb:human nonspecific crossreacting antig	2.54	5.96
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	2.52	4.27
	430200	BE613337	Hs.234896	geminin	2.52	4.19
	451035	AU076785	Hs.430	plastin 1 (I isoform)	2.51	4.15
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.48	3.66
50	441495	AW294603	Hs.127039	ESTs	2.45	3.60
	449246	AW411209	Hs.23353	hypothetical protein FLJ10983	2.45	3.52
	401780			NM_005557: Homo sapiens keratin 16 (foca	2.22	4.49
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.20	3.55
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.15	6.08
55	439394	AA149250	Hs.56105	ESTs	2.05	3.95
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.79	3.88

TABLE 6B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Pkey	CAT Number
	412636	13165_1
70	Accession	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789
		AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561
		BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576
		BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935
		AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157
		AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090
		BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159545 AW606553 AA099891 AA131128 AA337270 AA340777
		AW384371 AA852212 R58704 AW386566 AW364859 AA025851 AA025852 AA456100 AA719958 AW352220 AW996245 BE165351 BE073457
		AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529
		AW390272 C18467 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137
75		BE092136 AW177784 AJ022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077
		W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AJ190590 C03378 AJ554403
		AJ205263 AA128470 AJ392926 AF139055 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029

5
10
15
20
25

433470 3672_1

438091 44964_1

AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793
 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869
 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807
 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984
 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181
 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182
 AW015480 AW771865 AI270027 AA951816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500
 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
 AW960564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176445
 AA304671 AW583735 T61714 AA316958 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847
 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691
 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873
 AA180483 AA169546 F00242 AI940609 AI940602 AI189753 T97653 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452
 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510
 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384
 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452
 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956
 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682884
 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300
 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400
 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI856295 AA780994
 AI955913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096

TABLE 6C

30
35

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

40
45
50

Pkey	Ref	Strand	Nt_position
400750	8119067	Plus	198991-199168, 199316-199548
400843	9188605	Plus	5863-5970, 7653-7784, 8892-9023, 9673-9807, 10634-10789, 15254-15403, 23827-23958
401093	8516137	Minus	22335-23166
401192	9719502	Minus	69559-70101
401451	6634068	Minus	119926-121272
401780	7249190	Minus	28397-28617, 28920-29045, 29135-29296, 29411-29567, 29705-29787, 30224-30573
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 84237-84393, 84955-85037, 86290-86814
402230	9966312	Minus	29782-29932
402727	9211324	Plus	54596-54777
404875	9801324	Plus	96588-96732, 97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
405506	6466489	Plus	80014-80401, 80593-81125

TABLE 7A: Genes downregulated in bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of normal urothelium biopsy Als divided by 75th percentile of bladder tumor Als			
10	R2	90th percentile of normal urothelium biopsy and normal bladder Als divided by the 90th percentile bladder tumor Als			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	403010			C21000152:gi 6226483 sp Q52118 YMO3_ERWS	4.86 2.49
	426796	S78234	Hs.172405	cell division cycle 27	4.28 2.48
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	4.04 2.07
15	459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	3.82 2.66
	404917			Target Exon	3.78 2.00
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	2.64 1.79
	419543	AA244170		gb:nc05h02.s1 NCL CGAP_Pr1 Homo sapiens	2.63 3.42
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.32 3.24
20	428957	NM_003881	Hs.194679	WNT1 Inducible signaling pathway protein	2.20 3.80
	451529	AI917901	Hs.208641	ESTs	2.18 3.69
	417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.03 3.03
	425438	T62216	Hs.270840	ESTs	2.00 5.17
	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	1.89 2.46
25	432873	AW837268	Hs.279639	Homo sapiens mRNA; cDNA DKFZp586M2022 (f	1.70 2.79
	452123	AI267615	Hs.38022	ESTs	1.69 2.46
	424378	W28020	Hs.167988	neural cell adhesion molecule 1	1.65 4.67
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50 3.34
	402096			ENSP00000217725*:Laminin alpha-1 chain p	1.48 3.02
30	439563	AI018768	Hs.12482	glyceronephosphate O-acyltransferase	1.47 3.22
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	1.46 2.30
	458651	AW612481	Hs.104105	ESTs	1.39 2.89
	414033	AL079707	Hs.207443	hypothetical protein MGC10848	1.36 2.80
	433572	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti	1.35 3.49
35	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	1.34 2.93
	420412	AW976674	Hs.125103	ESTs	1.32 5.13
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	1.31 4.07
	417446	AL118671	Hs.82163	monoamine oxidase B	1.27 2.86
	452886	AI478250	Hs.13751	ESTs	1.26 1.95
40	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	1.25 3.44
	443105	X95753	Hs.9004	chondroitin sulfate proteoglycan 4 (meta	1.24 2.07
	421348	M94048	Hs.103724	peripheral myelin protein 22	1.24 2.63
	433070	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi	1.23 2.80
	420059	AF161488	Hs.94769	RAB23, member RAS oncogene family	1.22 3.43
45	408491	AI088063	Hs.7882	ESTs	1.20 6.01
	447384	AI377221	Hs.40528	ESTs	1.00 7.92
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	1.00 7.38
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	1.00 6.40
	444795	AI193356	Hs.160316	ESTs	1.00 5.53
50	408495	W68796	Hs.237731	ESTs	1.00 5.05
	417124	BE122762	Hs.25338	ESTs	1.00 4.73
	443998	AI620661	Hs.296276	ESTs	1.00 4.39
	406303			C16000922:gi 7499103 pir J120903 hypothe	1.00 4.37
	422994	AW891802	Hs.296276	ESTs	1.00 4.37
55	422195	AB007903	Hs.113082	KIAA0443 gene product	1.00 4.35
	452877	AI250789	Hs.32478	ESTs	1.00 3.90
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	1.00 3.90
	417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	1.00 3.82
	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	1.00 3.62
60	406274			Target Exon	1.00 3.59
	410611	AW954134	Hs.20924	KIAA1628 protein	1.00 3.06
	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	1.00 2.89
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.00 2.61
	413040	AA193338	Hs.12321	sodium calcium exchanger	1.00 2.51
65	429623	NM_005308	Hs.211569	G protein-coupled receptor kinase 5	1.00 2.05
	456607	AI660190	Hs.106070	cyclin-dependent kinase inhibitor 1C (p5	1.00 2.01
	429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.97 2.45
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.90 2.47
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	0.88 5.08
70	414449	AA557660	Hs.76152	decorin	0.88 3.13
	412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	0.78 1.88
	425100	AF051850	Hs.154567	supervillin	0.70 3.90
	432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	0.68 3.41
	427818	AW511222	Hs.193765	ESTs	0.63 3.75
75	TABLE 7B				
	Pkey:	Unique Eos probeset identifier number			

CAT number: Gene cluster number
Accession: Genbank accession numbers

5 Pkey CAT Number Accession
417159 1653899_1 R01761 R01760 N49787
419543 185745_1 AA244170 AJ018087 AA244355
450515 83710_1 AW304226 AW008420 AA349212 H15015 AA317021 A1829484 H25661 H81744 AJ906147 AA837938 AW167766 AW603578 AW842359
10 BE439926 AA902417 AW235409 AA010062 AW069319 AJ280242 AW672925 H06848 H05608 R51905 R45023 AW675471 H28475 AJ085597
AJ197815 AJ825355 N99134 AJ075956 AJ470122 AA449985 AW662633 AA860423 AA913342 T23825 AJ394207 AJ310319 T32467 AJ589870
AJ682293 AJ810633 BE223045 H14620 AA626645 AA876023 T33571 AA953982 AJ138631 H15016 AJ304356 AA983631 AJ350990 AJ143993
AJ708171 AA526961 H26247 W38485 AA847598 H81745 AW855486 BE299605 AJ079409 AJ278050 AJ223168 AJ860904 AW025415 AJ339003
AA393692 AJ354302 AJ492838 N80194 AJ015651 N34543 BE295397 AJ085154 W24135

15 TABLE 7C

Pkey: Unique number corresponding to an Eos probaset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
20 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

25 Pkey Ref Strand Nt_position
402096 8117697 Minus 24993-25186
403010 3132346 Plus 78385-79052
404917 7341851 Plus 49330-49498
406274 7543787 Plus 932-1123
30 406303 8575868 Plus 173622-173786

TABLE 8A: Genes predictive of bladder cancer progression

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	80th percentile of Ta or T1 tumor Als from patients who upstaged divided by 80th percentile of Ta or T1 tumor Als from patients who did not upstage			
10	R2	median of Ta or T1 tumor Als from patients who upstaged divided by the median of Ta or T1 tumor Als from patients who did not upstage			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	413324	V00571	Hs.75294	corticotropin releasing hormone	8.30 4.18
	437802	AI475995	Hs.122910	ESTs	7.51 2.50
	444444	AI149332	Hs.14855	ESTs	2.58 1.38
15	445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	2.26 1.13
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.27 5.33
	449618	AI076459	Hs.15978	KIAA1272 protein	2.70 3.33
	407242	M18728		gb:Human nonspecific crossreacting antigen	3.58 1.90
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.32 1.00
20	423441	R68649	Hs.278359	absent in melanoma 1 like	2.44 2.40
	405033			C1002652*gi544327[sp]Q04799[FM05_RABIT	1.75 3.48
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.72 1.28
	425118	AU076611	Hs.154572	methylene tetrahydrofolate dehydrogenase	2.40 2.78
	437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	2.20 1.53
25	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	1.38 2.33
	436608	AA628980		down syndrome critical region protein DS	3.32 4.53
	404440			NM_021048:Homo sapiens melanoma antigen,	2.64 1.00
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.06 1.09
	424098	AF077374	Hs.139322	small proline-rich protein 3	2.47 3.64
30	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.09 0.91
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	2.71 4.58
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.18 2.33
	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	2.61 1.81
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	1.90 2.02
35	401241	AB028989		mitogen-activated protein kinase 8 inter	1.26 2.55
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.12 1.23
	415989	AI267700		ESTs	1.60 1.00
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.73 1.50
	452140	AB007928	Hs.28169	KIAA0459 protein	2.44 2.95
40	443162	T49951	Hs.9029	DKFZP434G032 protein	2.98 1.00
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.56 1.20
	407379	AA332127	Hs.325804	transcription factor 17	2.10 1.72
	442712	BE465168	Hs.131011	ESTs	2.54 2.72
	411678	AI907114	Hs.71465	squalene epoxidase	1.12 3.11
45	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.69 1.38
	431805	NM_014053	Hs.270594	FLVCR protein	1.92 2.05
	438414	AA806794	Hs.131511	ESTs	1.04 2.15
	413924	AL119964	Hs.75616	seladin-1	1.69 2.05
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.27 2.26
50	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	1.42 2.74
	408349	BE546947	Hs.44276	homeo box C10	1.60 2.05
	422545	X02761	Hs.287820	fibronectin 1	1.77 3.02
	406643	N77976	Hs.347939	hemoglobin, alpha 2	1.57 1.35
	407228	M25079	Hs.155376	hemoglobin, beta	1.81 1.50
55	449644	AW960707	Hs.148324	ESTs	1.90 3.19
	402305			C19000735*gi4508027[ref]NP_003414.1 z	2.25 1.49
	427683	BE545490	Hs.15053	Homo sapiens HCMOGT-1 mRNA for sperm ant	1.08 2.25
	441690	R81733	Hs.33106	ESTs	1.80 2.65
	434487	AF143887	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.13 1.63
60	403352			NM_001615*:Homo sapiens actin, gamma 2,	2.33 2.22
	445496	AB007860	Hs.12802	development and differentiation enhancin	1.12 2.60
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I39022 hypotheti	1.83 3.05
	402366	AV648601		apolipoprotein B (including Ag(x) antige	1.32 2.05
	427254	AL121523	Hs.97774	ESTs	2.44 1.00
65	414533	AA149060	Hs.296100	ESTs	1.70 2.06
	430157	BE348706	Hs.278543	ESTs	2.54 3.00
	413433	NM_003199	Hs.326198	transcription factor 4	2.26 1.41
	410532	T53088	Hs.155376	hemoglobin, beta	1.52 1.56
	405779			NM_005367:Homo sapiens melanoma antigen,	2.42 1.22
70	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.48 2.13
	414081	AW969976	Hs.279009	maltrix Gla protein	1.81 1.53
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.65 2.08
	415062	H45100	Hs.49753	uveal autoantigen with coiled coil domai	1.62 3.75
	406317			C2002658*gi5625694[gb]AAF19354.1 AF185	1.68 2.11
75	453259	R93125	Hs.124187	ESTs	1.08 2.25
	445937	AI452943	Hs.321231	UDP-GalbetaGlcNAc beta 1,4- galactosylt	1.76 1.01
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.12 2.08
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.02 2.40

	432331	W37862	Hs.274368	MSTP032 protein	4.36	2.18
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.51	3.45
	413109	AW389845	Hs.110855	ESTs	4.34	5.98
	413643	AA130987	Hs.188727	ESTs	1.30	2.42
5	433217	AB040914	Hs.278628	KIAA1481 protein	1.70	2.49
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	1.79	1.66
	438006	BE148799	Hs.127951	hypothetical protein FLJ14503	1.76	2.04
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi]	2.32	2.45
	433656	AW974941	Hs.292385	ESTs, Weakly similar to I78885 serine/th	1.14	2.50
10	415714	NM_002290	Hs.78672	laminin, alpha 4	2.52	1.13
	450282	AA007655	Hs.93523	ESTs	1.40	2.58
	442855	AI074465	Hs.133469	ESTs	1.54	2.20
	432917	NM_014125	Hs.241517	PRO0327 protein	2.24	3.03
	429041	AJ132820	Hs.194768	a disintegrin and metalloproteinase doma	1.61	2.60
15	442807	AL049274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (fr	1.73	1.19
	427719	AI393122	Hs.134726	ESTs	1.46	2.00
	408778	AI500519	Hs.63382	hypothetical protein PRO2714	1.46	2.58
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	2.03
	424425	AB031480	Hs.146824	SPR1 protein	1.60	1.11
20	445391	T92576	Hs.191168	ESTs	1.69	2.40
	446899	NM_005397	Hs.16426	podocytin-like	1.22	2.42
	420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.68	2.98
	424909	S78187	Hs.153752	cell division cycle 25B	2.18	1.33
	413593	AA205248		gbzq78c12.r1 Stralagene hNT neuron (937	1.69	2.00
25	408734	AW264996	Hs.254299	ESTs	2.06	2.94
	413880	AJ660842	Hs.110915	interleukin 22 receptor	1.24	2.20
	437053	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.78	2.60
	418044	AJ640532	Hs.119830	ESTs, Weakly similar to ALUF_HUMAN IIII	1.54	2.53
	441971	W27060	Hs.265855	ESTs	1.62	2.13
30	450401	AW959281	Hs.8184	ESTs	1.42	2.30
	440157	AA868350	Hs.343636	ESTs	1.38	2.60
	457587	AA992841	Hs.27263	KIAA1458 protein	1.47	2.42
	440707	BE256751	Hs.22667	Homo sapiens cDNA: FLJ22073 fis, clone H	1.18	2.10
	402241			Target Exon	2.58	2.52
35	413428	AA430155	Hs.151343	KIAA1524 protein	1.22	2.45
	416735	R11275	Hs.194485	ESTs	1.14	2.14
	421582	AJ910275		trefoil factor 1 (breast cancer, estroge	1.25	1.03
	431031	AA830335	Hs.105273	ESTs	2.35	2.95
40	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	3.72	1.00
	420786	AW296466	Hs.43628	deleted in lymphocytic leukemia, 2	1.23	2.60
	401335			Target Exon	1.18	1.68
	417670	R07785		gb:yl15c06.r1 Soares fetal liver spleen	1.56	2.00
	406314			C14001020.gij12597441[gb]AAG60049.1[AF31	1.60	3.08
45	458981	AW968318	Hs.285996	hypothetical protein FLJ23375	1.70	2.50
	417509	AA203414	Hs.42009	ESTs	1.82	2.05
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	1.34	1.37
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.37	1.02
	457871	AJ168278		ESTs	1.20	2.19
50	444163	AJ126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.43	1.22
	413276	Z24725	Hs.75260	mitogen inducible 2	1.78	2.28
	421097	AJ280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.55	2.60
	417151	AA194055	Hs.293858	ESTs	1.68	1.67
	453566	AA425414	Hs.33287	nuclear factor I/B	2.06	2.40
55	440859	AW070865	Hs.346390	ESTs	1.12	1.70
	420629	AW204343	Hs.156823	ESTs, Weakly similar to T30868 RhoA-bind	1.21	2.38
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	1.58	2.15
	434831	AA248060	Hs.273397	KIAA0710 gene product	1.69	1.78
	412055	AA099907	Hs.271806	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.35	2.65
60	445468	AW450439		ESTs	1.52	2.50
	444550	BE250716	Hs.87614	ESTs	1.30	2.28
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.50	3.02
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (f	1.24	2.95
	413444	BE141019		gb:MR0-HT0067-201099-002-b10 HT0067 Homo	1.68	2.80
65	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	1.49	2.01
	427055	AJ301740	Hs.173381	dihydropyrimidinase-like 2	1.11	2.58
	454244	R51604	Hs.300842	KIAA1608 protein	1.00	2.02
	429503	AA394183	Hs.26873	ESTs	2.58	4.08
	422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	3.48	2.46
70	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.13	1.48
	437312	AA809350	Hs.246180	ESTs	1.10	2.05
	449426	T92251	Hs.198882	ESTs	1.22	2.08
	447620	AW290951	Hs.224955	ESTs	1.80	2.18
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	1.72	2.81
75	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	1.99	1.80
	415712	AW249188	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	1.66	2.98
	432877	AW974111	Hs.292477	ESTs	1.63	2.79
	412085	AW891667		gb:CM3-NT0089-110500-179-h09 NT0089 Homo	1.40	2.08

5	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	1.96	3.58
	409714	AW367812	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.24	2.10
	423013	AW875443	Hs.22209	secreted modular calcium-binding protein	1.49	2.09
	422663	AW500087	Hs.119014	zinc finger protein 175	1.01	2.78
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	1.54	2.57
10	413196	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	1.04	2.18
	439349	AI660898	Hs.195602	ESTs	2.03	2.43
	443005	AI027184	Hs.200918	ESTs	1.42	2.10
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.58	3.43
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	2.08	1.70
15	413916	N49813	Hs.75615	apolipoprotein C-II	0.70	0.42
	418332	R34976	Hs.78293	ESTs	2.74	2.43
	425552	BE297660	Hs.170328	moesin	1.28	1.52
	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	1.42	2.02
	447214	AI367288	Hs.273621	Homo sapiens cDNA: FLJ21350 fis, clone C	1.14	2.10
20	449254	W26908	Hs.172762	ESTs	2.04	2.50
	443651	W22152	Hs.282929	ESTs	2.94	3.08
	421021	AA808018	Hs.109302	ESTs	1.41	2.04
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.61	1.21
	432027	AI096678	Hs.272353	KIAA0957 protein	1.70	2.76
25	452688	AA721140	Hs.49930	ESTs, Weakly similar to putative p150 [H	1.80	2.95
	417042	C75563	Hs.113029	ribosomal protein S25	2.22	3.20
	443574	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io	1.21	2.51
	429372	AA451859	Hs.99253	ESTs	1.28	2.43
	424290	AA338396		gb:EST43386 Fetal brain I Homo sapiens c	1.82	2.03
30	428518	AW969656		gb:EST381733 MAGE resequences, MAGK Homo	1.72	2.52
	455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	1.65	3.03
	414665	AA160873	Hs.332053	serum amyloid A1	1.36	1.08
	418298	AA256014	Hs.85682	Homo sapiens cDNA: FLJ21578 fis, clone C	1.04	2.03
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	4.94	4.34
35	433924	AA618304	Hs.258785	ESTs	1.44	2.40
	452683	AI089575	Hs.9071	progesterone membrane binding protein	1.48	2.48
	439437	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.36	2.33
	432314	AA533447	Hs.312989	ESTs	0.96	2.78
	400881			NM_025080:Homo sapiens hypothetical prot	1.70	3.15
40	426477	AA379464		gb:EST92386 Skin tumor I Homo sapiens cD	2.01	2.37
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	2.12	3.44
	423977	AA333232		gb:EST37283 Embryo, 8 week I Homo sapien	1.38	2.13
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	2.13	3.28
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	1.90	2.23
45	415157	D63257		gb:HUM514B08B Clontech human placenta po	1.29	2.90
	418236	AW994005	Hs.337534	ESTs	1.74	2.37
	454390	AB020713	Hs.56966	KIAA0906 protein	1.47	1.38
	436143	AA705245	Hs.192189	ESTs	1.46	2.45
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.43	2.07
50	450735	AI732321		SRY (sex determining region Y)-box 4	1.36	2.02
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	2.70	1.68
	447100	AI361801	Hs.167130	hypothetical protein	1.66	2.03
	453577	AL043049		gb:DKFZp434A1523_r1 434 (synonym: htes3)	1.41	2.75
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.59	1.38
55	412632	AL120379	Hs.74294	aldehyde dehydrogenase 7 family, member	1.81	2.51
	423291	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	1.54	2.83
	456172	R99050		gb:yq65c02.r1 Soares fetal liver spleen	1.46	2.68
	452123	AI267615	Hs.38022	ESTs	1.24	1.93
	433900	AA721668	Hs.257761	ESTs	1.78	2.66
60	408436	R31954	Hs.7885	phosphatidylinositol binding clathrin as	1.21	2.35
	417123	BE326521	Hs.159450	ESTs	1.46	2.09
	436023	T81819	Hs.302251	ESTs	2.68	2.70
	454150	AA131893	Hs.154088	hypothetical protein FLJ22756	1.40	2.50
	444094	AI695764	Hs.202394	ESTs	1.28	4.03
65	429176	AW975021	Hs.193800	ESTs	1.08	2.53
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.80	3.03
	451164	AA015912	Hs.60659	ESTs, Weakly similar to T46471 hypotheti	1.47	1.17
	417501	AL041219	Hs.82222	sama domain, immunoglobulin domain (Ig),	2.92	2.70
	455642	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	1.70	2.70
70	443387	BE139135	Hs.254629	ESTs	1.48	2.32
	420995	AA282495	Hs.89014	ESTs	1.45	1.51
	407329	AA576061	Hs.269834	ESTs, Weakly similar to ALUD_HUMAN !!!!	1.13	2.38
	438797	C16161	Hs.283040	hypothetical protein PRO2543	0.99	2.75
	443357	AW016773		low molecular mass ubiquitome-binding pr	1.60	2.08
75	412656	AF005011	Hs.74375	dishevelled 1 (homologous to Drosophila	1.32	1.13
	427377	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.24	0.79
	412200	R08110	Hs.187462	ESTs, Weakly similar to I38022 hypotheti	1.35	1.54
	432586	AA568548		ESTs	1.50	2.25
	411590	T96183		gb:ye09f07.s1 Stratagene lung (937210) H	1.22	2.53
	422572	X12784	Hs.119129	collagen, type IV, alpha 1	2.27	2.20
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	1.59	2.11

	419900	AI469960	Hs.170698	ESTs	1.30	2.68
	410805	AW804742	Hs.84264	acidic protein rich in leucines	1.16	2.28
	452560	BE077084	Hs.99969	ESTs	1.44	2.58
5	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	4.02	1.00
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	1.10	2.00
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	1.45	1.28
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	1.82	2.10
	443696	AW607444	Hs.134622	ESTs	1.98	2.01
10	436094	AI798701	Hs.222222	ESTs	1.34	2.40
	420168	AF217508	Hs.95594	serine carboxypeptidase vitellogenic-like	1.58	2.45
	430325	AF004562	Hs.239356	syntactin binding protein 1	1.34	2.43
	439022	AA356599	Hs.173904	ESTs	2.76	2.40
	420563	AA278327	Hs.136237	ESTs, Moderately similar to Y140_HUMAN H	1.78	2.65
15	429494	AA769365	Hs.126058	ESTs	1.50	2.40
	420689	H79979	Hs.88678	ESTs	1.26	2.28
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.72	1.29
	439943	AW083789	Hs.124620	ESTs	1.45	2.84
	442300	AI765908	Hs.129166	ESTs	1.24	2.35
20	449614	AI989490	Hs.197703	ESTs	1.12	2.22
	444363	AI142827	Hs.143656	ESTs	1.32	2.08
	424479	AF064238	Hs.149098	smoothelin	1.59	1.10
	437321	AA768966	Hs.292026	ESTs, Weakly similar to 2109260A B cell	1.28	2.07
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	1.52	2.63
25	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.69	1.30
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.71	2.19
	437199	AL110175	Hs.306337	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	1.48	2.50
	457450	AW294163	Hs.146127	ESTs	1.07	2.60
	456678	AF141305	Hs.173736	ancient ubiquitously protein 1	1.44	2.35
30	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	0.95	3.00
	405944			Target Exon	1.48	2.45
	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	1.38	2.20
	446682	AW206532	Hs.211198	ESTs	1.38	3.00
	431380	AW610282	Hs.291003	ESTs	1.43	2.64
35	442027	AI652926	Hs.128395	ESTs	1.18	2.43
	423578	AW960454	Hs.222830	ESTs	1.56	2.18
	441495	AW294603	Hs.127039	ESTs	2.80	1.73
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.36	1.18
	443949	AW827419	Hs.235070	ESTs	1.30	2.28
40	440495	AA887212	Hs.14161	hypothetical protein DKFZp434I1930	1.74	2.78
	449948	R19156	Hs.20798	ESTs	1.12	2.23
	439564	W77911	Hs.110006	ESTs	1.34	2.85
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.24	1.09
	436139	AA765786	Hs.120936	ESTs	1.30	2.10
45	456968	AI174861	Hs.190623	ESTs	1.14	2.15
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	1.21	2.18
	411652	AW855393		gb:CM3-CT0275-191099-024-f10 CT0275 Homo	1.85	1.94
	420732	AA789133	Hs.88650	ESTs	1.66	2.71
	409291	AW373472		gb:RC3-BT0523-181299-011-d12 BT0523 Homo	1.56	2.30
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.56	1.39
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	1.58	1.24
	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	1.02	2.25
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	1.70	2.39
	415361	F06724		gb:HSC11G021 normalized infant brain cDN	1.34	2.40
55	406490			C5001926:gi7511572 pir T42245 probable	1.28	2.40
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	1.52	2.00
	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	1.12	2.20
	429508	AW369520	Hs.33944	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.33	2.28
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	1.88	2.18
60	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	1.65	1.16
	451870	AI820991	Hs.8377	ESTs	1.24	2.03
	444091	AV647924	Hs.282376	ESTs	1.05	2.13
	410793	AW581906	Hs.66392	Intersectin 1 (SH3 domain protein)	2.00	3.13
	452222	AW806287	Hs.21432	SEX gene	1.25	1.10
65	433010	AW970018		gb:EST382097 MAGE resequences, MAGK Homo	1.36	2.41
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	1.14	2.03
	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.24	1.77
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	1.52	2.65
	402685			Target Exon	2.04	2.46
70	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.66	2.05
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.89	4.98
	451225	AI433694	Hs.293608	ESTs	1.79	2.70
	441078	AI453268	Hs.323409	Homo sapiens cDNA FLJ14113 fis, clone MA	1.44	2.58
	409406	H83092	Hs.49605	ESTs	1.38	2.05
75	422297	AW961290		p30 DBC protein	1.20	2.73
	408711	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-fin	1.20	2.08
	426696	AW363332	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H	1.35	2.68
	417324	AW265494		ESTs	1.68	1.25

	408283	BE141579		gb:QV2-HT0083-071299-018-b05 HT0083 Homo	1.25	2.65
	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.34	1.09
	406300			Target Exon	1.61	2.47
5	411880	AW872477		gb:jhm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.60	4.03
	422287	F16355	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.16	1.44
	422567	AF111178	Hs.118407	glypican 6	1.57	2.03
	436855	AA732624	Hs.165852	ESTs	1.08	2.75
	403536			Target Exon	0.93	2.13
10	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.18	1.07
	417117	N46778		gb:yy52b02.r1 Soares_multiple_sclerosis_	1.70	2.85
	411690	AA669253	Hs.136075	RNA, U2 small nuclear	2.12	2.78
	443243	AI452496	Hs.132056	ESTs	1.15	2.83
	423074	AL109963		FSH primary response (LRPR1, rat) homolo	1.37	1.43
	408916	AW295232	Hs.429	ATP synthase, H transporting, mitochondr	1.63	2.23
15	449799	AI143456	Hs.125060	ESTs	1.40	2.08
	415378	T16964		gb:NIB2079-SR Normalized infant brain, B	1.88	1.85
	431089	BE041395		ESTs, Weakly similar to unknown protein	1.57	2.57
	434959	AW974949	Hs.186564	ESTs, Weakly similar to I38022 hypothe	1.30	2.30
20	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	1.58	4.35
	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.88	2.98
	456206	NM_006895	Hs.81182	histamine N-methyltransferase	1.24	2.08
	410583	AW770280	Hs.36258	ESTs, Moderately similar to JC5238 galac	1.56	4.33
	430410	AF099144	Hs.334455	tryptase beta 1	1.91	1.58
25	408139	AA451966		RAB9-like protein	1.42	2.14
	432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypothe	2.08	1.94
	441584	AW148329	Hs.175208	ESTs	1.12	2.05
	445940	D60438	Hs.34779	ESTs	1.86	2.70
	453022	AA031499	Hs.118489	ESTs	2.02	1.75
30	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.54	1.29
	442994	AI026718	Hs.16954	ESTs	3.60	3.78
	402085			C18000504*:gij2627436[gb]AAB86683.1] (AF	1.36	2.53
	411918	AW876354		gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.00	2.63
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.70	3.04
35	426106	AI678765	Hs.21812	ESTs	1.49	2.11
	425131	BE252230	Hs.99163	ESTs	2.04	2.65
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	1.17	2.55
	420447	AA687306	Hs.88448	ESTs	1.66	2.58
	428055	AA420564	Hs.101760	ESTs	1.08	2.15
40	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.76	1.82
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	1.08	2.10
	403280			C10001011*:gij4758212[ref]NP_004411.1] d	0.97	2.48
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	1.42	1.41
	432390	AA936177	Hs.274460	olfactory receptor, family 5, subfamily	1.26	2.05
45	443441	AW291196	Hs.92195	ESTs	1.52	2.13
	418925	AA159850	Hs.93765	lipoma HMGIC fusion partner	1.72	2.80
	445256	AI858635	Hs.144763	ESTs	1.97	3.33
	456381	AA236606		gb:zr99b10.r1 NCI_CGAP_GCB1 Homo sapiens	1.16	1.95
	422433	AA310560	Hs.153746	hypothetical protein FLJ22490	1.06	2.20
50	432529	AI989507	Hs.162245	ESTs	1.36	2.25
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	2.22	2.58
	420785	H89633	Hs.191346	ESTs	1.26	2.15
	411347	AW838126		gb:QV2-LT0051-240300-097-f01 LT0051 Homo	1.38	2.38
	438742	AW204126	Hs.196543	ESTs	1.10	2.30
55	414900	AW452420	Hs.248678	ESTs	2.01	3.08
	443284	AI369813	Hs.64783	ESTs, Weakly similar to T42705 hypothe	0.66	0.43
	402049			Target Exon	2.28	2.00
	429400	AW604940	Hs.201668	transcription factor 20 (AR1)	1.16	2.00
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	1.59	1.05
60	432495	AW973537	Hs.186734	ESTs, Weakly similar to I61746 pheromona	1.50	2.05
	414840	R27319	Hs.23823	hairly/enhancer-of-split related with YRP	1.89	2.09
	426711	R46414	Hs.56828	trinucleotide repeat containing 5	1.77	1.83
	448609	AW139420	Hs.7972	KIAA0871 protein	1.14	2.26
	443859	NM_013409	Hs.9914	folistatin	1.17	1.05
65	411141	AW819561		gb:RCS-ST0293-140200-013-G04 ST0293 Homo	1.44	2.40
	440116	AI798851	Hs.266959	hemoglobin, gamma G	1.18	2.08
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	2.10	1.37
	429640	U83508	Hs.2463	angiotensin 1	1.92	2.98
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	1.51	1.29
70	458218	AI435179	Hs.126820	ESTs	1.49	1.15
	443114	AI033377	Hs.153298	ESTs	1.38	2.05
	427788	AA412397	Hs.116858	ESTs	1.45	1.85
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	1.63	3.90
	457949	W89171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.01	2.00
75	419203	AA488719	Hs.190151	ESTs	1.94	2.45
	412510	AI056689	Hs.133538	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	2.20
	413885	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo	1.48	2.80
	426239	AA669515	Hs.214226	ESTs	1.36	2.50

	408866	AW292096	Hs.255036	ESTs	1.93	2.92
	412857	AI703484	Hs.128052	ESTs	1.72	1.60
	427340	BE167242	Hs.47099	hypothetical protein FLJ21212	1.46	2.13
5	412902	BE030818		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	0.90	2.05
	451141	AW772713	Hs.247186	ESTs	2.38	3.95
	412626	AA114945	Hs.151839	ESTs	1.75	2.15
	405667			Target Exon	2.62	3.79
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.24	2.08
10	401400			Target Exon	1.16	1.90
	426796	S78234	Hs.172405	cell division cycle 27	2.14	1.63
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.14	2.28
	448401	AI498509	Hs.346254	ESTs	2.50	2.83
	450832	AW970602	Hs.105421	ESTs	0.55	0.39
15	441057	AL043897	Hs.126483	ESTs	1.08	2.13
	438725	AA815163	Hs.127307	ESTs	1.31	2.65
	450062	AW001043	Hs.200854	ESTs	1.30	2.48
	441214	AI820648	Hs.129136	ESTs	1.43	1.71
20	431723	AW058350	Hs.15762	Homo sapiens mRNA; cDNA DKFZp56482062 (f	1.22	2.30
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.35	1.49
	423622	BE154847		gb:PM1-HT0345-121199-001-d05 HT0345 Homo	1.57	2.30
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.40	1.12
	444014	AI095718	Hs.135015	ESTs	2.30	1.78
	431603	AA807955	Hs.325984	EST	1.26	2.03
25	408697	AW419069	Hs.209570	ESTs	1.35	2.60
	444312	R44007		ESTs	1.95	2.07
	404286			C6001909:gi704441 dbj BAA18909.1 (D298	2.29	2.22
	438813	M27346		gb:Homo sapiens (clone HGP09/HGP32) T c	1.03	2.43
30	445534	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	1.00	2.16
	426046	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	1.59	2.73
	451907	AI822065	Hs.50749	ESTs, Moderately similar to ALU7_HUMAN A	1.74	2.65
	418796	AA228351	Hs.34060	ESTs	1.28	2.12
	422431	AI769410	Hs.221461	ESTs	1.80	3.58
	417557	AA225622	Hs.293589	ESTs	1.32	2.14
35	455313	AW894409	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	1.48	2.57
	415479	F10042	Hs.4840	ESTs	1.83	2.01
	450433	AW444538	Hs.231863	ESTs	1.31	2.58
	410581	AA018982	Hs.125036	tumor endothelial marker 7 precursor	1.54	1.62
	455407	AW936813		gb:PM2-DT0023-050400-003-b10 DT0023 Homo	1.32	2.15
40	417552	R00916	Hs.166510	ESTs	1.50	2.63
	428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	1.94	2.70
	432391	AI732374	Hs.339827	Human DNA sequence from clone RP5-881L22	0.96	2.38
	456283	U68182	Hs.84171	myeloproliferative leukemia virus oncoge	1.22	2.13
	438535	L09078		gb:Homo sapiens mRNA fragment	2.14	1.95
45	416564	AW795793	Hs.2575	Homo sapiens cDNA FLJ12257 fis, clone MA	2.28	1.93
	435200	AA670310	Hs.145903	ESTs	1.16	2.13
	457635	AV660976	Hs.3569	hypothetical protein	1.37	3.10
	449330	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	0.99	2.45
	449319	AA373630	Hs.188750	ESTs	1.56	3.28
50	418992	AW074143	Hs.87134	ESTs	1.88	2.20
	409367	AW382767		gb:PM0-HT0339-081199-001-h05 HT0339 Homo	1.30	2.50
	434973	AW449285	Hs.313636	EST	1.11	2.65
	408383	BE466959	Hs.144153	ESTs	1.30	2.44
	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.23	2.71
55	431996	AL122087	Hs.272304	Homo sapiens mRNA; cDNA DKFZp564C0371 (f	1.24	2.27
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfamily	1.70	1.68
	405146			C8001690*:gi15754446 ref NP_034760.1 ki	2.00	0.68
	436154	AA764950	Hs.119898	ESTs	1.43	3.00
	451233	AA047221	Hs.59752	ESTs	1.38	2.20
60	446856	AI814373	Hs.164175	ESTs	1.33	3.93
	448211	BE384592	Hs.6451	PRO0659 protein	1.48	2.73
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	1.33	2.68
	409609	AW444670	Hs.335685	ESTs	1.27	1.51
	450414	AI907735	Hs.21446	KIAA1716 protein	1.60	1.24
65	452929	AW954938	Hs.172816	neuregulin 1	2.01	3.70
	435112	AW976145	Hs.143198	Inhibitor of growth family, member 3	1.22	1.30
	439806	AA846824	Hs.180908	ESTs	0.80	2.04
	439910	H66765	Hs.339397	ESTs	1.28	2.16
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	1.06	2.82
70	441354	AA931221	Hs.126813	ESTs	1.20	2.28
	428951	AL138153	Hs.300410	ESTs, Moderately similar to A47582 B-cl	1.50	1.83
	438272	AI167963	Hs.143700	ESTs, Weakly similar to S65824 reverse t	1.34	2.51
	429642	X68264	Hs.211579	melanoma cell adhesion molecule	1.18	1.18
	422121	AI757949	Hs.179833	ESTs	1.18	2.26
75	411184	AW821117		gb:PM2-ST0303-170100-003-g03 ST0303 Homo	1.18	2.21
	435871	AF257077	Hs.283627	eukaryotic translation initiation factor	1.17	1.57
	430570	AI417881	Hs.292464	ESTs	1.49	3.17
	431995	AL080197	Hs.272302	hypothetical protein	1.52	2.11

	451326	AW296946	Hs.256078	ESTs	1.19	2.18
	437046	BE149154		gb:RC2-HT0252-271089-017-c11 HT0252 Homo	1.18	2.25
	410154	F06959		gb:HSC1QD011 normalized infant brain cDN	1.41	2.05
5	434373	AI565566	Hs.168587	ESTs	1.39	1.33
	444552	AW295211	Hs.230777	ESTs	1.36	2.20
	411808	AW853441		gb:RC1-CT0252-030100-023-g09 CT0252 Homo	2.12	1.80
	440573	BE550891	Hs.270624	ESTs	2.19	2.17
	443047	AW157377	Hs.132910	ESTs	1.81	2.28
10	451473	AW298047	Hs.346198	ESTs	1.18	2.30
	416265	AA177088	Hs.190065	ESTs	2.37	3.38
	435375	AI733610	Hs.187832	ESTs	1.12	2.18
	401469			NM_022137*:Homo sapiens secreted modular	1.32	1.61
	456152	AA174126	Hs.332163	ESTs	1.26	2.50
15	415808	R21439	Hs.334578	Homo sapiens, clone IMAGE:3929520, mRNA	1.39	2.43
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	0.92	2.20
	435127	AJ217926	Hs.179863	EST	1.36	2.65
	420772	AW752658	Hs.222707	KIAA1718 protein	1.19	1.50
	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	1.45	3.57
20	444678	AI741513	Hs.143739	ESTs	1.43	1.62
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	1.00	1.53
	416463	H59241		Homo sapiens cDNA FLJ11095 fis, clone PL	1.44	2.13
	405158			ENSP00000243337:CDNA FLJ13984 fis, clone	1.38	2.68
	403903			C5001632*:gij10645308[gb]AAG21430.1 AC00	1.32	1.43
25	407271	X98937		gb:H.sapiens rearranged lg heavy chain (1.40	2.68
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.59	1.33
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.17	1.10
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	1.92	2.80
	400075			Eos Control	1.76	2.60
30	433694	AI208611	Hs.12086	Homo sapiens cDNA FLJ11720 fis, clone HE	1.48	2.33
	454826	AW833676		gb:QV4-TT0008-181199-038-h04 TT0008 Homo	1.57	2.89
	415168	AA160805	Hs.199832	ESTs, Weakly similar to I78885 serine/th	2.08	1.76
	439486	AF086303	Hs.103185	ESTs	1.49	2.19
	403291			Target Exon	1.36	2.28
35	438618	AA897673	Hs.123457	ESTs	0.75	0.79
	455087	AW855389		gb:CM3-CT0275-191099-024-e06 CT0275 Homo	0.91	2.63
	408075	AA382881	Hs.42409	CGI-146 protein	1.46	2.15
	436826	AA731863	Hs.120276	ESTs	1.04	3.11
	408961	AW297475	Hs.323180	ESTs	1.25	1.39
40	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.64	2.05
	423300	AK000742	Hs.126774	L2DTL protein	1.47	3.44
	403217	AL134878		ribosomal protein, large P2	1.70	2.22
	437990	AI686579	Hs.121784	ESTs	2.14	1.69
	419156	AC002366	Hs.46329	amelogenin (X chromosome, amelogenesis i	1.40	1.45
45	411817	BE302900	Hs.72241	mitogen-activated protein kinase kinase	1.18	1.12
	425701	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.50	2.15
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	1.57	2.23
	415184	AA380436	Hs.211973	homolog of Yeast RRP4 (ribosomal RNA pro	1.32	2.09
	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.61	1.50
50	401723			Target Exon	1.01	2.68
	439010	AW170332	Hs.75216	Homo sapiens cDNA FLJ13713 fis, clone PL	1.28	1.65
	449166	BE168981	Hs.23131	kinesin family member C3	1.64	2.58
	410642	AW792784		gb:CM0-UM0001-010300-258-h11 UM0001 Homo	1.54	1.90
	409556	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	1.63	1.21
55	439894	AA853077	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.76	0.61
	401913			ENSP00000249158*:CDNA	0.97	2.59
	406097			Target Exon	1.11	1.23
	414745	AA160511	Hs.5326	amino acid system N transporter 2; porcu	1.29	1.12
60	445752	AI733942	Hs.344887	ESTs	2.03	1.68
	408052	AW501117	Hs.283585	ESTs	1.32	1.72
	407256	AA204763	Hs.288036	IRNA isopentenylpyrophosphate transferas	1.01	2.09
	423264	AJ133439	Hs.126076	Glutamate receptor interacting protein	1.51	2.39
	418859	AA229558		gb:nc15d10.s1 NCI_CGAP_Pr1 Homo sapiens	1.40	2.35
65	410370	AB037753	Hs.62767	KIAA1332 protein	1.34	2.00
	417264	AA195100	Hs.188695	ESTs	1.09	2.61
	444909	AI933051	Hs.192280	ESTs	1.56	2.92
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	1.14	2.28
	439212	AF087995	Hs.134877	ESTs	1.06	2.90
	437765	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.25	2.28
70	448951	AI611221	Hs.334802	hypothetical protein FLJ10101	1.88	2.17
	401659			Target Exon	1.63	2.05
	419145	N99638		gb:za39g11.1 Soares fetal liver spleen	2.63	3.85
	444813	AW054834	Hs.210356	ESTs	1.73	2.14
	433902	AW292820	Hs.144906	ESTs	1.88	2.46
75	403072			NM_003319*:Homo sapiens titin (TTN), mRN	1.32	2.91
	452484	AB033042	Hs.29679	cofactor required for Sp1 transcription	0.72	0.70
	456788	AA724612	Hs.133130	Homo sapiens mRNA; cDNA DKFZp566H0124 (f	1.90	3.40
	403315			Target Exon	1.22	2.00

	406432	AJ289116		CD1E antigen, e polypeptide	2.31	2.63
	457785	AA682670	Hs.160884	ESTs	0.96	2.38
	433259	AA580665	Hs.326082	ESTs	1.46	1.07
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor	1.38	2.13
5	401473			Target Exon	1.47	2.04
	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	1.64	2.15
	438029	H61502	Hs.10235	chromosome 5 open reading frame 4	1.44	2.25
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	1.26	2.21
	450817	N71597	Hs.29698	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.20	2.90
10	404427			C6000068*:g 5453579 ref NP_005120.1 bo	0.74	0.81
	430658	AW970093	Hs.24453	ESTs	1.45	2.55
	405723			Target Exon	1.60	2.28
	436896	AW977385	Hs.278815	ESTs	1.17	1.64
	411974	AW880414	Hs.84264	acidic protein rich in leucines	1.54	2.08
15	412528	AJ123478	Hs.32112	ESTs	1.72	2.85
	446425	AW295364	Hs.255418	ESTs	1.25	1.31
	424991	AA775471	Hs.241467	ESTs	0.62	0.37
	443100	AJ033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	1.15	2.34
	445332	AJ220225	Hs.321057	ESTs	1.07	2.00
20	414781	D50917	Hs.77293	KIAA0127 gene product	1.04	3.43
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	1.15	2.53
	424265	AF173901	Hs.144287	hairly/enhancer-of-split related with YRP	1.26	2.00
	446667	BE161878	Hs.224805	ESTs	1.12	2.13
	426399	AA652588	Hs.301348	Homo sapiens cDNA FLJ13271 fis, clone OV	2.26	1.29
25	438190	AA780020	Hs.136798	ESTs, Moderately similar to KBF3_HUMAN N	1.44	2.07
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.38	2.11
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	2.12	3.30
	446410	AJ361109	Hs.151721	ESTs, Weakly similar to I38022 hypothei	1.14	2.33
	427674	NM_003528	Hs.2178	H2B histone family, member Q	1.24	1.00
30	422526	AA311763	Hs.131056	ESTs	1.29	2.04
	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothei	1.26	2.12
	405126	AA063426		gb:zf70c08.s1 Soares_pineal_gland_N3HPG	1.28	2.20
	412093	BE242691	Hs.14947	ESTs	0.87	2.58
	420169	AA256126	Hs.16179	hypothetical protein FLJ23467	1.38	2.07
35	426096	D87436	Hs.166318	lipin 2	2.00	2.25
	402551			NM_005012*:Homo sapiens receptor tyrosin	0.80	0.82
	405760			Target Exon	1.44	2.85
	402901			NM_025206*:Homo sapiens hypothetical pro	1.63	1.27
	453982	AW014252	Hs.252837	ESTs	1.44	2.03
40	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.40	1.18
	438984	BE559514	Hs.275425	hypothetical protein	1.30	2.15
	457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	1.64	3.17
	415054	AJ733907		gb:zo86h09.y5 Stralagene ovarian cancer	1.00	2.20
	426273	AJ174861	Hs.190623	ESTs	1.19	1.16
45	405187			NM_014272*:Homo sapiens a disintegrin-like	1.31	1.35
	413939	AL047051	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.44	1.88
	427596	AA449505	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.06	1.50
	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	2.01	3.90
	406002			Target Exon	1.73	2.08
50	408284	AW248254	Hs.44101	protein kinase PKNbeta	1.28	1.31
	431377	AW178807	Hs.246182	ESTs	1.40	2.70
	451456	AW386183	Hs.210305	ESTs	1.44	2.08
	427530	AA405093	Hs.126519	ESTs	1.07	1.12
	431957	AK002104	Hs.272246	hypothetical protein FLJ11292	1.27	2.89
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.74	1.28
	419600	AA448958	Hs.91481	NEU1 protein	1.13	1.15
	423314	AJ400661	Hs.127811	disintegrin metalloproteinase with throm	1.44	2.53
	451690	AW451469	Hs.209990	ESTs	1.41	2.49
	454662	AW812715		gb:RC4-ST0185-271099-011-g01 ST0185 Homo	1.35	2.86
60	454413	AI653672	Hs.40092	PNAS-123	1.79	2.03
	416861	AW977206	Hs.151858	ESTs	1.52	2.10
	415908	H08623	Hs.22833	ESTs	1.37	2.13
	438942	AW875398	Hs.6451	PRO0659 protein	1.80	1.55
	407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.16	3.18
65	429177	AA447527	Hs.207429	ESTs	1.74	3.19
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	0.77	0.73
	422008	AJ000534	Hs.110708	sarcoglycan, epsilon	1.52	4.08
	434461	AA744046	Hs.133350	ESTs, Weakly similar to I78885 serine/th	1.66	2.16
	413489	BE144228		gb:MRO-HT0165-140200-009-d04 HT0165 Homo	1.28	2.23
70	405551			Target Exon	1.11	1.19
	441183	BE562910	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.20	1.20
	456034	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.98	2.53
	420611	AA994635	Hs.129929	ESTs	1.46	2.15
	422061	BE178434	Hs.267995	ESTs, Moderately similar to G02654 ribos	1.42	2.30
75	437908	AI082424		ESTs	1.38	2.21
	423052	M28214	Hs.123072	RAB38, member RAS oncogene family	0.74	0.43
	401927			C17000914*:g 8394367 ref NP_058549.1 s	2.26	2.14

	432967	AA572949	Hs.207566	ESTs	1.52	2.28
	439159	AF087972	Hs.120938	ESTs	2.03	2.08
	415357	H22757	Hs.13471	ESTs	1.82	2.07
	442327	AA991745	Hs.42522	ESTs	1.48	2.88
5	430186	AB020696	Hs.234791	KIAA0889 protein	1.46	2.23
	426971	AI809984	Hs.243209	ESTs, Weakly similar to NPA1_HUMAN NEURO	1.06	2.13
	422687	AW068823	Hs.119206	Insulin-like growth factor binding prote	1.61	1.37
	432954	AI076345	Hs.214199	ESTs	1.19	2.84
	429040	AL035542	Hs.248169	olfactory receptor, family 2, subfamily	1.25	1.44
10	414169	AA136169	Hs.149335	ESTs	1.59	2.51
	419882	AA687313	Hs.190043	ESTs	1.20	2.50
	426900	AW163564	Hs.142375	ESTs	1.87	1.77
	418773	T39748	Hs.325474	Target CAT	1.35	2.02
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	1.32	2.10
15	428712	AW085131	Hs.190452	KIAA0365 gene product	1.41	1.52
	408839	AW277084		gb:exp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	1.14	2.03
	450492	AW290961	Hs.201815	ESTs	1.17	2.21
	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	1.62	2.31
	457567	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1.80	3.73
20	452426	AI904823	Hs.31297	duodenal cytochrome b	2.15	1.84
	418559	AA225048	Hs.104207	ESTs	1.84	2.33
	439099	AB037800	Hs.5462	protein kinase C and casein kinase subst	1.07	1.15
	451984	R60571	Hs.27406	Homo sapiens mRNA; cDNA DKFZp566F1946 (f	1.18	1.22
	420789	AI670057	Hs.199882	ESTs	2.24	2.55
25	455396	AA236863	Hs.188894	ESTs, Weakly similar to APXL_HUMAN APICA	1.07	1.14
	402948			NM_025206:Homo sapiens hypothetical prot	2.41	1.83
	426405	AW296631	Hs.283403	ESTs	1.28	1.07
	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	0.85	0.77
	416784	AA334592	Hs.79914	lumican	1.88	1.27
30	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2 [Hsapiens	1.20	1.25
	415608	F12795	Hs.12286	ESTs, Moderately similar to ALU1_HUMAN A	1.03	2.31
	428671	BE297851	Hs.189482	zinc finger protein 179	1.26	2.20
	420007	H13700	Hs.31235	ESTs, Weakly similar to Y934_HUMAN HYPOT	1.60	2.25
	400850			Target Exon	1.22	1.03
35	404580			trichorhinopharyngeal syndrome 1 gene (T	1.00	1.00
	407680	AW064284	Hs.279153	ESTs	1.02	2.28
	410420	AA224053	Hs.172405	cell division cycle 27	1.64	1.00
	421234	AA907153	Hs.190060	ESTs	1.76	1.45
	426791	AA384910	Hs.46519	ESTs	1.12	2.15
40	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	1.00	1.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.40	1.00
	440304	BE159984	Hs.125395	ESTs	1.00	1.00
45	441699	AW511126	Hs.127572	ESTs	1.00	1.73
	443383	AI792453	Hs.166507	ESTs	2.04	1.00
	445660	AI702668	Hs.201955	ESTs	1.00	1.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	1.00
	456513	AA279143	Hs.88561	ESTs	1.00	1.40
50	457231	AI472022	Hs.301959	proline synthetase co-transcribed (bacte	0.98	0.63
	459565	W27085	Hs.209694	ESTs	1.00	1.00
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	1.00	1.00
	430971	M26150	Hs.248177	H3 histone family, member L	1.14	1.40
	408376	AW971303	Hs.292601	ESTs	1.08	1.60
55	411920	AW876263		gb:PM4-PT0019-131299-006-E09 PT0019 Homo	0.82	0.45
	457389	AW970989		gb:EST383074 MAGE resequences, MAGK Homo	0.92	0.71
	408565	BE502544	Hs.282244	ESTs, Weakly similar to peptidoglycan re	1.00	2.10
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.00	1.00
	446779	AI341135	Hs.156084	ESTs	1.06	2.02
60	441691	AI015418	Hs.127556	ESTs	1.13	2.03
	402039			Target Exon	0.44	0.36
	437133	AB018319	Hs.5460	KIAA0776 protein	0.95	0.63
	438089	W05391		nuclear receptor subfamily 1, group I, m	3.12	1.00
	409582	R27430	Hs.271565	ESTs	1.00	1.00
65	428769	AW207175	Hs.106771	ESTs	1.00	1.48
	442868	AI022701	Hs.336984	ESTs	1.27	1.62
	439559	AW364875	Hs.173921	ESTs, Weakly similar to 2109260A B cell	1.00	1.33
	426958	R18845	Hs.172979	zinc finger protein 177	1.24	2.25
	419015	T79262	Hs.14463	ESTs	1.16	2.03
70	415806	AA169560		gb:zo89d08.r1 Stratagene ovarian cancer	1.00	1.33
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothe	1.60	2.21
	458760	AI498631	Hs.111334	ferritin, light polypeptide	1.10	1.43
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.28	1.00
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.90	2.31
	438091	AW373052		nuclear receptor subfamily 1, group I, m	4.70	1.00
75	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.48	1.00
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.96	2.84
	416055	Z45423	Hs.13349	Homo sapiens cDNA FLJ14647 fis, clone NT	1.52	1.46

	417895	AA836392	Hs.56237	hypothetical protein FLJ20495	1.05	1.18
	422959	AV647015		paired immunoglobulin-like receptor beta	1.33	1.25
	408969	AW297929	Hs.328317	EST	1.88	2.07
5	409536	H59024	Hs.14485	Homo sapiens cDNA: FLJ23220 fis, clone A	1.18	2.38
	447449	AW137091	Hs.18624	KIAA1052 protein	1.07	1.13
	437315	AW976247	Hs.153248	ESTs	1.16	2.53
	459317	BRCA1b		Eos Control	1.36	1.32
	405137			Target Exon	1.11	1.18
	400366	M22333		Target	1.55	1.42
10	423413	AA325560	Hs.346401	ESTs	1.78	1.57
	433972	AI878910	Hs.278670	cisplatin resistance-associated overexpr	1.62	2.98
	440748	AW451780	Hs.130363	ESTs	1.42	2.14
	422637	AA399024	Hs.118836	myoglobin	1.46	2.38
	432342	AL036128	Hs.274404	plasminogen activator, tissue	1.67	1.10
15	442820	AW293459	Hs.172681	ESTs	1.02	1.13
	436573	AA723297	Hs.127138	ESTs	1.18	1.15
	403779			Target Exon	1.13	1.15
	447686	AI939440	Hs.345192	ESTs	1.66	2.78
	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	1.44	2.48
20	425853	BE348404	Hs.24740	ESTs	1.40	2.75
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	1.52	2.00
	424132	AA335715	Hs.200299	ESTs	1.34	1.32
	421707	NM_014921	Hs.107054	lectamedin-2	1.09	1.14
	442871	AI290691	Hs.131393	ESTs	1.40	2.50
25	448489	AI523875		gb:lg97d04.x1 NCI_CGAP_CLL1 Homo sapiens	1.31	2.20
	436365	AW444548	Hs.163118	ESTs	1.07	1.12
	415733	AI052628	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.91	2.01
	413888	AA580288		gb:nn12d01.s1 NCI_CGAP_Co12 Homo sapiens	1.75	1.93
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	1.92	1.73
30	442959	AI025248	Hs.6927	ESTs	1.05	1.12
	409610	AW444736	Hs.27854	ESTs	1.62	2.45
	424793	AI559696	Hs.298885	ESTs	1.37	2.78
	449977	C16939	Hs.297848	ESTs	1.52	4.57
	414051	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.68	2.84
35	422400	AA974434	Hs.128353	ESTs	1.04	2.20
	443908	AW295791	Hs.13040	G protein-coupled receptor 86	1.47	2.10
	439316	AF086126	Hs.118208	Homo sapiens cDNA FLJ11727 fis, clone HE	2.08	0.59
	438505	AA808948	Hs.173776	ESTs, Moderately similar to ALU1_HUMAN A	1.44	2.73
	436186	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.17	1.00
40	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	1.88	2.58
	431756	R69465	Hs.255889	ESTs	1.12	1.30
	424487	T08754	Hs.6259	KIAA1698 protein	1.15	1.15
	435392	R07195	Hs.19918	ESTs	1.38	2.64
45	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	0.92	2.12
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.44	2.51
	411664	BE065069	Hs.270833	amphiregulin (schwannoma-derived growth	1.94	2.33
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	1.72	2.68
	419612	AI498267	Hs.110613	KIAA0421 protein	2.28	2.46
	435800	AI248285	Hs.118348	ESTs	1.42	2.45
50	433363	AA584829	Hs.275163	non-metastatic cells 2, protein (NM23B)	2.07	2.53
	422936	AA319278		gb:EST21478 Adrenal gland tumor Homo sap	1.46	1.22
	413358	BE259160	Hs.75313	aldo-keto reductase family 1, member B1	1.43	1.43
	435357	N71620	Hs.118173	ESTs	1.44	2.93
	441063	AA913819	Hs.188025	ESTs	1.20	2.80
55	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.44	4.18
	430446	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	1.03	2.34
	401577			NM_000761:Homo sapiens cytochrome P450,	1.13	1.22
	403978			CS000010:gij10440464kbjBAB15765.1} (A	1.22	1.66
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.72	4.60
	416708	H78836	Hs.181900	ESTs, Moderately similar to ALU1_HUMAN A	1.36	2.03
	451410	AL110235	Hs.26358	DKFZP566K1924 protein	1.51	2.29
	451159	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.33	1.09
	448455	AI252625	Hs.269860	ESTs, Moderately similar to S65657 alpha	0.83	0.40
	444020	R92962	Hs.35052	ESTs	1.66	2.50
65	414623	BE391050		gb:601285674F1 NIH_MGC_44 Homo sapiens c	1.84	3.88
	454915	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	1.14	2.10
	444064	W85970	Hs.16292	ESTs	0.80	0.63
	454353	AW389693	Hs.300700	hypothetical protein FLJ20727	1.30	2.10
	447794	AI424999	Hs.161445	EST	1.26	2.05
70	426686	AI362802	Hs.171814	parathyromosin	1.16	1.11
	435815	AA700482	Hs.113157	ESTs	1.66	2.73
	432482	L19267	Hs.275924	dystrophin myotonia-containing WD repea	1.10	1.15
	431062	AA491270	Hs.187946	ESTs	1.44	2.60
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.35	1.06
75	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	1.21	3.45
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	1.23	2.10
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	1.11	2.71

	431868	BE246400	Hs.285176	acetyl-Coenzyme A transporter	1.03	3.10
	429321	AA449921		gb:zx37g07.r1 Soares_lotal_fetus_Nb2HF8_	1.68	2.93
	417890	R79048		gb:yi87g02.r1 Soares_placenta_Nb2HP_Homo	1.32	1.80
5	439590	AF086410		gb:Homo sapiens full length insert cDNA	1.32	2.43
	420232	AW450051	Hs.256295	ESTs	1.28	2.26
	418927	BE349635	Hs.190284	ESTs	1.46	1.23
	441940	AW298115	Hs.128152	ESTs	1.34	1.34
	401090			C9000193*:g[i]6330729[dbj]BAA86547.1[](AB	1.50	1.40
10	409136	AW206670	Hs.50748	chromosome 21 open reading frame 18	1.02	2.38
	438267	AW205708	Hs.292725	ESTs, Weakly similar to T18818 hypothetical	1.28	2.25
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCL_CGAP_Lym12 Homo sapien	1.05	2.81
	420067	TS2431	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (fr	1.77	2.40
	442180	AA983913	Hs.128929	ESTs	1.76	2.38
	434256	AI378817	Hs.191847	ESTs	1.05	2.06
15	444519	AI160304	Hs.28313	ESTs	0.55	0.63
	454459	AW855738	Hs.17767	KIAA1554 protein	1.10	2.05
	455988	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	1.70	2.64
	444510	AI367823	Hs.146872	ESTs	1.44	2.08
	456210	N49729	Hs.156875	ESTs	1.64	2.65
20	450569	AW192334	Hs.38218	ESTs	1.78	2.71
	414921	BE390551	Hs.77628	steroidogenic acute regulatory protein r	1.05	1.12
	401381			C14000165:g[i]12698069[dbj]BAB21853.1[](A	0.63	0.85
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	1.05	1.14
	453762	AW977286	Hs.17428	RBP1-like protein	1.42	2.68
25	419403	AA744520	Hs.87734	ESTs, Weakly similar to nonsyndromic hea	0.99	2.17
	423736	AW936874		gb:RC1-DT0029-120100-011-407 DT0029 Homo	2.05	1.56
	421186	AI798039	Hs.270563	ESTs, Moderately similar to T12512 hypot	1.29	1.31
	426435	AI827946	Hs.124854	hypothetical brain protein my040	1.35	1.59
	439312	AA833902	Hs.270745	ESTs	1.60	2.50
30	407924	BE537128	Hs.299797	ESTs	1.51	1.15
	409692	AI500724		KIAA1550 protein	1.72	2.21
	415449	H15034		gb:ym20a03.s1 Soares Infant brain 1NIB H	1.50	2.13
	423436	R21176	Hs.100926	ESTs	1.18	2.60
	458697	AI797713	Hs.156471	ESTs	1.54	2.20
35	415770	M79237		gb:EST01385 Subtracted Hippocampus, Stra	1.49	1.55
	449279	AI962312	Hs.224976	ESTs, Weakly similar to CRX_HUMAN CONE-R	2.50	3.60
	429735	AA458759	Hs.188794	ESTs	1.84	2.31
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 tis, clone PL	1.10	1.19
40	412557	AA761612	Hs.291557	ESTs	1.10	1.18
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	1.18	1.12
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	1.35	2.39
	420855	AA281092	Hs.33417	Homo sapiens cDNA: FLJ22806 tis, clone K	1.22	2.09
	450567	AA033904	Hs.269235	ESTs	1.60	2.20
	414197	W44877	Hs.55501	ESTs	1.06	2.08
45	448800	AI571294	Hs.298889	ESTs, Moderately similar to ALU1_HUMAN A	1.65	2.79
	421338	AA287443		gb:zs52c10.r1 NCL_CGAP_GCB1 Homo sapiens	1.47	2.90
	412679	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	1.32	2.53
	417882	R22311		gb:yh26c09.r1 Soares placenta Nb2HP Homo	1.58	2.43
50	425112	AW953291	Hs.64211	hypothetical protein MGC5601	0.70	0.63
	401658			C16000210:g[i]12585542[spj]O14771[Z213_HUM	1.68	2.04
	409325	AW377549	Hs.17865	ESTs	1.68	2.21
	437402	AI553976	Hs.121191	ESTs	1.20	2.35
	433455	AA360439	Hs.89319	ESTs	0.98	2.53
55	457329	AI634860	Hs.247043	type 1 tumor necrosis factor receptor sh	0.59	0.43
	434830	AW852235		gb:QV0-CT0225-230300-169-e11 CT0225 Homo	1.24	1.12
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	1.44	2.53
	446098	AW072215	Hs.208470	ESTs	1.38	2.93
	443310	BE552018	Hs.133152	ESTs	0.85	0.83
60	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.42	2.26
	420229	AA256675	Hs.194058	ESTs, Weakly similar to AF252293 1 PAR3	1.70	2.39
	403371			Target Exon	1.50	3.43
	410744	H86002		gb:ys92b01.r1 Soares retina N2b5HR Homo	1.32	2.13
	424160	T74062		gb:yc81f01.r1 Soares Infant brain 1NIB H	1.30	2.17
65	438818	AW979008	Hs.222487	ESTs	1.98	2.43
	438791	AA825750	Hs.129983	ESTs	1.12	2.15
	411206	AW827390	Hs.16689	ESTs	1.17	2.58
	432211	BE274530	Hs.273333	hypothetical protein FLJ10986	0.42	0.30
	448918	AB011152	Hs.22572	KIAA0580 protein	1.54	2.63
	424496	AI733451	Hs.167165	hypothetical protein FLJ12975	1.39	2.25
70	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	1.84	3.23
	457581	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	1.21	1.09
	435353	AW243062	Hs.190348	ESTs	1.90	2.98
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.21	1.24
	433682	AA642418	Hs.17381	ESTs	1.18	2.23
75	424915	R42755	Hs.23096	ESTs	1.60	2.73
	442201	AW516704	Hs.208726	ESTs	1.74	3.20
	429111	AI870811	Hs.7579	KIAA1151 protein	1.27	1.40

5	429282	N27596	Hs.21342	ESTs	1.84	3.73
	436604	AW105129	Hs.242158	ESTs	1.27	2.70
	448712	W01046	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	0.79	2.70
	412274	AA101443		gb:zn74a07.r1 Stratagene NT2 neuronal pr	1.40	2.53
	403859			C5001408*gl 12621134 ref NP_075244.1 M	1.76	2.00
10	451521	AA018237	Hs.128189	gb:ze53a02.r1 Soares ref na N2b4HR Homo	1.48	2.51
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	1.44	2.60
	442722	AL048889	Hs.131029	ESTs, Weakly similar to B28096 line-1 pr	1.20	2.25
	400840			Target Exon	0.66	0.60
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	1.23	1.41
15	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	1.77	2.12
	410725	AW799279		gb:RC0-UM0051-210300-012-h06 UM0051 Homo	1.08	2.55
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.94	2.29
	450717	T94709		gb:ye35d09.r1 Stratagene lung (937210) H	1.56	2.64
	400314	NM_018949	Hs.192720	G protein-coupled receptor 14	0.89	0.87
20	434947	AA654320	Hs.183819	Homo sapiens cDNA FLJ12304 fis, clone MA	1.19	2.14
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	1.24	2.19
	409005	AW299806	Hs.297256	ESTs	1.24	2.03
	405584			Target Exon	1.52	2.37
	420203	AA256374	Hs.191069	ESTs	1.16	1.37
25	406156			Target Exon	1.18	1.17
	422132	AB002337	Hs.112078	KIAA0339 gene product	1.08	1.16
	441371	AW452292	Hs.197354	ESTs	1.19	2.00
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	1.30	2.76
	424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.48	2.48
30	450893	AK002185	Hs.25625	hypothetical protein FLJ11323	1.15	1.57
	418481	M81945	Hs.85289	CD34 antigen	2.16	1.76
	443077	AI459490	Hs.60090	Homo sapiens cDNA FLJ13595 fis, clone PL	1.36	2.41
	437521	AA758756	Hs.121380	ESTs	1.07	2.05
	430265	L36033	Hs.237356	stromal cell-derived factor 1	2.34	1.35
35	446898	AV660906	Hs.184411	albumin	1.52	1.33
	429725	AA457367	Hs.191638	ESTs	1.38	3.00
	425114	AW409763	Hs.50699	ESTs, Weakly similar to 2109260A B cell	1.13	2.34
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	1.62	1.71
	435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	1.20	2.50
40	415634	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.46	2.35
	420565	AI806770	Hs.30258	ESTs	1.39	3.85
	419494	W01060	Hs.34382	ESTs	1.10	1.75
	458183	AL031591	Hs.7370	phosphatidylinositol transfer protein, b	1.28	2.24
	416620	R93080	Hs.35035	ESTs	1.81	2.58
45	431356	AW499632	Hs.288512	Homo sapiens cDNA FLJ11632 fis, clone HE	1.42	2.03
	433282	BE539101	Hs.5324	hypothetical protein	0.33	0.20
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.50	0.95
	458126	AW979136	Hs.124629	ESTs	1.34	1.32
	414005	AA134489	Hs.269379	ESTs	1.52	2.07
50	411496	AW849241		gb:IL3-CT0215-210200-088-E03 CT0215 Homo	1.10	2.21
	451147	AA016982	Hs.64341	ESTs	1.53	2.29
	450238	T89693	Hs.138777	ESTs	1.32	2.28
	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	1.46	1.40
	449479	AI797619	Hs.197659	ESTs	0.72	0.68
55	403066			Target Exon	1.32	1.19
	410118	AW590680	Hs.110802	von Willebrand factor	1.72	2.54
	437674	AI749921	Hs.205377	ESTs	1.38	2.21
	431065	AA491286	Hs.128792	ESTs	1.30	2.08
	416352	H78006	Hs.19553	ESTs	1.05	1.14
60	452565	BE066552		gb:RC3-BT0333-300300-017-h08 BT0333 Homo	1.46	2.53
	418115	AW005376	Hs.173280	ESTs	1.20	0.98
	422031	R66895	Hs.28788	ESTs	1.37	1.37
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	1.64	2.20
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	1.03	2.35
65	435521	W23814	Hs.6361	mitogen-activated protein kinase kinase	0.73	0.59
	438874	H02780	Hs.347520	gb:yl41a11.r1 Soares placenta Nb2HP Homo	1.56	2.73
	441167	AA921754	Hs.211781	ESTs	1.74	2.12
	455917	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	1.29	1.35
	419058	AW675039	Hs.1227	aminolevulinatase, delta, dehydratase	2.04	1.83
70	408651	BE266928	Hs.17126	hypothetical protein MGC15912	1.30	1.23
	442737	AB002319	Hs.8663	KIAA0321 protein	0.85	0.79
	407134	T51588		gb:yb27e06.s1 Stratagene fetal spleen (9	1.23	0.97
	447492	AI381619	Hs.20188	ESTs	1.26	2.28
	437840	AA884836	Hs.292014	ESTs	2.05	2.29
75	412294	AA689219	Hs.117176	poly(A)-binding protein, nuclear 1	1.47	3.55
	419909	AL136653	Hs.93675	decidual protein induced by progesterone	1.10	2.18
	432569	AI131140	Hs.152434	ESTs	1.34	1.83
	412252	AW903782		gb:CM4-NN1032-190400-527-g09 NN1032 Homo	1.26	2.00
	444298	Z17870		gb:HSDH1020 Stratagene cDNA library Hum	1.36	2.68
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	0.95	2.23
	418315	T06475	Hs.124962	Homo sapiens, clone IMAGE:3510191, mRNA,	0.82	0.82

	440357	AA379353	Hs.20950	phospholysine phosphohistidine inorganic	0.83	0.68
	440867	AI417007	Hs.166338	ESTs	1.45	1.50
	410956	AW938322		gb:PM1-DT0054-231299-002-c02 DT0054 Homo	1.06	2.95
	446574	AI310135	Hs.335933	ESTs	1.54	2.45
5	447912	AW576549	Hs.165728	ESTs, Weakly similar to I38022 hypothe	1.22	2.07
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	1.89	2.08
	433762	AA732484	Hs.169399	ESTs	1.24	2.58
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	3.71	1.38
10	409282	AW966480		gb:EST378554 MAGE resequences, MAGI Homo	1.70	1.70
	425169	AW292500	Hs.128514	ESTs	1.13	1.12
	458497	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	1.26	2.28
	405673			NM_022775:Homo sapiens hypothetical prot	2.00	1.00
	442691	AW341438	Hs.278036	ESTs	1.38	2.28
	424316	AA676403	Hs.145078	regulator of differentiation (in S. pom	1.06	2.10
15	444508	AI174683	Hs.329863	ESTs	1.95	1.82
	447345	BE247767	Hs.18166	KIAA0870 protein	1.26	2.10
	438488	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	1.68	2.63
	428946	D42046	Hs.194665	DNA2 (DNA replication helicase, yeast, h	1.32	2.33
20	403214			NM_016232*:Homo sapiens Interleukin 1 re	1.02	2.15
	404495			C8001441*:gij8923061jrefNP_060114.1) hy	2.20	2.49
	443471	AW236939	Hs.172154	Homo sapiens clone FLB3442 PRO0872 mRNA,	1.58	1.74
	437116	AL049253	Hs.190162	ESTs	1.22	2.53
	451357	AB020640	Hs.26319	Human DNA sequence from clone RP3-467L1	0.94	2.35
25	408255	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	1.12	1.39
	448931	AI597805	Hs.192671	ESTs	1.30	3.29
	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	1.86	2.32
	407140	AA059106	Hs.271780	ESTs, Weakly similar to I38022 hypothe	1.37	1.01
	429187	AA447648	Hs.163872	ESTs, Weakly similar to S65657 alpha-1C-	1.74	1.55
30	423614	AI457640	Hs.206532	ESTs	1.48	2.83
	428073	AA446167	Hs.47385	ESTs	1.24	2.00
	415732	AA167566	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.31	2.34
	412634	U55984	Hs.289088	heat shock 90kD protein 1, alpha	0.42	0.22
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.94	1.27
35	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	0.78	0.71
	402654			Target Exon	0.90	0.85
	457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	0.86	0.90
	405340			C2002952:gij1345964jsepP10079jFBP1_STRPU	1.46	2.33
40	426259	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	1.63	2.75
	442237	AW905607	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCLE	1.08	3.38
	456370	AA234938	Hs.87384	ESTs	0.77	2.83
	407041	X15673		gb:Human pTR2 mRNA for repetitive sequen	2.00	1.84
	452001	AI827675	Hs.274281	fidgetin	1.38	2.03
	445137	AI733837	Hs.145661	ESTs	1.60	3.00
45	440808	AK001339	Hs.7432	hypothetical protein FLJ10477	1.17	2.10
	404418			Target Exon	1.90	3.36
	447658	AI916872	Hs.213424	ESTs	1.90	2.21
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.58	1.24
	400834			NM_002240*:Homo sapiens potassium inward	1.25	2.33
50	449542	AW857362	Hs.268855	ESTs, Weakly similar to I38022 hypothe	1.46	1.28
	441043	AA913422	Hs.192104	ESTs	1.26	1.09
	403391			C3001164*:gij1730196jsepP50573jGAR3_RAT	1.46	2.55
	449129	AI631602	Hs.258949	ESTs	1.27	2.48
	418321	D63477	Hs.84087	KIAA0143 protein	0.56	0.52
55	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fs, clone HE	1.31	2.06
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	1.34	1.22
	428554	R46070	Hs.6407	ESTs	1.04	2.08
	401890			Target Exon	1.24	1.14
	419501	AW843822		gb:CM4-CN0045-010200-514-f08 CN0045 Homo	1.74	1.38
60	457096	AI809202	Hs.208343	ESTs, Weakly similar to carboside sulf	0.82	0.87
	426123	AA370352		gb:EST82246 Prostate gland I Homo sapien	1.28	2.35
	449445	AW197349	Hs.232197	ESTs	1.24	2.13
	430683	AC004862	Hs.247768	Homo sapiens PAC clone RP4-697H17 from 7	1.30	2.00
	440642	AI744995		ESTs, Moderately similar to ALU4_HUMAN A	1.29	2.44
65	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	1.78	2.95
	449822	AW013915	Hs.196578	ESTs	1.42	2.20
	415116	AA160363	Hs.269956	ESTs	2.02	1.03
	457269	AI338993	Hs.134535	ESTs	1.93	1.35
	427877	AW138725	Hs.178057	ESTs	1.91	2.42
70	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	1.00	3.13
	458390	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!	1.02	2.21
	435844	AA700856	Hs.59651	ESTs, Weakly similar to I78885 serine/th	0.85	0.81
	427237	AA399964	Hs.97763	ESTs	1.57	1.44
	406855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	1.20	3.13
75	442151	AI733404	Hs.128865	ESTs	1.50	2.13
	412708	R26930	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	1.16	3.00
	417262	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot	1.25	2.40
	419362	N64116	Hs.24624	hypothetical protein FLJ21945	1.38	2.48

	447248	AW295831	Hs.6496	ESTs	1.56	2.03
	415522	F13010	Hs.12400	ESTs	1.48	2.30
	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 lis, clone PL	1.26	2.88
	414585	W46954	Hs.334716	hypothetical protein MGC16291	1.24	2.05
5	443197	Z43613		gb:HSC1GD091 normalized infant brain cDN	1.11	2.04
	428266	AJ382001	Hs.43590	ESTs	1.09	2.03
	447083	AJ472124	Hs.157757	ESTs	1.66	3.53
	412302	AW936334		gb:QV4-DT0021-281299-070-g05 DT0021 Homo	1.74	3.00
	445555	AW974013		ESTs	1.32	1.29
10	453117	AW162044	Hs.104203	hypothetical protein MGC12981	0.73	0.81
	436757	AW975663	Hs.293404	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	1.88
	431976	AA719001	Hs.291065	ESTs	1.23	2.01
	430557	AA482910	Hs.279664	ESTs	1.64	2.65
	438744	BE314727	Hs.75721	profilin 1	0.85	0.85
15	439325	AF086139	Hs.150423	cyclin-dependent kinase 9 (CDC2-related	1.16	2.05
	438117	AA328041	Hs.194329	hypothetical protein FLJ21174	0.79	0.76
	401686			NM_014587*:Homo sapiens SRY (sex determi	1.32	2.31
	420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	0.78	0.53
20	434288	AW189075	Hs.116265	fibrillin3	2.42	4.23
	433215	AB040912	Hs.191098	hypothetical protein FLJ11598	1.36	1.36
	413429	BE139117	Hs.278881	ESTs	1.30	2.98
	426417	AA377908	Hs.13254	ESTs	1.36	1.77
	413882	AA132973	Hs.184492	ESTs	1.55	2.10
	413346	AA128586		gb:z124h06.r1 Soares_pregnant_uterus_NbH	1.29	1.77
25	445020	AI205655	Hs.147221	ESTs	1.90	2.00
	418175	AW967054	Hs.206312	ESTs, Weakly similar to I38022 hypothei	1.60	3.70
	429582	AJ569068	Hs.22247	ESTs	1.06	2.38
	409134	AW340389	Hs.250585	ESTs	1.64	2.57
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	0.73	2.33
30	435867	F13625	Hs.124183	ESTs	1.10	2.33
	440513	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mRNA,	0.85	2.03
	419711	C02621	Hs.159282	ESTs	1.22	2.00
	434249	AA987537	Hs.129875	ESTs	1.29	2.48
	437355	AL359557	Hs.306508	Homo sapiens mRNA; cDNA DKFZp762O1415 (f	1.86	2.08
35	428360	H10291	Hs.30974	ESTs	1.40	2.05
	435339	AJ358300	Hs.129827	ESTs	1.38	2.18
	435345	AW360966	Hs.6653	ESTs	1.49	2.27
	435105	AJ878982	Hs.131859	Homo sapiens F-box protein FBX11 mRNA, p	1.78	2.33
	459645	AA074346	Hs.250715	ESTs	1.50	2.40
40	449691	AA002143	Hs.21413	solute carrier family 12, (potassium-chl	0.74	0.69
	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	1.42	2.76
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.00	2.16
	456955	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	0.84	0.81
45	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	1.30	2.21
	457926	AA452378	Hs.11637	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	1.27	2.12
	444557	AI167637	Hs.146924	ESTs	1.83	2.35
	434476	AW858520	Hs.84264	acidic protein rich in leucines	1.43	3.80
	458059	AW015588	Hs.137232	ESTs, Weakly similar to S65657 alpha-1C-	1.30	2.23
	413595	AW235215	Hs.16145	ESTs	2.10	2.43
50	417281	R98773	Hs.268883	ESTs	1.26	2.10
	445689	BE158869		gb:QV0-HT0398-210100-096-f08 HT0398 Homo	1.15	2.15
	423249	AA323682	Hs.125374	ESTs, Weakly similar to S26689 hypothei	1.76	1.50
	408366	AW511255	Hs.346442	ESTs	1.74	2.91
	441359	AJ435179	Hs.126820	ESTs	2.43	1.59
55	413068	BE063792		gb:QV3-BT0295-260100-066-d06 BT0295 Homo	1.52	2.09
	441322	AW071851	Hs.130628	ESTs	1.42	2.10
	409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfil	1.11	2.20
	432413	AK000257	Hs.274505	Homo sapiens mRNA; cDNA DKFZp564A216 (fr	1.10	2.25
60	425391	AI248252	Hs.160672	ESTs	1.17	2.38
	443861	AW449462	Hs.134743	ESTs	1.44	2.30
	454609	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.30	1.33
	425893	AA629895		gb:ad43b07.s1 Stratagene lung carcinoma	1.76	2.51
	443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)-related k	1.81	2.90
65	410359	R38624	Hs.106313	ESTs	1.78	2.05
	406308			NM_025192:Homo sapiens hypothetical prot	1.92	2.24
	432476	T94344	Hs.326263	ESTs	1.40	2.45
	435073	AA664078		gb:ac04a05.s1 Stratagene lung (937210) H	1.66	2.26
	420581	AA278469	Hs.151940	ESTs	1.48	2.58
70	435579	AJ332373	Hs.156924	ESTs	1.46	2.68
	439633	AF086464	Hs.86248	ESTs	1.40	2.48
	430551	AA481150	Hs.136343	ESTs	1.40	2.28
	450855	T97988	Hs.295605	mannosidase, alpha, class 2A, member 2	1.48	2.40
	444326	AI939357	Hs.270710	ESTs	0.88	2.28
	412149	R49355	Hs.273824	ESTs	1.58	2.19
75	455116	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	1.56	2.50
	449626	AA774247	Hs.301637	zinc finger protein 258	0.60	0.53
	410047	AI167810	Hs.132390	zinc finger protein 36 (KOX 18)	0.66	0.58

	418865	AW117500	Hs.104241	ESTs	1.58	2.63
	402762			ENSP00000235171*:GAP Junction beta-4 pro	0.81	0.82
	436449	AI418027	Hs.120361	ESTs	1.46	1.46
5	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	1.38	2.23
	431235	AA318271	Hs.250905	hypothetical protein	1.14	2.55
	448576	AB026730	Hs.21495	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	0.70	0.78
	408100	AW205382	Hs.42676	KIAA0781 protein	1.36	2.66
	433436	AW162474		Bruno (Drosophila) -like 6, RNA binding	1.50	2.15
	422337	R38572		gb:yc87c11.s1 Soares infant brain 1N1B H	2.23	1.71
10	426160	AA206020	Hs.167460	splicing factor, arginine/serine-rich 3	1.08	2.09
	447008	BE010189		nuclear receptor subfamily 1, group I, m	1.26	1.27
	420141	AA702951	Hs.124103	ESTs, Weakly similar to I38344 tlin, ca	1.45	2.60
	423840	AA332434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	1.26	2.47
	447793	AI424924	Hs.211203	ESTs	2.38	1.83
15	407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.11	2.54
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	2.05
	421311	N71848	Hs.283609	hypothetical protein PRO2032	0.51	0.44
	444649	AW207523	Hs.197628	ESTs	1.21	2.24
	448688	R94570	Hs.266869	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	3.25
20	428847	AI954833	Hs.98881	ESTs	1.48	2.66
	413750	BE161453		gb:IL2-HT0437-290200-045-A06 HT0437 Homo	1.22	1.00
	429355	AW973253	Hs.292689	ESTs	1.86	2.35
	427798	AA412499	Hs.104779	ESTs	1.82	2.33
25	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	0.80	2.00
	451719	AI373532	Hs.157910	ESTs	1.29	3.85
	438094	AI821755	Hs.131805	ESTs, Weakly similar to A56194 thromboxa	1.74	2.54
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	0.52	0.49
	407414	AF072164		gb:Homo sapiens HSFE-1 mRNA, partial cds	1.67	2.28
	416410	H53777	Hs.36822	ESTs	1.85	2.28
30	439141	AI241470	Hs.268982	ESTs	1.08	2.28
	441181	AA416925	Hs.121076	peptidylprolyl isomerase (cyclophilin)-I	1.81	2.02
	434482	AF143331	Hs.16073	ESTs	1.22	2.00
	455757	BE079531		gb:RC5-BT0624-240300-013-D08 BT0624 Homo	1.53	2.16
35	425787	AA363867	Hs.155029	ESTs	0.76	2.13
	405727			CX001244:gi11420428[ref][XP_004814.1] be	1.70	2.21
	441846	AW850980		gb:IL3-CT0220-150200-068-803 CT0220 Homo	1.16	2.14
	451945	BE504055	Hs.211420	ESTs	0.84	2.73
	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	1.60	2.43
40	451140	AW411354	Hs.26002	LIM domain binding 1	1.14	1.20
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.03	2.42
	453041	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	1.69	3.43
	437613	R19892	Hs.10267	MIL1 protein	1.16	2.11
	451507	AW291109	Hs.208787	ESTs, Weakly similar to T31611 hypotheti	1.22	2.05
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.85	1.00
45	453669	AL049029	Hs.7258	hypothetical protein FLJ22021	0.75	0.64
	455065	AW854352		gb:RC3-CT0255-200100-024-g10 CT0255 Homo	1.49	2.20
	442220	AL037800	Hs.8148	selenoprotein T	0.50	0.18
	437936	AW798475	Hs.288549	hypothetical protein FLJ14710	1.50	2.44
	442556	AL137781	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	0.54	0.37
50	405223			Target Exon	1.09	2.80
	437225	AW975982	Hs.292935	ESTs	1.03	2.47
	421101	AF010446	Hs.101840	major histocompatibility complex, class	0.72	0.57
	436200	R51386	Hs.124881	ESTs	1.64	2.93
55	402025			NM_021624:Homo sapiens histamine H4 rece	1.52	2.28
	407019	U49973		gb:Human Tigger1 transposable element, c	2.40	2.12
	451305	AW003571	Hs.211191	ESTs, Weakly similar to A46010 X-linked	1.24	3.23
	423450	AJ290445	Hs.128759	KIAA0524 protein	1.64	2.13
	423139	AW402725	Hs.288560	hypothetical protein FLJ21106	1.61	2.28
60	451763	AW294647	Hs.233634	hypothetical protein FLJ14220	1.39	2.08
	456915	AI915689	Hs.212781	EST	1.62	2.02
	452829	AI955579	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	0.60	0.41
	446383	T05816	Hs.92511	ESTs	2.08	1.48
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypotheti	1.88	2.49
	433820	AI401627	Hs.174067	ESTs	1.30	2.00
65	419719	AA844700	Hs.39297	ESTs, Moderately similar to ALU1_HUMAN A	1.33	2.00
	415868	H06728	Hs.21017	ESTs	1.34	2.08
	420738	NM_004185	Hs.258575	wingless-type MMTV integration site fami	1.42	2.29
	446614	AK001733	Hs.15562	hypothetical protein FLJ10871	0.79	0.78
70	404167			NM_021956*:Homo sapiens glutamate recept	1.62	2.55
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	0.72	0.75
	401215			C12000457*:gi17512178[pl][T30337] polypr	1.14	2.08
	421600	AW893889	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.66
	426248	T18988	Hs.293668	ESTs	1.17	3.44
	454523	AW803980		gb:PMO-UM0084-240300-001-G11 UM0084 Homo	1.34	2.40
75	420656	AA279098	Hs.187636	ESTs	1.22	2.43
	402833			C1002508:gi16691937[emb][CAB65797.1] (ALO	1.31	2.00
	438910	AA827921	Hs.291858	ESTs, Weakly similar to ALUC_HUMAN IIII	1.39	3.13

	416170	H42454	Hs.220645	ESTs	0.99	2.18
	433598	A1762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	2.04	1.28
	417699	T91491	Hs.119670	ESTs	1.36	2.50
5	459605	AL045773		gb:DKFZp434F246_r1 434 (synonym: hies3)	1.21	2.13
	453204	R10799	Hs.191990	ESTs	3.12	2.98
	458971	AL119206	Hs.126257	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.34	2.09
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.68	2.00
	400414	AF083118	Hs.283968	Homo sapiens CATX-2 mRNA, complete cds	1.70	2.54
10	426263	A1908774	Hs.259785	camitline palmitoyltransferase I, liver	0.96	2.14
	439334	A148976	Hs.112062	ESTs	1.50	2.45
	455527	AW984479		gb:PM1-HN0012-220300-001-b12 HN0012 Homo	1.46	2.28
	408084	AL040832	Hs.160422	Homo sapiens clone PP902 unknown mRNA	1.61	2.23
	432059	AF227131	Hs.272387	taste receptor, type 2, member 4	1.66	2.15
15	429791	AW015667	Hs.119427	ESTs	1.51	2.83
	438695	A1885190	Hs.156089	ESTs, Weakly similar to repressor protei	1.19	2.03
	458139	A1525711	Hs.253147	ESTs	1.42	2.10
	413035	BE155563		gb:PM4-HT0352-171199-001-C05 HT0352 Homo	1.62	2.30
	422444	AA310688		gb:EST181501 Jurkat T-cells V Homo sapie	1.38	2.05
20	409546	AW410190	Hs.250624	hypothetical protein MGC4473	1.87	2.18
	411432	AW846272		gb:QV0-CT0179-300999-024-d12 CT0179 Homo	1.04	2.03
	445327	A1220082	Hs.147722	ESTs	1.16	2.10
	424628	AB011136	Hs.151385	KIAA0564 protein	0.61	0.63
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	0.56	0.39
25	409894	BE081731		gb:QV2-BT0635-220400-158-e04 BT0635 Homo	1.50	2.45
	422776	AA316987	Hs.129846	ESTs	1.36	2.20
	428255	A1627478	Hs.187670	ESTs	1.34	2.40
	412484	AA112090	Hs.269961	ESTs	0.97	2.00
	432789	D26361	Hs.3104	KIAA0042 gene product	1.44	2.73
30	430100	AA766178	Hs.291601	ESTs, Highly similar to T00350 hypothei	1.06	2.02
	419528	AA244000	Hs.222365	ESTs	1.34	2.06
	441793	AA968459	Hs.158785	ESTs	1.80	2.70
	429468	AF033579		T-box 10	0.71	0.61
	410248	AA166553	Hs.268171	ESTs	2.55	2.10
35	401818			NM_000664*:Homo sapiens acetyl-Coenzyme	1.76	2.58
	451724	A1903765		gb:UT-BT037-301298-102 BT037 Homo sapien	1.64	2.28
	431866	NM_012098	Hs.8025	angiotensin-like 2	1.56	2.36
	432719	AW935411	Hs.314460	ESTs	1.36	2.25
	418977	AA233094	Hs.191517	ESTs	2.06	3.60
40	404220			C6000989*:gil7573285[emb CAB87644.1] (AL	1.54	2.23
	446708	BE549905	Hs.231754	ESTs	1.35	2.16
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	1.42	2.38
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	1.40	2.50
	400704			Target Exon	1.48	1.00
45	406104			Target Exon	1.22	2.03
	411008	AW813238		gb:MR3-ST0191-020200-207-d04 ST0191 Homo	1.00	2.13
	426582	AA381797	Hs.281121	ESTs	1.35	2.45
	430853	A1734179	Hs.105876	ESTs	1.43	2.23
	432420	AL044659	Hs.43791	ESTs	1.15	2.03
50	403197			C2002793*:gil1353148[sp Q09568]YR86_CAE	0.52	0.47
	432407	AA221036		gb:zr0312.r1 Stratagene NT2 neuronal pr	1.93	2.23
	414996	AW747800	Hs.55016	hypothetical protein FLJ21935	1.56	2.72
	401016			ENSP00000227126:NAALADASE II PROTEIN.	1.25	2.45
	433335	AA584134	Hs.269454	ESTs	1.31	2.24
55	459668	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.16	2.03
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypothei	3.75	2.72
	452277	AL049013	Hs.28783	KIAA1223 protein	0.33	0.26
	425712	AA412548	Hs.21423	ESTs, Moderately similar to ALU1_HUMAN A	1.34	2.21
	427598	AA406057	Hs.97998	ESTs	1.06	2.05
60	412565	M85975	Hs.344069	gb:EST02500 Fetal brain, Stratagene (cat	1.24	2.59
	422043	AL133649	Hs.110953	retinoic acid induced 1	0.48	0.41
	421814	L12350	Hs.108623	thrombospondin 2	0.48	2.45
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	1.32	2.45
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	0.39	0.28
65	452396	H10302	Hs.112577	ESTs	1.60	2.45
	440612	BE561384		gb:601344969F1 NIH_MGC_8 Homo sapiens cD	1.08	2.60
	454721	AW815588		gb:QV0-ST0216-061299-066-a09 ST0216 Homo	1.44	1.65
	417796	AA206141	Hs.6786	ESTs	1.68	3.85
	432864	D16217	Hs.279607	calpastatin	0.43	0.35
70	454480	AA088375	Hs.22612	hypothetical protein DKFZp566D1346	2.19	1.91
	434490	AF143870	Hs.15246	ESTs	2.26	2.07
	403871	AA515814		gb:ng64b03.s1 NCI_CGAP_Lip2 Homo sapiens	1.42	2.55
	441283	AA927670	Hs.131704	C5001783*:gil780367[gb AAB05844.1] (L416	1.60	2.63
75	442250	AW290871	Hs.129121	ESTs	1.31	3.63
	456747	AL037357	Hs.125864	ESTs	1.14	2.38
	425757	AA363171		tropomodulin 2 (neuronal)	1.61	1.26
	405494			gb:EST72986 Ovary II Homo sapiens cDNA 5	1.29	2.95
				C2001837*:gil12697903[gb BAB21770.1] (A	2.09	1.00

5	432250	AA452088	Hs.274170	Opa-interacting protein 2	1.26	2.71
	431911	AK000156	Hs.272193	Homo sapiens cDNA FLJ20149 fis, clone CO	1.46	2.60
	413923	AI733852	Hs.199957	ESTs	1.62	2.10
	449590	AA694070	Hs.268835	ESTs	1.20	2.53
	438467	AA808027	Hs.123277	ESTs	1.48	2.10
	432121	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	1.27	3.13
	412298	AW936300		gb:QV4-DT0021-281299-070-a04 DT0021 Homo	1.42	2.60
	408519	AA679082	Hs.43481	hypothetical protein DKFZp564K192	1.84	3.70
	416067	T79732	Hs.14633	ESTs	1.11	3.08
10	420497	AW206285	Hs.253548	ESTs	1.90	2.48
	405704			NM_001844*:Homo sapiens collagen, type I	1.42	2.90
	423443	AI432601	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	1.42	2.03
	415904	Z44679	Hs.336391	ESTs	1.62	2.94
	413786	AW613780	Hs.13500	ESTs	0.33	0.17
15	404031			C5001700*:gij9256616jrefjNP_061761.1 pr	1.94	2.29
	457412	NA0711	Hs.333300	hypothetical protein FLJ14026	1.92	3.20
	439719	AF086554	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	1.62	2.30
	418161	AI950754	Hs.81716	ESTs	1.81	2.42
	425894	AW954011	Hs.180711	ESTs	0.92	2.20
20	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, com	1.34	2.57
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	1.67	2.66
	450177	AI698091	Hs.107845	ESTs	1.50	2.25
	459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp434N011 (fr	1.27	3.35
	410357	AW663614		gb:hj22e04.x1 NCI_CGAP_L38 Homo sapiens	0.69	0.59
25	459234	AI940425		gb:CMO-CT0052-150799-024-c04 CT0052 Homo	1.67	2.08
	421313	NM_014923	Hs.103329	KIAA0970 protein	0.57	0.26
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.80	2.73
	423086	AB028994	Hs.123420	KIAA1061 protein	0.40	0.56
30	425980	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.33	2.50
	423185	BE299590	Hs.125078	omithine decarboxylase antizyme 1	0.60	0.56
	410840	AW806924		gb:QV4-ST0023-160400-172-h10 ST0023 Homo	1.50	2.88
	403917			Target Exon	1.82	2.02
	437384	AI674710	Hs.174397	ESTs	1.26	2.05
35	444389	AW439340	Hs.189720	ESTs	1.26	2.13
	443318	AI051603	Hs.133141	ESTs	1.46	2.20
	441093	AI698138	Hs.126918	ESTs	1.40	2.35
	439432	AI984203	Hs.57874	ESTs	0.88	2.18
	454629	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.96	2.31
40	406207			Target Exon	2.77	2.55
	444872	AI936264		p30 DBC protein	1.48	2.45
	401908			C17000154:gij12003980 gb AAG43830.1 AF21	1.15	2.28
	404730			Target Exon	1.84	2.78
	457498	AI732230	Hs.191737	ESTs	1.49	2.55
45	448471	AA158617	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	0.37	0.36
	438978	AI095207	Hs.307972	ESTs	1.57	2.39
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.86	3.34
	400416	AF083130		Homo sapiens CATX-14 mRNA, partial cds	2.03	1.55
	450446	AI696334	Hs.14450	ESTs	1.32	2.38
50	419791	AI579909	Hs.106104	ESTs	0.41	0.27
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	2.01	1.50
	430808	L08603	Hs.247980	melanocortin 4 receptor	1.09	2.18
	443116	AI033325	Hs.132225	ESTs	1.30	2.25
	437923	BE088433	Hs.334696	hypothetical protein KIAA1335	1.40	2.50
55	403294			Target Exon	0.98	2.18
	436007	AI247716	Hs.232168	ESTs	1.38	1.00
	430649	AB040941	Hs.247713	KIAA1508 protein	1.52	2.85
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	1.29	2.59
	444500	AV651273	Hs.282966	ESTs, Moderately similar to 2109260A B c	1.22	2.05
60	447434	R16890	Hs.137135	ESTs	1.72	2.85
	400830			NM_025006:Homo sapiens hypothetical prot	2.04	2.68
	428114	AI821548	Hs.98363	ESTs, Weakly similar to I38022 hypotheti	1.09	2.74
	409688	AI150485		gb:qf36a10.x1 Soares_testis_NHT Homo sap	1.67	1.38
	440781	BE561823	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.28	2.50
65	442662	U78168	Hs.8578	Rap1 guanine-nucleotide-exchange factor	1.92	2.28
	443078	M78728	Hs.132694	Homo sapiens cDNA: FLJ23149 fis, clone L	1.42	2.03
	440179	AI990151	Hs.125904	ESTs	1.49	2.63
	446780	R31107		gb:yh61g01.s1 Soares_placenta Nb2HP Homo	1.96	2.78
	444173	AI126432	Hs.149493	ESTs	1.50	2.10
70	417939	R53863	Hs.337512	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.60	2.03
	428490	BE301738	Hs.49806	ESTs, Weakly similar to A46010 X-linked	0.47	0.44
	443869	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.25	2.68
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.12	1.15
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	0.64	0.48
75	454701	AW854930		gb:PM0-CT0263-201099-003-005 CT0263 Homo	1.30	2.33
	439795	N77294	Hs.194294	ESTs	1.17	2.33
	425546	BE409762	Hs.26118	hypothetical protein MGC13033	1.17	2.85
	411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	1.90	3.98

	434957	AF283775	Hs.35380	x 001 protein	0.47	0.41
	425724	AA362525		gb:EST72223 Namalwa B cells I Homo sapie	1.38	2.63
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.34	0.28
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.28	2.19
	421718	AL117574		Homo sapiens mRNA; cDNA DKFZp434L2221 (f	2.04	1.79
	415924	H18047	Hs.335821	ESTs	2.02	3.17
	450850	AA648886	Hs.151999	ESTs	1.68	2.45
	443153	AI371823	Hs.34079	ESTs	1.13	2.41
10	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	1.34	2.38
	426128	AL118747	Hs.26691	ESTs	1.31	2.25
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	1.48	2.40
	459563	AI590487	Hs.49760	gb:tl77d04.x1 NCI_CGAP_HSC3 Homo sapiens	1.74	3.33
	453006	AI362575	Hs.303171	ESTs	1.17	2.24
15	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	0.54	0.46
	417016	AA837098	Hs.269933	ESTs	1.04	2.18
	420223	N27807	Hs.286	ribosomal protein L4	2.08	3.10
	425303	AA354785		gb:EST63098 Jurkat T-cells V Homo sapien	2.18	2.85
	400375	NM_014115		NM_014115:Homo sapiens PRO0113 protein	1.83	2.14
20	456169	Y07909	Hs.79368	epithelial membrane protein 1	1.54	2.08
	409707	AA861773	Hs.313501	ESTs	0.79	0.84
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.46	2.06
	443162	AI803470	Hs.204529	KIAA1806 protein	1.07	2.43
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	0.45	0.34
25	415110	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo	1.62	2.07
	443251	BE185436	Hs.278839	ESTs	1.34	2.05
	433441	R37094	Hs.13742	ESTs	1.76	2.05
	434612	R76513	Hs.301183	molecule possessing ankyrin repeats Indu	0.83	2.88
	417807	R17806	Hs.269452	gb:yg09b06.r1 Soares infant brain 1NIB H	1.30	2.23
30	426902	AI125334	Hs.97408	ESTs	1.94	2.20
	436028	AA731124	Hs.120931	ESTs	2.01	1.73
	428878	AA436884	Hs.48926	ESTs	1.22	2.17
	439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	1.32	2.75
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypothe	2.09	3.13
35	416527	T62507	Hs.11038	ESTs	1.66	2.12
	441808	AW118601	Hs.127887	ESTs, Moderately similar to 1609195B blo	1.22	2.58
	417054	AF017060	Hs.174151	aldehyde oxidase 1	2.57	1.48
	446536	AC002563	Hs.15767	cltron (rho-interacting, serine/threonin	1.16	2.23
	418442	AI873471	Hs.186898	ESTs	1.39	2.26
40	416640	BE262478	Hs.79404	neuron-specific protein	0.31	0.26
	403146			Target Exon	1.49	2.18
	457397	AW969025	Hs.109154	ESTs	1.32	2.26
	439189	AI951185	Hs.144530	nuclear receptor subfamily 2, group F, m	1.76	2.90
	423969	AI830571	Hs.34969	hypothetical protein DKFZp566N034	1.18	2.00
45	455683	AI674906	Hs.199460	gb:wc73f02.x1 NCI_CGAP_Pan1 Homo sapiens	1.74	2.00
	426826	AK001890	Hs.172654	guanine nucleotide binding protein beta	2.04	1.60
	414462	BE522743	Hs.301064	araplatin 1	0.40	0.29
	438027	N93047	Hs.19131	transcription factor Dp-2 (E2F dimerizat	1.08	2.40
	408623	AW811978	Hs.254037	ESTs	1.64	3.08
50	433765	AA909619	Hs.112668	ESTs	1.52	2.02
	417132	N56605	Hs.269053	ESTs	1.64	2.51
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.28	0.16
	435186	AL119470	Hs.145631	ESTs	1.74	3.10
	411107	AW958042	Hs.95870	PTD015 protein	0.49	0.24
55	406930	U04691		gb:Human olfactory receptor (OR17-219) g	2.21	3.88
	411026	AW813786		gb:RC3-ST0197-120200-015-b05 ST0197 Homo	1.64	1.03
	415766	H01613	Hs.50628	adaptor-related protein complex 4, sigma	1.64	2.51
	446018	AW631111	Hs.249727	gb:hh92e12.y1 NCI_CGAP_GU1 Homo sapiens	1.56	2.48
60	440125	AW238410	Hs.253888	ESTs	1.46	2.25
	449832	AA694264	Hs.60049	ESTs	1.27	2.33
	431899	AA521381	Hs.187726	ESTs	1.11	2.53
	431531	BE142052	Hs.62654	kringle-containing transmembrane protein	1.06	2.00
	441077	AI241273	Hs.15312	ESTs	1.12	2.13
	426799	H14843	Hs.303154	popeye protein 3	0.61	0.51
65	419480	BE536584	Hs.122546	hypothetical protein FLJ23017	1.88	2.38
	455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	1.77	2.55
	403332			Target Exon	1.46	2.60
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	1.40	2.43
	404429			Target Exon	1.31	2.01
70	436941	AF075047	Hs.31864	ESTs	1.34	2.21
	428745	AA433896	Hs.201634	ESTs	1.72	2.06
	411567	AW851630		gb:MR2-CT0222-211099-002-h06 CT0222 Homo	1.60	2.70
	458714	R20916	Hs.344777	ESTs	0.93	2.07
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	1.39	2.71
75	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	1.66	2.18
	407322	AA171892	Hs.324570	ESTs, Weakly similar to ALU3_HUMAN ALU S	1.30	2.65
	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	1.52	2.73
	435695	AA694324	Hs.257675	ESTs	1.24	2.00

	402294		Target Exon	1.80	3.08
	417759	R13567	ESTs	1.63	2.58
	417527	AA203524	gb:zx55e10.r1 Soares_fetal_liver_spleen_	1.52	2.02
	427526	AA405062	gb:zu12e04.r1 Soares_testis_NHT Homo sap	2.03	1.90
5	455300	AW691707	gb:CM3-NT0090-040500-171-e02 NT0090 Homo	1.12	2.20
	448121	AL045714	hypothetical protein DKFZp564F013	0.93	2.28
	415855	AJ921875	gb:wp07e04.x1 NCL_CGAP_Kd12 Homo sapien	1.43	2.08
	425702	N59555	gb:yv76f05.s1 Soares fetal liver spleen	1.61	2.80
10	441056	H37860	ESTs	1.11	2.10
	400311	AF072164	Homo sapiens HSFE-1 mRNA, partial cds	2.04	2.95
	451478	NM_012331	methionine sulfoxide reductase A	0.50	0.20
	425288	AA354502	gb:EST62799 Jurkat T-cells V Homo sapien	0.99	2.08
	456397	W28339	PTD010 protein	1.11	2.29
15	405654		C12001521:gil7513934 pir T31081 cca3 pr	2.30	1.00
	450151	AJ088196	Homo sapiens clone IMAGE:451939, mRNA se	1.21	2.60
	418851	AA287987	ESTs, Weakly similar to 1207289A reverse	1.28	2.60
	406016		Target Exon	0.57	0.48
	440903	AM58079	ESTs	2.02	1.61
20	445026	W90337	ESTs, Moderately similar to 2109260A B c	1.56	2.23
	414182	AA136301	KIAA1105 protein	1.32	2.55
	457048	AA400352	ESTs	1.54	2.05
	440542	AA899143	ESTs, Weakly similar to PC4259 ferritin	1.48	2.15
	422857	R71461	gb:yi51h07.r1 Soares placenta Nb2HP Homo	1.42	2.78
25	445948	AW444562	ESTs	1.50	2.48
	454002	BE299567	ESTs, Moderately similar to ALU8_HUMAN A	1.31	2.25
	413656	T91703	gb:ye20g09.s1 Stratagene lung (937210) H	2.10	1.69
	420441	AJ986160	dual specificity phosphatase 6	0.99	2.33
	412062	H09124	Homo sapiens cDNA: FLJ23573 fis, clone L	2.14	1.61
30	408991	BE501816	ESTs	1.76	2.83
	432534	AW361626	hypothetical protein FLJ11240	0.41	0.28
	435136	R27299	ESTs	0.76	3.40
	451052	AA281504	Homo sapiens cDNA: FLJ22165 fis, clone H	2.16	1.85
	413928	AA442498	ESTs, Moderately similar to Z195_HUMAN Z	1.30	2.00
35	439448	AA970788	ESTs	1.87	2.23
	403344		NM_000341:Homo sapiens solute carrier fa	1.36	2.22
	418056	AA524886	gb:nh34f02.s1 NCL_CGAP_P3 Homo sapiens	1.42	2.85
	435428	AJ791745	ESTs	2.44	1.32
	419964	AA811657	ESTs	1.32	2.08
40	440926	AW196772	ESTs	1.80	2.65
	452625	AA724771	ESTs	1.64	2.18
	452797	AJ369787	ESTs	1.47	3.16
	436120	AJ248193	ESTs	1.41	2.83
	449567	AJ990790	ESTs	1.48	2.45
45	409628	AB021865	potassium voltage-gated channel, Shal-re	1.70	2.23
	416617	H69311	ESTs	1.83	2.04
	452266	AJ767250	ESTs	0.58	0.43
	404606		Target Exon	1.47	3.75
	401814		Target Exon	2.00	1.91
50	428403	AJ393048	leucine rich repeat (in FLJ) Interactin	0.33	0.21
	433390	AA566950	Homo sapiens mRNA; cDNA DKFZp761G18121 (2.00	4.90
	451443	AW295527	ESTs	1.87	2.25
	411188	BE161168	gb:PMO-HT0425-170100-002-a10 HT0425 Homo	2.15	1.69
	452704	AA027823	Homo sapiens PNAS-130 mRNA, complete cds	2.64	1.65
55	424060	X92108	H.sapiens mRNA for subtelomeric repeat s	2.40	2.58
	433331	AJ738815	ESTs	1.46	2.10
	428520	AA331901	hypothetical protein FLJ10097	0.44	0.19
	439492	AF086310	ESTs	0.42	0.26
	426736	AA431615	ESTs	1.90	2.45
60	416225	AA577730	ESTs, Weakly similar to PC4259 ferritin	2.72	6.25
	404917		Target Exon	1.60	2.15
	448955	AW207597	ESTs	2.08	1.75
	402797		Target Exon	2.12	1.37
	457951	U23860	gb:Human clone mcag19 chromosome 16 CTG	1.72	2.00
65	426982	AA149707	ubiquitin-like 3	0.36	0.17

TABLE 8B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	408139	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA652438 AW172843 W19794 N21460 AJ743862 AW130622 AA991348 AJ204553 AA992664 N80848 AA699329 AI824676 R26624 R49653 AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866
	408255	1049351_1	

408283	1050275_1	BE141579 AW807555 AW807502 BE141596 AW845845 AW807500 AW845854 AW807480 AW807486 AW807478 AW178109 AW807228 AW807374 AW807125 AW846124 AW807470 AW807477 AW807510 AW807208 BE141573 AW807465
408839	1085657_1	AW277084 R27662 R26970 D79194
409126	110159_1	AA063426 AW962323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
409282	111512_1	AW966480 AA069840 AA384646
409291	1115745_1	AW373472 AW373484 BE071899 BE071898
409367	1123651_1	AW382767 BE153835 BE153702 BE153572
409688	114831_3	AI150485 AW938392 AA076894 AW883422
409692	114869_1	AI500724 AA399661 AA397891 AI471084 AI423511 T07531 AI094336
409894	1157906_1	BE081731 AW861738 AW503629 BE081969
410154	117950_1	F06959 Z43559 AA082002
410357	1197159_1	AW663614 BE046540 BE045760 AW827443 BE046544
410642	1213736_1	AW792784 Z44444 H06639
410725	1218207_1	AW799279 AW799395 AW799392 AW799276 AW799479 H57885
410730	121847_1	AW368860 AA457091 AI903441 AA088823 W88852 AW979154 AA826016 R94779
410744	1219485_1	H85002 W92289 AW801558 AW801324 AW801270 AW801307 AW801351 AW801357 AW801299 AW801609 AW801356 AW801420 AW801425 AW801358 AW801429 AW801428 AW801427 AW801424 AW801306
410840	1223800_1	AW806924 AW866537 AW866473 AW866298 AW866390 AW866478 AW866454 AW866309 AW866539 AW866521 AW866547 AW866517 AW866403 AW866369
410956	1227882_1	AW938322 AW938307 AW938320 AW938323 AW811840
411008	1229027_1	AW813238 AW813474 AW813334 AW815081 AW813296 AW813363 AW813397 AW813327 AW813328 AW816031 AW816140
411026	1229373_1	AW813786
411141	1233793_1	AW819561 AW819682 AW819563 AW819688 AW819499 AW819498 AW819690 BE065081
411184	1234977_1	AW821117 AW855541 AW855405 AW855374
411188	1235093_1	BE161168 BE162466 AW821260
411245	1236412_1	AW833441 AW833552 AW833700 AW833610 AW833673 AW833675
411347	1239834_1	AW838126 AW838294 AW838247 AW838251 AW838292 AW838299 AW838374
411432	1245636_1	AW846272 AW846564 AW846545 AW846285 AW846135 AW846317 AW846200 AW846265 AW846326 AW846196 AW846357 AW846153 AW846286 AW846319 AW846277 AW846381 AW846438 AW846481 AW846352
411496	1248073_1	AW849241 AW849569 AW849243
411567	1249774_1	AW851630 AW851703 AW851735 AW851723 AW851708 AW851712
411590	125064_1	T96183 T64070 AA094134
411608	1251259_1	AW853441 BE145228 BE145218 BE145162 BE145283
411652	1252836_1	AW855393 AW855560 AW855424
411880	1263110_1	AW872477 BE088101 T05990
411918	1265807_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198
411920	1265812_1	AW876263 AW876257 AW876261 AW876273 AW876231 AW876398 AW876334 AW876134 AW876371 AW876308 AW876314 AW876328 AW876169 AW876331 AW876426 AW876407 AW876412 AW876322 AW876363 AW876218 AW876240 AW876141 AW876138 AW876326 AW876181 AW876131 AW876378 AW876206 AW876191 AW876188 AW876376 AW876289 AW876415 AW876209 AW876366 AW876343 AW876347 AW876165
412085	1276467_1	AW891667 H93096
412252	1285293_1	AW903782 AW903668 AW903672 AW903763 AW903784
412274	128647_1	AA101443 R20332 F07484
412298	1288098_1	AW936300 AW936538 AW936386
412302	1288128_1	AW936334 AW936371 AW936474
412679	1321229_1	BE144762 AW979091
412902	1335166_1	BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
413035	1346295_1	BE155663 BE155574 BE155556 BE061294
413068	1348104_1	BE063792 BE063803 BE063775 BE063801 BE063809 BE063777 BE063784 BE063808 BE066125 BE063782 BE063805 BE063812
413196	135322_1	AA127386 R15844 AA127404
413346	136323_1	AA128586 AA463667 AA235203
413444	1370831_1	BE141019 BE141473 BE141529
413489	1373392_1	BE144228 BE144291
413593	137891_1	AA205248 AA130658 AA204737
413645	138145_1	AA130992 AA503835 AW969537
413656	1381628_1	T91703 BE155222 BE155240 BE155274 BE155275 T92469
413750	1386250_1	BE161453 W28808
413885	1397288_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433
413888	139750_1	AA580288 AA315655 AA133031 AA377748
414051	1413185_1	BE244127 BE246216
414623	1466952_1	BE391050 BE389191 BE389697
415054	151827_1	AI733907 AA159708 AI732614
415110	1522905_1	H04043 D60988 D60337
415157	1525616_1	D63257 D78918 D63214
415381	1534970_1	F06724 Z43690 R21681
415378	1535274_1	T16964 F07075 H10256
415449	1537026_1	H15034 T17195 F09069
415770	155437_1	M79237 AI267298 AA169260
415806	155668_1	AA169560 AA169840
415855	155930_1	AI921875 AA170835 AA866613
415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416311	158797_1	D80529 D81719 C14833 AA179446 AA357794
416463	1595999_1	H59241 H57540 R00795
417086	164830_1	AA194446 AA194603 AA193162 AA196396 Z24810
417117	1651230_1	N45778 W86339 N75221
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370

5	417527	168576_1	AA203524 W88451
	417670	1692163_1	R07785 T85948 T86972
	417882	1705458_1	R22311 R23982 R23997
	417890	1706141_1	R79048 R23111
	418056	171841_1	AA524886 AW971347 AA211537
	418797	1790395_1	AA515814 AA515037 AA230024 AA228343
	418859	179717_1	AA229558 AA345492 AA229582
	419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
10	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419501	185354_1	AW843822 AW844020 AA825923 AW968657 AW854173 BE084673
	421338	201378_1	AA287443 AA419385 BE084078 AI478347
	421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818
15			AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126
			BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539
			BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292
	421718	20595_1	AL117574 AI681945 BE503055 AW015330 C16652 AA441855 AA329853 AW962502 AA441830 AF114049
	421926	209246_1	AA300591 AW963893 AA300493
	422259	214322_1	AA307584 AW795791 AW795790
20	422297	214851_1	AW961290 AA308338 R60841 BE378716 R13001
	422337	215447_1	R38572 R49597 H51730 F10468 AA309198 BE011889 AA613236
	422444	216595_1	AA310688 AA355321 AW962134
	422657	222190_1	R71461 AA328744 AA318128 BE081817 BE081587 BE081751
	422936	223099_1	AA319278 AA319712 AW961504 AW954956
25	422940	223106_1	BE077458 AA337277 AA319285
	422959	22327_3	AV647015 AV647162 AA477047 AW392066 BE168052 AA657684 AL040747 AL043589 AL041618 W24630 AA419002 AA778650 AI028269
			AW378085 AW780241 AI984255 AW129462 AI271476 AL040967 AA835991 AL040910 AW273346 AA132452 AI375545 AI436321 N53166
			AA598667 AA423804 AA889495 AI954063 AI923968 AW194576 AI400578 AA748499 AA860230 AW519209 AA339537 AA476935 AA67391
			AI017695 AI860419 N93437 AW452389 AI051533 AA806940 AA609569 AI524860 AI356952 AI115116 AI439198 AA749268 AI206880
			AI784422 AI431957 AI187038 AI678429 AI273421 AI358604 AI691155 AA586499 AA897667 AA524576 AI417772 AW799936 BE241923
30			AA013428 BE164987 AW602710 AI933540 AA757772 AW015132 AI954159 AW956377 W69468 AI807580 AI871746 AI922524 N80292
			AI676213 BE467086 N92405 AV656311 AI678172 AW339455 AI949278 AI872882 AI123785 AA016257 AI961623 AW168519 F28686 F37181
			AA908333 AW020788 AW374027
	423074	22470_1	AI109963 AA134692 BE273642 M78295 AI825179 AA228029 BE538677 AW589948 AW241564 AA732224 AA228030 AW977225
35	423622	230333_1	BE154847 BE154890 AA328702
	423736	231511_1	AW936874 AW936923 AW936924 AA330274
	423977	233868_1	AA333232 AW962695 R54896
	424060	23490_1	X92108 AW295478 AI768675 AI086644 AW190160 AA313783 AA322741 AA354698 AW962099 AL044667 AA282648 AA973897 AL036586
			AA386055 AL135179 AW882199
40	424160	236151_1	T74062 F12441 AA336207 BE185031
	424290	237857_1	AA338396 AW966247 AW753612
	424951	245273_1	AW964082 AA348838 AA348839
	425288	249569_1	AA354502 AA355215 AW962122
	425303	249780_1	AA354785 AA354792 AW958427
45	425702	255206_1	N95555 AA362113 AA362136
	425724	255509_1	AA362525 AW979199 AA857501
	425757	255956_1	AA363171 AW963347 AA371863
	425893	257742_1	AA629695 AA365582 AA365581 AW959799 AW876559 AW876588
	425980	258778_1	AA366951 AA470999 AA469425
50	426123	261304_1	AA370352 AA370860 AW962776
	426477	267804_1	AA379464 AA379611 AA379463
	428036	28620_1	AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M54110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875
			AI888836 AA864291 AI685080 AW088029 AI924908 AW466328 AI903800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330
			AL046953 AA852866 AW391995 W30846 AW662928 W25261 AA042863 R99045 H97060 W03910 H94687 T88984 AL048165 T29632 N31556
55			N36484 AI798679 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047816 R24137 R63433
			AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370271 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594
			AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA808425 R63380 AA384736 AA384738 AA852352 AI073645
			AA527960 AA525036 AA044414 AI752450 AA703064 R01216 AA897183 AI751996 T81078 H95047 AA573642 D58348 N20953 AA437143
			N95439 AA579540 AW867055 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020
60			AW994984 H20896 AW964438 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309
			AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813
			AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 AW608407 R05674 H16712 N85426 N42354
			H85516 BE147991 T28113 R32662 AA384678 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409
			AA042828 AA363555 AJ223812 AA344709 BE149590 R70995 W46881 W90778 N71242 AA534826 AL040676 R23797 H96450 AA082957
65			D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343590 AW888731
			AI751527 AA937490 AA937506 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046508 AW384981 AA043908
			AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821
			AI626043 N37087 AI624140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022
			AW069069 AW069454 AA342989 AI077712 AI311467 AI087361 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356670
70			AA873156 AI004219 AI189585 AA478018 AA076063 AI445222 AI753124 AI521569 AI925026 AI022368 AI475993 H20846 AI223234 AI635123
			AA579170 N30442 AW117889 AA807935 AA558975 AI306636 AA888983 AI92591 AI935835 AA45293 H16713 AW139833 AA622122
			AA972051 AI280828 H09543 AI453725 AW069613 AI855615 AI753921 AI368782 AI633208 AI446651 W46961 N22201 H82276 C16555
			AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N67873 AW023948 C15881 C16601 AI251465 AW079187
			BE045090 AI273006 C16390 C16503 AI620823 F13661 N66864 Z21311 C16108 C16089 C16400 AA758273 AI287781 AA864676 AW608074
75			AW585583 AI589944 AA665817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C161487 N29477 AW189997
			AI370492 C16471 AA652809 AA938687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662
			T94414 AI567041 AI619654 AW009486 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA659781
			AA026678 AW132002 AW263919 C16562 AA759137 AA693351 Z40779 C16577 AA85045 AW073763 R45484 AI520895 U54708 T49285

			AI568126 AW006569 AI093317 AL119781 T61046 AI053563 H51958 AF114144 AA305739 AW950394 AW793928 AW793910 AL047737 AV659047 AV659632 AI750389 AA092053 AA092798 H85367 T61597 R23745 Z20418 T78485 AI751528 AW068121 AA853188 AI752459 AA853711 AW950663 R78954 R36359 R21626 R21522 AW969656 AA501412 AA905186 AA429703 AA431958 AA449921 AA449922 C75309 AF033579 NM_005995 AA464964 M85405 AA947566 AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 BE041395 AA491826 AA621945 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AW972724 AA522631 AA877998 AI204995 AW827539 AW969908 AW440776 AA528756 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA666403 AA601627 AW869639 BE061833 BE000620 AW951170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AA568548 AI050036 AA554053 AI911659 AI826259 AW970018 AA573669 AA573622 R08736 AW162474 AA588442 AI972440 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218557 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW832836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045584 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AW852235 AF156166 R07008 AA664078 AW363313 AA805009 AA628980 AI126603 BE504035 BE149154 BE149151 X60138 AW975957 AA747943 AA811289 AI082424 AI740586 AA771764 AA771806 AI033879 BE500996 AW204531 D38676 W05391 X56197 H75313 AW770789 AA281642 AV654440 AA344646 R00244 T83378 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859108 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096 L09078 L03145 L09094 L09098 L03165 L09102 M27346 AF086410 W94386 W74609 AW979249 D63277 AA846968 BE561384 AW732707 AI744995 AI973099 R19291 AA935215 AA897534 AI698070 BE179102 AI694912 AW850980 AA969613 AW366793 AI033188 BE004743 AW804074 BE004795 BE178660 BE089438 BE089378 BE089439 BE089437 BE089423 BE089420 BE089425 BE089424 BE089426 Z43613 AA320191 AW954963 H15889 R83872 AW016773 AI052778 AI452937 AW085293 AI126098 AI184746 AI148521 Z17870 AL039867 AI139927 R44007 N54521 AI140476 AW418649 T95308 AI936254 AI219228 AI200740 BE300771 AI635739 AI690626 AW044010 R60842 R40388 AW450439 AW297340 AI239849 AI613119 AW974013 AA557257 N36812 AI597998 AA873565 BE158869 AI248241 BE158865 BE158868 R31107 AI341136 AI653198 H04953 BE010169 AW879041 BE008038 AW905325 AA343575 AW844209 AL038020 BE010133 BE010083 AW903901 BE174377 AI309717 AI349651 AI903726 BE176661 AW905394 AI523875 R45782 R45781 T94709 AI820675 AI732253 R55428 AI820704 AI732283 R54983 AI732321 R55640 R55639 AI820744 AI903765 AI811194 BE007147 AW130760 BE066552 BE066341 AI907683 AL043049 T95976 AL137967 BE064160 BE064186 AL138129 AL138179 BE064231 AW753456 AW753036 AW854868 AW854862 AW803980 AW803974 AW810204 AW810555 AW810196 AW810619 AW810507 AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157 AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335 AW811633 AW811652 AW811898 AW812715 AW812646 AW812714 AW854930 AW814431 AW814190 AW814115 AW854941 AW815588 AW815571 AW815493 AW815898 AW815613 AW815490 AW815808 AW815426
5	428518	292383_1	
	429321	302955_1	
	429468	30498_1	
	430068	312849_1	
	430439	31808_1	
10	431089	327825_1	
	431322	331543_1	
	431926	339082_1	
	432222	343347_1	
	432407	34624_1	
15	432586	350432_1	
	433010	357372_1	
	433436	366107_1	
	434414	38585_1	
20			
25	434830	39406_1	
	435073	399701_1	
	436608	42361_3	
	437046	43210_1	
	437272	435447_1	
	437908	445001_1	
	438089	44963_1	
	438091	44964_1	
30			
35			
40	438535	45946_1	
	438813	46553_1	
	439590	47413_1	
	439848	477806_1	
	440612	49847_1	
	440642	499098_1	
45	441846	527227_1	
	443100	559752_1	
	443197	56261_1	
	443357	567506_1	
50	444163	593658_1	
	444298	600160_1	
	444312	600647_1	
	444872	623948_1	
	445468	640681_1	
55	445555	64334_1	
	445689	647829_1	
	446780	692897_1	
	447008	70358_1	
60	448489	765247_1	
	450717	844561_1	
	450724	844585_1	
	450735	844617_1	
	451724	882130_1	
65	452565	922372_1	
	453577	972216_1	
	453823	982526_1	
	453826	982669_1	
	454457	1207274_1	
70	454523	1221564_1	
	454609	1226517_1	
	454629	1227240_1	
	454631	1227443_1	
	454639	1227728_1	
75	454662	1228537_1	
	454701	1229702_1	
	454721	1230747_1	

	454741	1232559_1	BE154396 AW817959 BE154393
	454826	1236377_1	AW833676 AW833814 AW833798 AW833677 AW833449 AW833630 AW833626 AW833444 AW833366 AW833791 AW833659 AW833432
			AW833534 AW833556 AW833553
5	454915	1242343_1	AW841619 AW851958 AW851851 AW851985
	455065	1251980_1	AW854352 AW854311 AW854340 AW854461
	455087	1252832_1	AW855389 AW855556 AW855420
	455116	1254206_1	AW857271 AW857308 AW857296 AW857258
	455236	1255662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
10	455300	1276482_1	AW891707 AW891696 AW891917 AW891913 AW891912 AW891909 AW891890 AW891892 AW891889 AW891697 AW891880 AW891898
	455407	1288347_1	AW936813 AW936731 AW936728 AW936600 AW936681 AW936651
	455508	1318507_1	AW976165 C04000
	455527	1322125_1	AW984479 AW984498 AW984495 AW984477 AW984480 AW984504
	455642	1348163_1	BE063965 BE063968 BE064034 BE064028 BE063874 BE063966 BE063869 BE064043 BE064033 BE063884
	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
15	455753	1356070_1	BE075124 BE075229 BE075278
	455757	1358657_1	BE079531 BE079371 BE079372 BE079593 BE079468 BE079504 BE079505
	455908	1382301_1	BE156306 BE156188 BE156298 BE156377 BE156374
	455917	1382784_1	BE156765 BE156770 BE156767 BE156769 BE156803 BE156802 BE156847 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779
			BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
20	455988	1397740_1	BE177983 BE178322
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
	456172	1603643_1	R99050 R99067 H67642
25	456332	179104_1	AA228357 AW841786 AW841716
	456381	184123_1	AA236606 AA459341 AA237079
	457297	313764_1	AW968188 AA468196 AA468269 AA468298
	457389	331080_1	AW970989 AA502167 AA507546
	457567	357346_1	AW939074 AW939073 BE160476 AW939938 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
30	457581	359936_1	AA578512 AA595535 BE177533
	457741	395767_1	BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046561 AA653908 BE166581
	457871	426637_1	AI168278 AA668238 BE550792 AI522194 AI819707 AA973538 AI990086 AI628424 AI095270 AI991608 AA730741
	457951	44251_1	U23860 U80739
	459234	945240_1	AI940425

35 TABLE 8C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
45 400704	8118864	Minus	63110-63241
400830	8570385	Plus	157683-163035
400834	8705192	Plus	121963-122288
400840	9188586	Plus	113882-114121
400850	1927150	Minus	4506-4691
50 400881	2842777	Minus	91446-91603,92123-92265
401016	8117441	Plus	126234-126359,128050-128236
401090	8492704	Minus	201281-201460
401215	9858408	Plus	103739-103919
401241	4827300	Minus	30503-30844,31056-31248
55 401335	9884881	Plus	15736-16352
401381	8570226	Minus	118629-119146,119392-119657
401400	7708226	Minus	33028-33585
401469	6682292	Minus	125521-125639
60 401473	7249001	Plus	115142-117305
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401658	9100864	Plus	89638-90028
401659	7689875	Minus	183379-183521
401686	6468551	Plus	5005-5426,6810-7042
65 401723	7656694	Plus	147273-147503
401814	7408052	Plus	136003-136726
401818	7467933	Minus	10964-11084,11674-11817
401890	8516144	Plus	148955-149396,149569-150002
401908	8698760	Minus	126888-127024
401913	9369520	Minus	33753-33904
70 401927	3873185	Minus	112000-112137
402025	7547159	Plus	173835-173998
402039	7770432	Plus	560-1294
402049	8072512	Plus	100065-100419
402085	7249154	Plus	90533-90687,94949-95158
75 402241	7690131	Minus	125073-125206,130996-131125
402294	2282012	Minus	2575-3000
402305	7328724	Plus	40832-41362

	402366	9454515	Plus	195808-196863
	402551	9856793	Minus	37346-37633
	402654	8076879	Plus	44058-44803
5	402685	8318556	Plus	58962-59294
	402762	9230904	Minus	123298-124035
	402797	3421043	Minus	15758-15930
	402833	8918545	Plus	26987-27778
	402901	8894222	Minus	175426-175667
10	402948	9368458	Minus	143456-143626,143808-143935
	403066	8954202	Plus	158189-158433
	403072	8954241	Plus	141829-142005
	403146	9799812	Plus	162877-163118
	403197	9930749	Plus	79990-80237
15	403214	7630945	Minus	76723-77027,79317-79484
	403217	7630969	Plus	54089-54163,55427-55623
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403294	8096496	Plus	41565-41881
20	403315	8247953	Minus	125117-125287
	403332	8568139	Minus	31409-31674
	403344	8569726	Plus	70823-70990
	403362	8571772	Plus	64099-64260
	403371	9087278	Plus	105655-106050
25	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,87970-88110
	403488	9966615	Minus	12450-12753
	403536	8076924	Plus	34972-35182
	403779	8018040	Minus	95602-95969
	403859	7708954	Plus	113738-113858
30	403871	7709262	Plus	104545-104757
	403903	7710671	Minus	101165-102597
	403917	7710849	Plus	109718-109847,109927-110202
	403978	8576014	Plus	97326-97808
	404031	7671252	Plus	171477-172316
35	404167	9926594	Minus	77030-77280
	404220	6706820	Plus	46107-46439
	404286	2326514	Plus	51086-51301
	404418	7382420	Minus	153339-153481,155099-155294
	404427	7407959	Plus	127170-127358
40	404429	7407979	Plus	31352-31498
	404440	7528051	Plus	80430-81581
	404495	8151634	Minus	59449-60477
	404580	6539738	Minus	240588-241589
	404606	9212936	Minus	22310-23269
45	404730	8389582	Plus	119832-120016,124110-124275
	404917	7341851	Plus	49330-49498
	405033	7107731	Minus	142358-142546
	405137	8570507	Plus	158969-159423
	405146	9438278	Minus	102529-102633
50	405158	9966252	Plus	42873-43056,43815-43949
	405187	7229826	Plus	117025-117170,118567-118736
	405223	7239614	Plus	106184-106313
	405340	6094635	Plus	49644-49760
	405494	8050952	Minus	70284-70518
55	405551	1552506	Plus	12525-12997
	405654	4895155	Minus	53624-53759
	405667	4726099	Plus	5798-5914
	405673	4589984	Plus	50700-50842
	405704	4204244	Plus	135842-139051
60	405723	9801668	Plus	114896-115831
	405727	9838331	Minus	78865-78664
	405760	6066938	Minus	37424-38045
	405779	7280331	Minus	33048-33856
	405944	7883702	Minus	5143-5684
65	406002	8247797	Minus	154007-154579
	406016	8272661	Plus	41341-41940
	406097	7107918	Minus	36698-37269
	406104	9124028	Plus	35309-35977
	406156	7144867	Plus	379-597
70	406207	5923650	Minus	162607-162800
	406300	6479046	Minus	19234-19401
	406308	9211532	Plus	358408-358651
	406314	9211609	Minus	12899-13011,18022-18136
	406317	9211652	Plus	108018-108410
75	406432	9256504	Plus	3804-3930,4026-4120,4929-5109
	406490	7711309	Minus	80295-80480
	406584	3983530	Minus	3989-4497

TABLE 9A: Genes predictive of no bladder cancer progression

	Pkey: Unique Eos probeset identifier number					
	ExAccn: Exemplar Accession number, Genbank accession number					
5	UnigeneID: Unigene number					
	Unigene Title: Unigene gene title					
	R1: 80th percentile of Ta or T1 tumor AIs from patients who did not upstage divided by the 80th percentile of Ta or T1 tumor AIs from patients who did upstage					
	R2: median of Ta or T1 tumor AIs from patients who did not upstage divided by the median of Ta or T1 tumor AIs from patients who upstaged					
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	408000	L11690	Hs.198589	bulbos pemphigoid antigen 1 (230/240kD)	4.64	5.88
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.54	5.10
	459290	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	4.37	1.63
	400844			NM_003105*:Homo sapiens sortilin-related	3.69	5.90
15	419555	AA244416		gbnc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.61	2.03
	414522	AW518944	Hs.76325	step II splicing factor SLU7	3.60	1.00
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.58	1.04
	445182	AW189787		ESTs	3.57	2.70
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.56	1.48
20	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	3.28	3.25
	429663	M68674	Hs.211587	phospholipase A2, group IVA (cytosolic,	3.25	2.50
	430702	U56979	Hs.278568	H factor 1 (complement)	3.20	2.70
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.20	2.30
	420729	AW964897	Hs.290825	ESTs	3.20	1.53
25	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.00	4.10
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.94	2.78
	407981	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.93	1.43
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.93	1.33
	428030	AJ915228	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.92	2.47
30	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.89	3.33
	414407	AA147026	Hs.76704	ESTs	2.87	2.87
	450779	AW204145	Hs.155044	ESTs	2.78	1.86
	411243	AB039886	Hs.69319	CA11	2.73	1.00
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.68	2.32
35	441519	NM_014056	Hs.7917	DKFZP564K247 protein	2.67	2.98
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.66	1.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.64	1.77
	426252	BE176980	Hs.28917	ESTs	2.63	7.30
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.60	2.53
40	429429	AA829725	Hs.334437	hypothetical protein MGC4248	2.59	3.34
	427450	AB014526	Hs.178121	KIAA0626 gene product	2.57	2.28
	420180	AJ004035	Hs.25191	ESTs	2.56	1.68
	434061	AW024973	Hs.283675	NPD009 protein	2.54	2.10
	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.54	3.25
45	419355	AA428520	Hs.90061	progesterone binding protein	2.53	3.63
	446215	AW821329	Hs.14368	SH3 domain binding glutamic acid-rich pr	2.52	4.38
	432442	AJ672516	Hs.178485	ESTs, Weakly similar to S65657 alpha-1C-	2.50	4.60
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	2.49	2.23
	401155			Target Exon	2.48	2.30
50	404530			Target Exon	2.48	1.00
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	2.48	2.35
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.47	2.88
	446535	AF257175	Hs.15250	peroxisomal D3,D2-enoyl-CoA isomerase	2.46	2.19
	408636	BE294925	Hs.46680	CGI-12 protein	2.45	1.60
55	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	2.44	3.75
	427008	Z45258	Hs.286013	short coiled-coil protein	2.42	3.40
	459711	BE386801	Hs.21858	trinucleotide repeat containing 3	2.40	2.78
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	2.40	1.00
	410337	M83822	Hs.62354	cell division cycle 4-like	2.39	3.88
60	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.39	3.23
	437181	AJ306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.39	1.00
	410968	AA199907	Hs.67397	homeo box A1	2.38	1.33
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.38	6.40
	450775	AA902384	Hs.73853	bone morphogenetic protein 2	2.38	2.71
65	442433	BE243044	Hs.8309	KIAA0747 protein	2.37	3.68
	454000	AA040620	Hs.5672	hypothetical protein AF140225	2.36	1.14
	447701	BE619526	Hs.255527	hypothetical protein MGC14128	2.36	2.02
	427985	AJ770170	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	2.36	2.18
	442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	2.35	3.53
70	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	2.35	3.60
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.35	2.48
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	2.35	1.00
	407793	AW080879	Hs.236572	gbxc38g04.x1 NCI_CGAP_Co20 Homo saplens	2.35	1.21
	442061	AA774284	Hs.285728	abl-interactor 12 (SH3-containing protei	2.34	3.03
75	402845			ENSP00000246267:KIAA0444 PROTEIN (FRAGME	2.34	1.52
	411407	R00903	Hs.169793	ribosomal protein L32	2.34	0.77
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.34	0.72

	424637	NM_015057	Hs.151411	KIAA0916 protein	2.32	2.56
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	2.32	1.46
	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN	2.32	2.90
5	430028	BE564110	Hs.227750	Target CAT	2.32	2.28
	417720	AA205625	Hs.208067	ESTs	2.32	2.09
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.31	1.13
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.30	4.38
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prol	2.30	1.86
10	408179	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyla	2.29	2.19
	442679	R53718	Hs.107882	hypothetical protein FLJ10659	2.29	2.79
	458949	AW291777	Hs.346137	ESTs, Weakly similar to T08599 probable	2.28	1.85
	407191	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma	2.27	2.42
	448367	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	2.27	1.18
15	405155			Target Exon	2.26	1.94
	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	2.26	1.55
	417458	NM_005655	Hs.82173	TGFB inducible early growth response	2.25	1.95
	430315	NM_004293	Hs.239147	guanine deaminase	2.24	1.84
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	2.24	2.73
20	408937	AA210734	Hs.291386	ESTs	2.24	3.18
	431474	AL133990	Hs.190642	CEGP1 protein	2.23	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.22	4.08
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	2.22	2.15
	420164	AW339037	Hs.24908	ESTs	2.22	2.16
25	414099	U11313	Hs.75760	sterol carrier protein 2	2.21	4.05
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.21	3.53
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	2.90
	416290	NM_000016	Hs.79158	acyl-Coenzyme A dehydrogenase, C-4 to C-	2.20	4.00
	439208	AK000299	Hs.180952	dynactin 4 (p62)	2.20	1.88
30	401563			C15001262:gi7304981 ref NP_038528.1 ca	2.20	1.77
	404687			C9000375:gi11994617 dbj BAB02754.1 (A	2.19	2.60
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.19	2.08
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.19	2.21
35	400835	AW853954		chromosome 2 open reading frame 2	2.18	3.00
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Or	2.18	2.45
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.17	1.83
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	2.17	2.67
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.17	1.71
	406038	Y14443		zinc finger protein 200	2.17	1.71
40	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.17	1.00
	441623	AA315805		desmoglein 2	2.17	1.81
	459244	AW503990	Hs.142442	HP1-BP74	2.17	4.03
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.17	2.93
	404204			ENSP00000252204:Zinc finger protein 165	2.17	1.02
45	453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.16	2.85
	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (Hv	2.16	3.60
	454949	AW847318	Hs.290131	KIAA1819 protein	2.16	1.96
	409223	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory su	2.16	1.48
	418030	BE207573	Hs.83321	neuromedin B	2.16	2.07
50	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.16	2.32
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.16	1.85
	437559	AI678033	Hs.121476	ESTs	2.15	1.43
	418827	BE327311	Hs.47166	HT021	2.15	3.84
	417470	AF112219	Hs.82193	esterase D/ornithineglutathione hydrolase	2.15	1.74
55	421012	X53281	Hs.101025	basic transcription factor 3	2.15	1.26
	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	2.15	4.05
	439601	AB029032	Hs.6606	KIAA1109 protein	2.15	2.15
	434417	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (f	2.15	1.45
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.15	2.63
60	400752			NM_003105:Homo sapiens sortilin-related	2.14	2.67
	438918	AW188464	Hs.101515	ESTs	2.14	2.38
	430024	AI808780	Hs.227730	Integrin, alpha 6	2.14	2.00
	409345	AI949109		hypothetical protein FLJ20763	2.14	1.40
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.13	1.58
65	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.13	2.67
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.13	2.00
	458025	AI275406	Hs.32450	gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapi	2.12	0.89
	428582	BE336699	Hs.185055	BENE protein	2.12	2.65
	422749	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified	2.12	2.73
70	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.11	0.91
	456421	AL157485	Hs.91973	hypothetical protein	2.11	2.51
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.11	3.13
	402750			NM_021797:Homo sapiens eosinophil chemo	2.09	1.79
	406274			Target Exon	2.09	1.60
75	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	2.09	1.00
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.09	2.92
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	2.09	3.20
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.09	1.90

5	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.08	1.15
	405165			ENSP00000238974: Homeobox protein NKX2-3	2.07	2.83
	416999	AW195747	Hs.21122	hypothetical protein FLJ11830 similar to	2.07	3.71
	453865	AA307279	Hs.35947	methyl-CpG binding domain protein 4	2.07	1.71
	439924	AI985897	Hs.125293	ESTs	2.07	1.00
10	439004	AW979062		gb:EST391172 MAGE resequences, MAGP Homo	2.07	2.13
	407955	BE536739	Hs.109909	ESTs	2.06	1.91
	412998	BE046254		gb:hn38g09.x2 NC1_CGAP_RDF2 Homo sapiens	2.06	2.58
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	2.05	5.00
	415249	R40515	Hs.21248	ESTs	2.05	2.18
15	427332	R09418	Hs.261101	ESTs, Weakly similar to I38022 hypotheti	2.05	3.35
	426521	AF161445	Hs.170219	hypothetical protein	2.05	1.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.05	6.03
	423851	R39505	Hs.133342	Homo sapiens clone 24566 mRNA sequence	2.05	1.88
	410028	AW576454	Hs.346502	ESTs	2.04	1.95
20	406575			Target Exon	2.04	1.56
	457148	AF091035	Hs.184627	KIAA0118 protein	2.04	3.11
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	2.04	2.42
	429837	NM_003896	Hs.225939	slatyltransferase 9 (CMP-NeuAc lactosyl	2.04	1.97
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	2.04	2.06
25	411998	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	2.04	2.65
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	2.04	2.35
	446187	AK001241	Hs.14229	hypothetical protein FLJ10379	2.04	2.03
	420838	AW118210	Hs.42321	ESTs	2.03	1.00
	445481	AW661846	Hs.346630	ESTs	2.03	2.49
30	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	2.03	2.25
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.02	2.10
	401177			Target Exon	2.02	2.59
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	2.02	4.23
	434782	NM_005032	Hs.4114	plastin 3 (T isoform)	2.02	1.48
35	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	2.02	2.93
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.02	2.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.02	3.43
	414721	X90392	Hs.77091	ribosomal protein L10	2.02	1.89
	429859	AJ907018	Hs.15977	Target CAT	2.02	1.47
40	439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	2.01	1.94
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.01	1.64
	452046	AB018345	Hs.27657	KIAA0802 protein	2.01	4.31
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	2.01	6.75
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.00	2.75
45	408232	AL137269	Hs.43899	Homo sapiens mRNA: cDNA DKFZp434C1714 (I	2.00	2.02
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.00	1.95
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	2.00	0.91
	426969	AJ936504	Hs.2083	CDC-like kinase 1	2.00	3.60
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.00	1.95
50	444916	AB028956	Hs.12144	KIAA1033 protein	2.00	1.23
	452286	AJ358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.00	5.30
	414906	AA157911	Hs.72200	ESTs	1.99	1.22
	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	1.99	3.83
	414557	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	1.99	2.31
55	452846	AA082160	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	1.99	3.43
	408437	AW957744	Hs.278469	lacrimal proline rich protein	1.98	2.15
	439205	AF087990	Hs.42758	Homo sapiens, clone IMAGE:3354845, mRNA,	1.98	2.28
	442506	BE566411		ESTs	1.98	3.95
	447731	AA373527	Hs.19385	CGI-58 protein	1.98	2.67
60	410579	AK001628	Hs.64691	KIAA0483 protein	1.97	2.43
	426716	NM_006379	Hs.171921	sama domain, Immunoglobulin domain (Ig),	1.97	2.50
	456141	AJ751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.97	3.03
	419576	AK002060	Hs.91251	hypothetical protein FLJ11198	1.96	2.88
	407241	M34516		gb:Human omega light chain protein 14.1	1.96	1.09
65	420654	AJ681270	Hs.99824	BCE-1 protein	1.96	1.75
	448586	AF285120	Hs.283734	CGI-204 protein	1.95	3.28
	408089	H59799	Hs.42644	thioredoxin-like	1.95	4.00
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.95	2.12
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.95	3.45
70	432015	AL157504	Hs.159115	Homo sapiens mRNA: cDNA DKFZp586O0724 (I	1.94	2.80
	434263	N34895	Hs.44648	ESTs	1.94	4.60
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	1.94	1.79
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	1.94	2.30
	401835			Target Exon	1.94	2.27
75	406557			C5000893:gi 6226859 sp P38525 EFG_THEMA	1.94	3.28
	440062	AJ350518	Hs.129692	ESTs	1.94	3.18
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.94	2.70
	457281	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.94	2.60
	420230	AL034344	Hs.284186	forkhead box C1	1.93	2.28
	452970	NM_012238	Hs.31176	sirtuin (silent mating type information	1.93	4.35
	403728			Target Exon	1.92	1.70

5	415789	H01581	gb:33f08.r1 Soares placenta Nb2HP Homo	1.92	2.15
	406759	AA654582	Hs.77039 ATP synthase, H transporting, mitochondr	1.92	2.10
	442073	AW973443	Hs.8086 RNA (guanine-7-) methyltransferase	1.92	4.43
	438023	AF204883	Hs.6048 FEM-1 (C.elegans) homolog b	1.92	4.00
	445502	AW379160	Hs.12813 DKFZP434J214 protein	1.92	2.13
	405474		NM_001093*:Homo sapiens acetyl-Coenzyme	1.92	2.58
	430007	NM_014892	Hs.227602 KIAA1116 protein	1.92	3.78
	439937	AF151906	Hs.6776 CGI-148 protein	1.91	2.32
10	418068	AW971155	Hs.293902 ESTs, Weakly similar to ISHUS protein d	1.91	1.88
	444630	AI753230	Hs.323562 hypothetical protein DKFZp564K142	1.91	1.61
	451184	T87943	Hs.173638 transcription factor 7-like 2 (T-cell sp	1.90	3.35
	414715	AA587891	Hs.904 amylo-1,6-glucosidase, 4-alpha-glucanotr	1.90	3.55
	445841	AL080115	Hs.13370 DKFZP564G0222 protein	1.80	1.46
15	425284	AF155568	Hs.348043 NS1-associated protein 1	1.90	3.65
	437943	NM_016353	Hs.5943 rec	1.89	1.73
	442426	AI373062	Hs.332938 hypothetical protein MGC5370	1.89	2.79
	400111		Eos Control	1.89	3.84
	437762	T78028	Hs.154679 synaptotagmin I	1.89	1.00
20	404069		Target Exon	1.89	2.51
	434809	AW974687	gb:EST386776 MAGE resequences, MAGM Homo	1.88	2.35
	414220	BE298094	Hs.323806 gb:601118231F1 NIH_MGC_17 Homo sapiens c	1.88	1.00
	422506	R20909	Hs.300741 sorcin	1.87	2.99
	417439	AW602154	Hs.82143 E74-like factor 2 (ets domain transcript	1.87	1.13
25	404391		Target Exon	1.87	3.00
	420187	AK001714	Hs.95744 hypothetical protein similar to ankyrin	1.86	2.93
	446950	AA305800	Hs.5672 hypothetical protein AF140225	1.86	1.90
	400634		C10000818*:gil7661882[ref NP_055697.1] K	1.86	2.80
	408455	C19034	Hs.286613 Homo sapiens cDNA FLJ14175 fis, clone NT	1.86	1.32
30	422366	T83882	Hs.97927 ESTs	1.85	1.44
	452170	AF064801	Hs.28285 patched related protein translocated in	1.85	2.64
	430604	AV650537	Hs.247309 succinate-CoA ligase, GDP-forming, beta	1.85	1.81
	426484	AA379658	Hs.272759 KIAA1457 protein	1.85	2.60
	411609	AW993680	gb:RC3-BN0034-290200-013-d08 BN0034 Homo	1.85	2.10
35	431129	AL137751	Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.84	3.70
	412843	AF007555	Hs.74624 protein tyrosine phosphatase, receptor I	1.84	2.58
	401512		NM_014080:Homo sapiens dual oxidase-like	1.84	1.52
	415969	H11294	Hs.31047 ESTs	1.84	3.08
	444736	AA533491	Hs.23317 hypothetical protein FLJ14681	1.84	1.20
40	426418	M90464	Hs.169825 collagen, type IV, alpha 5 [Alport syndr	1.84	2.35
	416968	AA412686	Hs.97955 ESTs	1.84	2.18
	442961	BE614474	Hs.289074 F-box only protein 22	1.84	2.18
	418650	BE386750	Hs.86978 prollyl endopeptidase	1.84	1.98
	420923	AF097021	Hs.273321 differentially expressed in hematopoieti	1.84	1.00
45	432634	F06459	Hs.289113 cytochrome b5 reductase 1 (BSR-1)	1.83	3.93
	442485	BE092285	Hs.29724 hypothetical protein FLJ13187	1.83	3.10
	427699	AW965076	Hs.180378 hypothetical protein 669	1.83	3.03
	447387	AI268331	Hs.102237 lubby super-family protein	1.83	1.78
	418663	AK001100	Hs.41690 desmocollin 3	1.82	1.53
50	419733	AW382955	Hs.224961 Homo sapiens cDNA FLJ14415 fis, clone HE	1.82	1.00
	409267	NM_012453	Hs.52515 transducin (beta)-like 2	1.81	1.57
	413341	H78472	Hs.191325 ESTs, Weakly similar to T18967 hypotheli	1.81	2.05
	423810	AL132685	Hs.132955 BCL2/adenovirus E1B 19kD-interacting pro	1.81	1.98
	416274	AW160404	Hs.79126 guanine nucleotide binding protein 10	1.80	1.91
55	400843		NM_003105*:Homo sapiens sortilin-related	1.80	4.88
	442187	N23532	Hs.288963 Homo sapiens cDNA: FLJ23034 fis, clone L	1.80	2.61
	458285	AW295984	Hs.255595 ESTs, Weakly similar to A46302 PTB-assoc	1.80	2.33
	413753	U17760	Hs.75517 laminin, beta 3 (nicotin (125kD), kalinin	1.80	3.17
	428004	AA449563	Hs.151393 glutamate-cysteine ligase, catalytic sub	1.80	1.00
60	401613		Target Exon	1.79	2.66
	407173	T64349	gb:yc10d08.s1 Stralagene lung (937210) H	1.79	2.30
	443145	AI049671	Hs.307763 EST, Weakly similar to I38022 hypothetic	1.79	2.00
	418596	AW976721	Hs.293327 ESTs	1.79	3.92
	437374	AL359571	Hs.44054 ninein (GSK3B interacting protein)	1.79	1.24
65	439569	AW602166	Hs.222399 CEGP1 protein	1.79	2.39
	430677	Z26317	Hs.94560 desmoglein 2	1.78	2.02
	436749	AA584890	Hs.5302 lectin, galactoside-binding, soluble, 4	1.78	0.96
	453016	AW295466	Hs.232051 ESTs, Weakly similar to dJ403A15.3 [H.s	1.78	2.60
	426885	AA393130	Hs.193894 ESTs, Weakly similar to A47582 B-cell gr	1.78	2.47
70	452848	AI417193	Hs.288912 hypothetical protein FLJ22604	1.78	2.17
	412560	R24601	Hs.72249 CCR4-NOT transcription complex, subunit	1.78	3.13
	411821	BE299339	Hs.193516 threa-POZ containing protein similar to	1.78	1.55
	428788	AF082283	Hs.17448 B-cell CLL/lymphoma 10	1.78	2.36
	443963	AA878183	Hs.259737 Homo sapiens cDNA FLJ13618 fis, clone PL	1.78	2.20
75	435479	AF197137	Hs.75187 ATP synthase, H transporting, mitochondr	1.77	2.03
	413073	AL038165	Hs.75187 translocase of outer mitochondrial membr	1.77	2.29
	442473	W27992	gb:43d9 Human retina cDNA randomly prime	1.77	2.93
	418060	AA211589	Hs.208047 ESTs	1.77	4.19

	400773		NM_003105*:Homo sapiens sortilin-related	1.77	1.76	
	400175		Eos Control	1.77	2.04	
	421501	M29971	Hs.1384	Q-6-methylguanine-DNA methyltransferase	1.77	2.32
5	451234	AJ914901	Hs.24052	ESTs, Weakly similar to I38022 hypothe	1.77	2.43
	423332	AJ091466	Hs.127241	sorting nexin 7	1.76	1.82
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	1.76	2.00
	450489	AJ697990	Hs.346002	ESTs	1.76	3.15
	457265	AB023212	Hs.225967	KIAA0895 protein	1.76	2.37
10	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	1.75	2.18
	421948	L42583	Hs.334309	keratin 6A	1.75	1.00
	453578	R06875	Hs.81810	ESTs	1.75	3.10
	412430	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	1.75	2.14
	439396	BE562958	Hs.74346	hypothetical protein MGC14353	1.75	1.78
15	431448	AL137517	Hs.306201	hypothetical protein DKFZp56401278	1.75	2.36
	449538	AI559444	Hs.104679	ESTs	1.75	3.07
	453146	AI338952	Hs.32194	ESTs	1.74	2.82
	426122	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	1.74	2.88
	408989	AW361666	Hs.49500	KIAA0746 protein	1.74	2.07
20	441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.74	2.06
	412718	X79204	Hs.74520	spinocerebellar ataxia 1 (olivopontocere	1.74	2.46
	450798	AW167780	Hs.50438	ESTs	1.74	2.02
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.73	2.58
	400190			Eos Control	1.73	2.40
25	416309	R84694	Hs.79194	cAMP responsive element binding protein	1.73	1.48
	410219	T98226	Hs.171952	occludin	1.73	2.75
	419814	AW402478	Hs.93213	BCL2-antagonist/killer 1	1.73	2.70
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	1.73	2.07
	422387	AA309996	Hs.148656	ESTs, Weakly similar to T12453 hypothe	1.73	2.02
30	417386	AL037228	Hs.82043	D123 gene product	1.73	2.44
	405812			Target Exon	1.72	2.94
	436270	C03769	Hs.339669	Homo sapiens, clone IMAGE:3947554, mRNA,	1.72	2.85
	409855	AW502461		gb:U1-HF-BR0p-giv-b-08-0-ULr1 NIH_MGC_5	1.72	2.63
35	411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	1.72	1.88
	400846			sortilin-related receptor, L(DLR class)	1.72	1.63
	401660			Target Exon	1.72	2.63
	402190			C19000835*:gij10946730[ref NP_067362.1]	1.72	3.33
	439191	AA281177	Hs.41182	Homo sapiens DC47 mRNA, complete cds	1.71	2.17
40	410444	W73484	Hs.132554	gb:z54e04.s1 Soares_fetal_heart_NbHH19W	1.71	2.70
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.71	1.33
	445066	AI343931	Hs.149383	ESTs	1.71	2.32
	411299	BE409857	Hs.69499	hypothetical protein	1.71	2.92
	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.71	2.00
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12538 fis, clone NT	1.71	1.93
45	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.70	3.70
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	1.70	1.60
	400750			Target Exon	1.70	2.82
	455842	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.70	2.17
50	429966	BE081342	Hs.283037	HSPC039 protein	1.70	1.18
	418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	1.70	2.47
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	1.70	3.03
	415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncha	1.70	2.34
	405245			Target Exon	1.70	1.99
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypothe	1.70	2.05
55	413611	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	1.70	2.05
	410190	AW072328	Hs.59728	Homo sapiens mRNA; cDNA DKFZp566C0546 (f	1.69	2.20
	434608	AA805443	Hs.179909	hypothetical protein FLJ22995	1.69	2.36
	432170	T56887	Hs.18282	KIAA1134 protein	1.69	1.83
	448182	AF244137	Hs.20597	host cell factor homolog	1.69	2.11
60	436293	AI601188	Hs.120910	ESTs	1.69	2.37
	448524	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	1.68	2.48
	404231			Target Exon	1.68	2.50
	453906	AW444952	Hs.257054	ESTs	1.68	2.45
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	1.68	1.00
65	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.68	3.51
	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	1.68	1.69
	429162	AK001250	Hs.197642	hypothetical protein FLJ10388	1.68	3.13
	425556	H27225	Hs.9444	hypothetical protein FLJ13114	1.67	2.02
	405630			Target Exon	1.67	3.00
70	421405	AA251944	Hs.104058	CGI-29 protein	1.67	3.25
	422640	M37984	Hs.118845	troponin C, slow	1.67	1.23
	450857	AA629075	Hs.190090	ESTs	1.67	2.48
	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.66	2.55
	433821	AW182416		ESTs	1.66	2.65
75	405595			NM_000721*:Homo sapiens calcium channel,	1.66	2.23
	433892	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	1.66	1.97
	443558	AA376798	Hs.286122	MDS024 protein	1.66	2.00
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.66	2.65

	424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	1.66	2.88
	400845			NM_003105*:Homo sapiens sortilin-related	1.66	1.61
	447816	NM_007233	Hs.274329	TP53 target gene 1	1.66	2.63
	404438			Target Exon	1.66	2.34
5	451543	AA397651	Hs.301959	proline synthetase co-transcribed (bacte	1.65	2.08
	433233	AB040927	Hs.301804	KIAA1494 protein	1.65	3.13
	420938	AL049698	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	1.65	1.37
	435438	H84421	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homo	1.65	2.35
10	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.65	1.00
	433235	AB040929	Hs.35089	contactin 3 (plasmacytoma associated)	1.65	1.44
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	1.65	2.35
	409324	W76202	Hs.343812	lipic acid synthetase	1.65	2.00
	452207	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	1.65	2.33
15	423630	AB011132	Hs.129952	KIAA0560 gene product	1.65	2.13
	443358	H65417	Hs.17757	pleckstrin homology domain-containing, f	1.65	1.63
	427417	AA341061	Hs.177861	CGI-110 protein	1.64	1.28
	450333	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	1.64	1.60
	445677	H96577	Hs.6838	ras homolog gene family, member E	1.64	1.91
20	447503	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810	1.64	2.04
	431234	AL389985	Hs.301637	zinc finger protein 258	1.64	1.53
	418032	AW964695	Hs.9436	Homo sapiens, clone MGC:15763, mRNA, com	1.64	2.05
	407796	AA195509	Hs.39733	postsynaptic protein CRIP1	1.64	2.30
	445298	AF187813	Hs.14637	kidney- and liver-specific gene	1.64	2.05
25	439578	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.64	2.26
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	1.64	2.10
	433646	AA603319	Hs.155195	ESTs	1.64	2.05
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	1.64	1.00
	419982	AA252544	Hs.55610	solute carrier family 30 (zinc transport	1.64	2.16
30	401603			NM_022041*:Homo sapiens giant axonal neu	1.64	2.73
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	1.64	2.75
	400788			C6000994*:gij10435784 dbj BAB14658.1 (A	1.63	2.04
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	1.63	2.64
	422491	AA338548	Hs.117546	neuronatin	1.63	0.96
35	424737	BE301883	Hs.152707	glioblastoma amplified sequence	1.63	3.45
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	1.63	1.39
	403988			C5001831:gij11056014 ref NP_067651.1 ac	1.62	2.11
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	1.62	2.63
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	1.62	2.19
40	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	1.62	3.03
	438184	AA779897	Hs.122125	ESTs	1.62	2.79
	405502			C7000609*:gij628012 pir A53933 myosin I	1.62	2.55
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	1.62	2.48
	457961	AA772119	Hs.270721	ESTs, Weakly similar to I38022 hypotheti	1.62	2.30
45	438774	AW975810	Hs.159054	hypothetical protein FLJ13224	1.62	2.17
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	1.62	2.03
	458660	AI299739	Hs.99601	hypothetical protein FLJ12553	1.62	2.25
	405806			Target Exon	1.62	2.15
	421205	AL137540	Hs.102541	netrin 4	1.62	1.00
50	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	1.62	1.74
	427016	AA397525	Hs.191579	ESTs	1.61	2.16
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	1.61	2.74
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.61	2.59
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.61	1.78
55	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.61	2.10
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.61	1.75
	439944	AA856767	Hs.124523	ESTs	1.61	2.41
	414692	H06831	Hs.164557	ESTs, Moderately similar to ALUC_HUMAN1	1.60	3.05
	433187	R53995	Hs.293381	ESTs, Moderately similar to ALU7_HUMAN A	1.60	2.63
60	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	1.60	2.43
	441166	AA921738	Hs.132473	ESTs	1.60	2.69
	425571	AJ007292	Hs.158306	ephrin-A2	1.60	1.49
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	1.60	1.08
65	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.60	1.47
	449268	AW369278	Hs.23412	hypothetical protein FLJ20160	1.60	2.89
	400772			NM_003105*:Homo sapiens sortilin-related	1.60	2.57
	445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosyl	1.60	2.03
	428172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	1.60	2.68
	421887	AW161450	Hs.109201	CGI-86 protein	1.59	1.39
70	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	1.59	1.67
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	1.59	2.19
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	1.59	2.26
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	1.59	1.76
	418067	AI127958	Hs.83393	cystatin E/M	1.59	1.26
75	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	1.59	2.25
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	1.59	2.10
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	1.58	2.43
	410796	Z44547	Hs.3731	ESTs, Moderately similar to I38022 hypot	1.58	1.28

5	417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.58	2.84
	416643	U62531	Hs.79410	solute carrier family 4, anion exchanger	1.58	1.26
	400847			NM_003105: Homo sapiens sortilin-related	1.58	1.48
	436760	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	1.57	1.57
	433427	A1816449	Hs.171889	cholinephosphotransferase 1	1.57	1.64
10	451986	BE246996	Hs.318401	hypothetical protein DKFZp564D1378	1.57	1.83
	426901	A1929568	Hs.146668	KIAA1253 protein	1.57	2.23
	426028	NM_0011110	Hs.172028	a disintegrin and metalloproteinase doma	1.57	3.07
	444604	AW327695	Hs.11441	chromosome 1 open reading frame 8	1.57	1.86
	439686	W40445	Hs.235857	ESTs, Weakly similar to I38022 hypotheti	1.57	3.07
15	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	1.57	2.01
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.57	2.83
	418942	A1566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	1.57	1.21
	418555	A1417215	Hs.87159	hypothetical protein FLJ12577	1.56	3.08
	402358			NM_021155: Homo sapiens CD209 antigen (C	1.56	2.05
20	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	1.56	2.08
	404977			Insulin-like growth factor 2 (somatomedi	1.56	5.50
	441872	BE567100	Hs.154938	hypothetical protein MDS025	1.56	2.30
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	1.56	2.56
	451743	AW074266	Hs.23071	ESTs	1.56	1.85
25	423184	NM_004428	Hs.1624	ephrin-A1	1.56	1.41
	408041	AW138782	Hs.243607	ESTs	1.56	2.21
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	1.56	2.00
	428013	AF151020	Hs.181444	hypothetical protein	1.56	1.53
	410072	BE384447	Hs.16034	hypothetical protein MGC13186	1.55	1.52
30	411495	AP000693	Hs.70359	KIAA0136 protein	1.55	2.88
	408162	AA938333	Hs.118527	ESTs	1.55	2.70
	413350	U02556	Hs.75307	t-complex-associated-testis-expressed 1-	1.55	1.99
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	1.55	1.60
	425229	AU076961	Hs.155212	methylmalonyl Coenzyme A mutase	1.55	2.57
35	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	1.55	1.45
	419011	H55244	Hs.89552	glutathione S-transferase A2	1.55	2.77
	417538	AW050865	Hs.275711	hypothetical protein MGC2452	1.55	2.76
	409806	AW500960		gb:U1-HF-BP0p-aly-b-01-0-U1r1 NIH_MGC_5	1.55	2.45
	402737			Target Exon	1.54	2.58
40	419825	A1754011	Hs.7326	ESTs	1.54	1.00
	410001	AB041036	Hs.57771	kallikrein 11	1.54	0.62
	407813	AL120247	Hs.40109	KIAA0872 protein	1.54	2.33
	415906	A1751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.54	2.77
	427886	AA417083	Hs.104789	ESTs	1.54	2.60
45	437018	AA889078	Hs.187033	ESTs	1.54	2.48
	415049	N67334	Hs.50158	ESTs	1.54	2.57
	422315	U16296	Hs.115176	T-cell lymphoma invasion and metastasis	1.54	2.57
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	1.54	1.98
	447144	A1630759	Hs.17481	Homo sapiens clone 24606 mRNA sequence	1.54	2.48
50	438924	BE535511		transmembrane trafficking protein	1.53	3.08
	445166	A1656116	Hs.147451	ESTs	1.53	2.08
	414073	AF068293	Hs.75737	pericentriolar material 1	1.53	1.70
	402378			Target Exon	1.53	2.83
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.53	1.60
55	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.53	3.59
	402817			C1003551:gi5678593 ref NP_033547.1 win	1.53	2.75
	406837	R70292	Hs.156110	immunoglobulin kappa constant	1.53	1.01
	410573	AF151057	Hs.64595	aminoadipate-semialdehyde dehydrogenase-	1.53	1.23
	426359	AA376409	Hs.10862	Homo sapiens cDNA: FLJ23313 fis, clone H	1.53	0.67
60	434445	A1349306	Hs.11782	ESTs	1.53	2.80
	452717	AW160399	Hs.30376	hypothetical protein	1.53	2.01
	420465	AL080276	Hs.70488	similar to prokaryotic-type class I pept	1.53	2.25
	437404	AA858974	Hs.180992	ESTs	1.53	2.00
	459192	AW176180		gb:RC2-BT0214-010999-001-E07 BT0214 Homo	1.52	3.20
65	446457	A1300580	Hs.345281	ESTs, Moderately similar to ALU1_HUMAN A	1.52	2.35
	441466	AW673081	Hs.54828	ESTs	1.52	1.99
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	1.52	2.98
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	1.52	2.47
	414882	D79994	Hs.77546	Homo sapiens cDNA: FLJ21983 fis, clone H	1.52	2.55
70	442169	W21813	Hs.8125	Homo sapiens mRNA; cDNA DKFZp586E1521 (f	1.52	1.31
	404349			Target Exon	1.52	2.74
	416278	AA356365	Hs.79137	protein-L-isaspartate (D-aspartate) O-m	1.52	2.93
	431846	BE019924	Hs.271580	uropod 1B	1.52	1.01
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.52	0.93
75	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.52	2.70
	441617	AA581863	Hs.178485	Homo sapiens cDNA FLJ13919 fis, clone Y7	1.52	1.65
	440079	A1557284	Hs.6900	ring finger protein 13	1.52	1.76
	432831	A1821702	Hs.115959	ESTs, Weakly similar to I38022 hypotheti	1.52	2.13
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.52	2.13
	442149	AB014550	Hs.8118	KIAA0650 protein	1.52	1.00
	457747	AW975000		gb:EST387105 MAGE resequences, MAGN Homo	1.51	2.38

5	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	1.51	2.50
	431812	AA515902	Hs.130650	ESTs	1.51	1.64
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	1.51	2.62
	447580	AB53360	Hs.133487	ESTs	1.51	2.02
	416926	H03109	Hs.108920	HT018 protein	1.51	2.22
	442755	W57656	Hs.109701	ubiquitin-like 5	1.51	1.34
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.51	2.24
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.51	1.49
10	404397			ENSP00000251675* KIAA1550 protein (Fragm	1.51	2.18
	412927	AA284018	Hs.75063	human Immunodeficiency virus type 1 enha	1.51	1.33
	402371			Target Exon	1.51	3.22
	431730	AF208856	Hs.268122	hypothetical protein	1.51	1.57
	417715	AW969587	Hs.86366	ESTs	1.51	1.59
15	451117	AA015752	Hs.205173	ESTs	1.50	2.70
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	1.50	3.53
	442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	1.50	2.24
	425883	AL137708	Hs.161031	Homo sapiens mRNA: cDNA DKFZp434K0322 (f	1.50	1.13
	452658	N88604	Hs.30212	thyroid receptor interacting protein 15	1.50	1.62
20	428695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	1.50	1.00
	438967	H30340	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	1.50	1.05
	419847	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA,	1.50	2.53
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.49	0.97
	433265	AB040971	Hs.35096	KIAA1538 protein	1.49	1.44
25	408136	AL041135	Hs.42959	KIAA1012 protein	1.49	2.24
	455485	AA102287	Hs.26756	hypothetical protein FLJ20896	1.49	2.40
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.49	2.84
	405193			C7000789:gil1943947[gb]AAC48716.1.(U901	1.48	2.20
	408948	AW296713	Hs.221441	ESTs	1.48	2.20
30	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.48	2.24
	405932			C15000305:gil3806122[gb]AAC69198.1.(AF0	1.48	1.48
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.48	1.16
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.48	1.20
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.48	2.38
35	418166	AW501907	Hs.261734	Homo sapiens cDNA: FLJ22807 fis, clone K	1.48	1.28
	430453	BE387080	Hs.3903	Cdc42 effector protein 4; binder of Rho	1.48	2.73
	401600	BE247275		U5 snRNP-specific protein, 116 kD	1.48	2.53
	432638	AI017717		chromosome 21 open reading frame 15	1.48	2.03
	405194			C7000789:gil1943947[gb]AAC48716.1.(U901	1.48	2.00
40	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.48	1.25
	450272	AI075170	Hs.20010	ESTs	1.48	2.35
	413709	BE158687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	1.48	2.08
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	1.48	1.00
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.47	1.91
45	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	1.47	2.26
	404769			NM_007037*Homo sapiens a disintegrin-li	1.47	1.24
	420132	BE079847	Hs.301914	gb:RC6-BT0627-220300-012-D06 BT0627 Homo	1.47	2.00
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.47	2.90
	421628	AL121317	Hs.106210	hypothetical protein FLJ10813	1.47	4.08
50	449059	AJ000566	Hs.98135	hypothetical protein FLJ20559	1.47	3.13
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.47	1.06
	422119	AI277829	Hs.111862	KIAA0590 gene product	1.47	1.51
	438713	H16902		ESTs	1.47	2.39
	418248	NM_005000	Hs.83916	NM_005000*Homo sapiens NADH dehydrogena	1.47	1.00
55	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.46	2.20
	420548	AA278246	Hs.920	ESTs	1.46	2.13
	424258	AA433848	Hs.107882	hypothetical protein FLJ10659	1.46	1.98
	414683	S78296	Hs.76888	hypothetical protein MGC12702	1.46	1.45
	427045	H86504	Hs.173328	protein phosphatase 2, regulatory subunl	1.46	2.31
60	446646	BE552004	Hs.26192	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.46	1.30
	427257	AI026805	Hs.97726	ESTs	1.46	2.48
	422971	AI879223	Hs.145409	RAB, member of RAS oncogene family-like	1.46	1.05
	451334	AI122691	Hs.13268	ESTs	1.46	2.12
	403326			C2000428*gil7705383[ref]NP_057536.1.(GC	1.46	2.40
65	453827	AF201948	Hs.35560	BUPI protein	1.46	1.65
	423599	AI805664	Hs.31731	peroxiredoxin 5	1.46	1.56
	410691	AW239226	Hs.65450	reticulum 4	1.46	1.49
	430688	AL022101	Hs.104991	hypothetical protein similar to preferen	1.46	2.45
	438083	AI949940	Hs.121924	ESTs	1.46	2.00
70	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	1.45	1.60
	437325	AF142481	Hs.5548	I-box and leucine-rich repeat protein 5	1.45	1.26
	403342			Target Exon	1.45	2.21
	438808	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mRNA, complete	1.45	2.40
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	1.45	3.65
75	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	1.44	2.71
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	1.44	1.08
	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	1.44	2.24
	432901	AI554929	Hs.281866	ATPase, H transporting, lysosomal (vacuo	1.44	1.63

	412210	AW901492		gb:RCO-NN1012-270300-031-h10 NN1012 Homo	1.44	2.15
	421685	AF169723	Hs.106778	ATPase, Ca transporting, type 2C, member	1.44	1.83
	428115	AB023194	Hs.300855	KIAA0977 protein	1.44	1.31
5	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	1.44	2.47
	414685	L39874	Hs.76894	dCMP deaminase	1.44	1.25
	413798	AA336708	Hs.75546	capping protein (actin filament) muscle	1.44	1.26
	410937	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homolog)	1.44	1.41
	400397	AJ270770		transcription factor 7-like 2 (T-cell sp)	1.44	3.43
	405902			Target Exon	1.44	2.65
10	433976	AA620987	Hs.190268	ESTs	1.44	2.46
	405376			Target Exon	1.44	2.28
	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	1.44	1.34
	418182	AW016405	Hs.16648	ESTs	1.44	2.35
	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	1.43	1.55
15	434524	AA443164	Hs.23259	hypothetical protein FLJ13433	1.43	2.05
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	1.43	2.15
	404744			Target Exon	1.43	1.99
	405418			Target Exon	1.43	2.83
	402899			Target Exon	1.43	2.40
20	451608	AA384525	Hs.26745	hypothetical protein	1.43	1.22
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	1.43	2.45
	401041			C11000425.gij4507721[ref]NP_003310.1} i	1.43	2.90
	417839	AJ815732	Hs.82712	fragile X mental retardation, autosomal	1.43	2.84
	409245	AA361037	Hs.288036	tRNA isopentenylpyrophosphate transferase	1.43	2.65
25	447808	NM_007265	Hs.19673	suppressor of S. cerevisiae gcr2	1.43	2.00
	456492	AA330047	Hs.191187	ESTs	1.43	2.73
	449244	AW859979	Hs.32204	ESTs	1.42	1.57
	413094	H24184	Hs.25413	TOLLUP protein	1.42	1.33
	452407	AA582909	Hs.29353	brain-specific protein p25 alpha	1.42	2.50
30	407674	AW064061	Hs.279145	ESTs	1.42	2.35
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	1.42	2.20
	421832	W51778	Hs.323949	kangal 1 (suppression of tumorigenicity)	1.42	1.48
	426348	BE466586	Hs.17433	hypothetical protein FLJ20957	1.42	1.83
	432554	AJ479813	Hs.278411	NCK-associated protein 1	1.42	2.46
35	431735	AW977724	Hs.75868	thymosin, beta 4, X chromosome	1.42	1.30
	429853	NM_004376	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	1.42	1.50
	444037	AV647686	Hs.42733	CHMP1.5 protein	1.42	1.38
	402144			Target Exon	1.42	2.38
40	456758	AA325170	Hs.224627	ESTs, Weakly similar to FAHUA alpha-act	1.42	2.23
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	1.42	2.18
	426863	AL137657	Hs.172803	hypothetical protein MGC10327	1.41	1.38
	410684	AA086500	Hs.170298	ESTs	1.41	1.28
	401784			NM_002280*:Homo sapiens keratin, hair, a	1.41	1.37
45	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.41	1.32
	449269	AI564682	Hs.175870	ESTs	1.41	1.37
	406467			Target Exon	1.41	1.80
	444339	T96555	Hs.31562	ESTs	1.41	2.94
	431563	AI027643	Hs.120912	ESTs	1.41	1.41
50	413343	BE392026	Hs.334346	hypothetical protein MGC13045	1.41	1.21
	447537	AW295072	Hs.346408	ESTs, Weakly similar to AF193556 1 sacsi	1.41	2.07
	428211	AA424211	Hs.183176	ESTs	1.41	1.25
	406248			Target Exon	1.41	2.40
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.41	1.39
55	414653	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	1.41	1.33
	403885			Target Exon	1.41	2.58
	439459	AF086279	Hs.58013	ESTs	1.41	2.08
	419075	T84266	Hs.123927	ESTs	1.41	2.84
	405022			Target Exon	1.40	2.55
60	401346	BE041451		hypothetical protein	1.40	2.38
	415660	AI909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo)	1.40	2.38
	448023	AI693299	Hs.170388	ESTs	1.40	2.38
	435962	AA702820	Hs.291294	ESTs	1.40	2.10
	432480	AA205475	Hs.275865	ribosomal protein S18	1.40	1.37
65	414309	AK000639	Hs.75884	DKFZP588A011 protein	1.40	1.18
	440256	U23841	Hs.18851	hypothetical protein FLJ10875	1.40	1.91
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human)	1.40	2.80
	408176	AK001553	Hs.43436	adenylate kinase 3 alpha like	1.40	2.73
	433960	AW629188	Hs.188929	ESTs	1.40	1.99
70	404178			C6001430*.gij4503521[ref]NP_001559.1} mu	1.40	2.83
	402449			Target Exon	1.40	1.51
	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	1.40	2.30
	429221	AI821060	Hs.198271	Target CAT	1.40	1.22
	422122	AA383642	Hs.111894	lysosomal-associated protein transmembra	1.40	1.42
75	406231			Target Exon	1.40	2.60
	405879			Target Exon	1.40	2.73
	450936	AI033745		gb:ow23a10.x1 Soares_parathyroid_tumor_N	1.40	1.13
	403381			ENSP00000231844*:Ecotropic virus Integra	1.39	6.03

5	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.39	3.20
	448261	BE244072	Hs.20815	macrophage erythroblast attacher	1.39	1.33
	427656	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	1.39	2.30
	413659	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.39	1.53
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.39	1.34
10	430138	AA936296	Hs.234265	DKFZP586G011 protein	1.39	2.38
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	1.39	2.88
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.39	1.34
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	1.61
	450092	AW139606	Hs.221057	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.39	2.78
15	400275			NM_006513:Homo sapiens seryl-tRNA synth	1.39	2.03
	403725			Target Exon	1.39	2.03
	443211	AJ128388	Hs.143655	ESTs	1.39	1.83
	421510	AK000919	Hs.105191	hypothetical protein FLJ11057	1.39	2.83
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	1.38	3.54
20	451545	AJ802128	Hs.208647	ESTs	1.38	2.21
	439897	NM_015310	Hs.6763	KIAA0942 protein	1.38	3.65
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.38	1.00
	410344	AW978436	Hs.62515	KIAA0494 gene product	1.38	2.25
	404439			ENSP00000067222:Mitochondrial 28S ribos	1.38	2.25
25	448581	NM_002709	Hs.21537	protein phosphatase 1, catalytic subunit	1.38	1.47
	408569	BE066047	Hs.86412	chromosome 9 open reading frame 5	1.38	1.27
	447643	H10767	Hs.238465	nGAP-like protein	1.38	1.22
	401593			Target Exon	1.38	2.58
	403807			NM_031889:Homo sapiens enamelin (ENAM),	1.38	2.38
30	406356	N47812		CGI-35 protein	1.38	2.25
	401886			NM_021783:Homo sapiens XEDAR (XEDAR), mR	1.38	2.00
	421110	AJ250717	Hs.1355	cathepsin E	1.38	8.93
	427449	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAVL	1.38	1.44
	427451	AJ690916	Hs.178137	transducer of ERBB2, 1	1.38	2.81
35	440681	AW449696	Hs.166547	ESTs	1.38	2.95
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	1.38	2.10
	446044	H57567	Hs.13572	calcium modulating ligand	1.37	2.62
	400967			Target Exon	1.37	3.12
	414506	AF075337	Hs.76293	thymosin, beta 10	1.37	1.18
40	402599			NM_021186:Homo sapiens zona pellucida g	1.37	2.68
	422932	AI191813	Hs.308220	ESTs	1.37	2.38
	433889	AK002082	Hs.3623	hypothetical protein FLJ11220	1.37	2.23
	429802	H09548	Hs.5367	ESTs, Weakly similar to I38022 hypothe	1.37	2.25
	443856	AK000574	Hs.9908	nitrogen fixation cluster-like	1.37	1.28
45	453489	AA300067	Hs.33032	hypothetical protein DKFZp434N185	1.37	2.15
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.37	1.66
	428995	AW004975	Hs.194716	MAD (mothers against decapentaplegic, Dr	1.37	1.33
	441551	AA318224	Hs.295141	ESTs	1.37	2.95
	450528	NM_014072	Hs.25063	PRO0461 protein	1.37	1.19
50	427605	NM_000997	Hs.337445	ribosomal protein L37	1.37	1.31
	459237	AA031675	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	1.37	2.50
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.37	1.31
	404906			NM_025213:Homo sapiens spectrin, beta, n	1.36	3.08
	436246	AW450963	Hs.119991	ESTs	1.36	1.00
55	441478	AA350018	Hs.301342	hypothetical protein MGC4342	1.36	1.43
	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.36	1.28
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.36	2.16
	400129			Eos Control	1.36	2.03
	450447	AF212223	Hs.25010	hypothetical protein P15-2	1.36	2.13
60	434697	AL133033	Hs.4084	KIAA1025 protein	1.36	2.01
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.36	2.03
	434767	AF153201		C2H2 (Kruppel-type) zinc finger protein	1.36	2.87
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	1.36	1.27
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.35	2.20
65	408912	AB011084	Hs.46924	KIAA0512 gene product; ALEX2	1.35	2.68
	409844	AW502336		gb:U1-HF-BR0p-aka-b-05-Q-U1.r1 NIH_MGC_5	1.35	2.29
	402517			Target Exon	1.35	2.10
	447042	AB035863	Hs.182217	succinate-CoA ligase, ADP-forming, beta	1.35	1.25
	405000			Target Exon	1.35	2.32
70	452065	AK000360	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.35	2.38
	404666			C9000748:gi8324209 gb AAB34384.2 (S775	1.35	2.55
	451081	AJ078645	Hs.431	murine leukemia viral (bmt-1) oncogene h	1.35	1.70
	427979	BE379776	Hs.181309	proleasome (prosome, macropain) subunit,	1.35	2.23
	435825	R16702	Hs.91147	ESTs	1.35	2.39
75	426469	BE297886	Hs.293970	methylmalonate-semialdehyde dehydrogenas	1.35	1.40
	447002	BE242866	Hs.16933	HepA-related protein	1.34	2.88
	410946	AW811502		gb:QV2-ST0145-061299-015-b04 ST0145 Homo	1.34	2.02
	454383	AW500332	Hs.11114	hypothetical protein dJ1181N3.1	1.34	2.13
	440512	AA887845	Hs.19673	suppressor of S. cerevisiae gcr2	1.34	2.05
	409655	AW502208		gb:U1-HF-BR0p-aju-a-09-Q-U1.r1 NIH_MGC_5	1.34	2.63
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	1.34	1.00

5	450293	N36754	Hs.171118	hypothetical protein FLJ000026	1.34	2.45
	445831	NM_006055	Hs.13351	LanC (bacterial lanthiotic synthetase c	1.34	1.60
	418610	AW24593	Hs.223394	hypothetical protein MGC2742	1.34	1.39
	441946	AW298716	Hs.120775	ESTs	1.34	2.30
	446192	H49944	Hs.14231	selenoprotein W, 1	1.34	1.17
	416285	BE537973	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	1.34	2.22
	425590	A1954686	Hs.158321	beaded filament structural protein 2, ph	1.34	2.50
	407498	U28131		gb:Human HMGL-C chimeric transcript mRNA	1.34	2.13
10	441331	A1216764	Hs.149971	ESTs, Moderately similar to ALUB_HUMAN I	1.34	2.05
	411789	AF245505	Hs.72157	Adlcan	1.34	1.27
	420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	1.33	1.25
	413892	A1878921	Hs.75607	myristoylated alanine-rich protein kinas	1.33	1.41
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	1.33	1.99
	414861	AL119396	Hs.77508	glutamate dehydrogenase 1	1.33	1.66
15	421687	AL035306	Hs.106823	hypothetical protein MGC14797	1.33	2.18
	410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	1.33	2.07
	443937	R66571	Hs.24601	ESTs	1.33	2.02
	432360	BE045243	Hs.274416	Target CAT	1.33	1.12
20	443119	AA312264	Hs.7980	hypothetical protein MGC12966	1.33	2.68
	438464	AA659735	Hs.324743	protein phosphatase 4 regulatory subunit	1.33	1.99
	401371			ENSP00000198192:BA438F9.1 (novel protei	1.33	1.10
	405443			Target Exon	1.33	2.11
	453764	BE008180	Hs.282846	Homo sapiens cDNA FLJ14353 fis, clone Y7	1.33	2.88
25	424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.33	1.24
	453555	N23574	Hs.123649	ESTs, Moderately similar to ALU7_HUMAN A	1.33	2.23
	404343			C7002191:gi5053028[gb]AAD3881.1JAF155	1.33	1.04
	412383	AW947577		gb:RC0-MT0004-140300-031-b09 MT0004 Homo	1.33	2.06
	404250			Target Exon	1.33	2.53
30	413899	AF083892	Hs.75608	flgh1 junction protein 2 (zona occludens	1.33	2.81
	422716	A1702835	Hs.124475	ESTs, Weakly similar to YEF4_YEAST HYPOT	1.33	2.30
	448862	A1351979	Hs.152717	hypothetical protein FLJ13725	1.33	1.08
	409540	AW409569		gb:fn01e09.x1 NIH_MGC_17 Homo sapiens cD	1.33	2.18
	431186	NM_012249	Hs.250697	ras-like protein	1.32	1.39
35	402754			NM_022469: Homo sapiens hypothetical pro	1.32	1.16
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.32	2.02
	459710	A1701596	Hs.121592	ESTs	1.32	2.70
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor	1.32	2.22
	401383			Target Exon	1.32	2.18
40	453394	AW960474	Hs.40289	ESTs	1.32	2.20
	421820	AW662990	Hs.294133	heme-binding protein	1.32	1.24
	444047	A1097452	Hs.135095	ESTs	1.32	2.95
	440860	R10482	Hs.132876	ESTs	1.32	2.83
	425808	AA364109	Hs.177990	ESTs	1.32	2.11
45	456558	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	1.32	2.05
	447015	AB033029	Hs.16953	KIAA1203 protein	1.32	1.30
	414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C	1.32	1.39
	414843	BE386038	Hs.77492	heterogeneous nuclear ribonucleoprotein	1.32	1.28
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	1.32	2.01
50	401196			Target Exon	1.32	2.13
	450147	AW373713	Hs.146324	CGI-145 protein	1.32	1.32
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	1.32	1.33
	405172			Target Exon	1.32	2.11
	434087	AF116675	Hs.334476	hypothetical protein PRO1942	1.32	2.30
55	416720	H05435	Hs.11110	hypothetical protein MGC2508	1.32	2.18
	426621	NM_001329	Hs.171391	C-terminal binding protein 2	1.32	1.53
	442685	AB033017	Hs.8594	KIAA1191 protein	1.32	1.43
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	1.31	2.24
	405180	NM_002649		phosphoinositide-3-kinase, catalytic, ga	1.31	1.36
60	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.31	0.98
	402087			Target Exon	1.31	1.31
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.31	2.05
	409935	AW511413	Hs.276025	ESTs	1.31	1.20
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	1.31	1.31
	400172			Eos Control	1.31	1.05
65	421742	AW970004	Hs.107528	androgen induced protein	1.31	1.79
	404273			Target Exon	1.31	2.35
	416204	AW972270	Hs.144054	ESTs	1.31	2.15
	435076	AW298113	Hs.92909	SON DNA binding protein	1.31	2.05
70	452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, clone C	1.30	1.57
	404596			Target Exon	1.30	2.23
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.30	1.15
	427195	W27230	Hs.173912	eukaryotic translation initiation factor	1.30	1.34
	438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.30	2.55
75	402138			Target Exon	1.30	2.09
	404029			NM_018936: Homo sapiens protocadherin be	1.30	2.83
	402731	AL042818		E3 ubiquitin ligase SMURF1	1.30	3.32
	458766	AW183618	Hs.55810	solute carrier family 30 (zinc transport	1.30	1.56

5	434585	AW451715	Hs.184075	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.30	2.73
	417219	AW973473	Hs.220936	ESTs	1.30	2.45
	428125	AA393071	Hs.182579	leucine aminopeptidase	1.30	2.00
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.30	1.00
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.30	0.94
10	408621	X57809	Hs.181125	immunoglobulin lambda locus	1.29	1.02
	436653	AW410458	Hs.5258	chromosome 11 open reading frame2	1.29	1.20
	417250	N58241	Hs.332115	ESTs	1.29	3.43
	434978	AA321238	Hs.4310	eukaryotic translation initiation factor	1.29	1.91
	448079	R76981		thyroid hormone receptor-associated prot	1.29	2.01
15	450626	AW190989	Hs.1508	insulin-degrading enzyme	1.29	2.09
	456059	BE543127	Hs.336948	Homo sapiens, clone IMAGE:3530891, mRNA,	1.29	2.23
	417809	H75797	Hs.233550	zinc finger protein 208	1.29	2.20
	454771	AWB19939	Hs.273629	ESTs	1.29	2.10
	413895	BE178160		gb:RC3-HT0600-060400-022-h10 HT0600 Homo	1.29	2.08
20	404649			Target Exon	1.29	1.32
	440676	NM_004987	Hs.112378	LJM and senescent cell antigen-like doma	1.29	2.08
	405891			Target Exon	1.29	2.00
	418965	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	1.29	2.41
	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.29	1.27
25	420037	BE295598	Hs.135559	hypothetical protein FLJ14708	1.29	1.23
	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	1.28	2.48
	458551	AW612481	Hs.104105	ESTs	1.28	2.35
	422984	W28614		chorionic somatomammotropin hormone 1 (p	1.28	1.37
	455365	BE087754		gb:MR4-BT0358-140400-006-g10 BT0358 Homo	1.28	1.06
30	418254	AA732511	Hs.86650	ESTs	1.28	2.38
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.28	1.99
	448456	AI521830	Hs.171050	ESTs	1.28	2.18
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.28	1.68
	405053			Target Exon	1.28	3.23
35	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	1.28	4.25
	443721	AW450451	Hs.266355	ESTs	1.28	1.15
	452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B BINDING FA	1.28	2.30
	440213	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	1.28	1.19
	452900	AA626794		prothymosin, alpha (gene sequence 28)	1.28	1.27
40	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	1.28	2.76
	458911	AA373131	Hs.24322	ATPase, H transporting, lysosomal (vacuo	1.28	1.21
	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.28	2.43
	431831	AA548906	Hs.122244	ESTs	1.27	1.51
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	1.27	3.08
45	430316	NM_000875	Hs.235176	insulin-like growth factor 1 receptor	1.27	1.37
	416272	AA178882		gb:z38b09.r1 Stratagene muscle 937209 H	1.27	2.00
	437456	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.27	3.18
	456327	H68741	Hs.38774	ESTs	1.27	2.35
	403349	NM_001406		ephrin-B3	1.27	2.28
50	428821	H91282	Hs.286232	Homo sapiens cDNA: FLJ23190 fis, clone L	1.27	2.13
	454555	AW807095		gb:MR4-ST0062-040100-024-e02 ST0062 Homo	1.27	2.05
	408872	AI760903		gb:wi09h08.x1 NCL_CGAP_CLL1 Homo sapiens	1.27	1.44
	401720			NM_014587:Homo sapiens SRY (sex determi	1.27	2.07
	400082			Eos Control	1.27	1.26
55	420183	W92885	Hs.143408	ESTs	1.27	2.24
	411579	AC006258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	1.27	1.17
	402191			NM_021733:Homo sapiens testis-specific	1.27	2.44
	457118	AI245525	Hs.182469	Homo sapiens mRNA; cDNA DKFZp564K1972 (I	1.27	2.17
	408576	NM_003542	Hs.46423	H4 histone family, member G	1.27	2.78
60	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.27	3.15
	414909	R80316	Hs.132569	PP2135 protein	1.27	1.37
	416114	AI695549	Hs.183868	glucuronidase, beta	1.26	2.48
	455476	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo	1.26	2.18
	445926	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	1.26	1.35
65	432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.26	1.16
	405436			Target Exon	1.26	2.38
	406140			Target Exon	1.26	3.20
	426201	AW182614	Hs.128499	ESTs	1.26	1.17
	433334	AJ927208	Hs.231958	matrix metalloproteinase 28	1.26	2.30
70	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	1.26	2.61
	422929	AA356694	Hs.94011	ESTs, Weakly similar to MGB4_HUMAN MELAN	1.26	2.11
	445605	AJ906088	Hs.67159	hypothetical protein FLJ12577	1.26	3.11
	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	1.26	2.18
	420539	AA282735	Hs.44004	AD031 protein	1.26	2.03
75	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.25	1.19
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.25	1.18
	434202	BE382411	Hs.3764	guanylate kinase 1	1.25	1.14
	439528	BE613180	Hs.288368	Homo sapiens cDNA: FLJ21314 fis, clone C	1.25	2.12
	400178			Eos Control	1.25	2.15
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	1.25	1.20
	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	1.25	1.39

5	425655	BE614551	Hs.738	ribosomal protein L14	1.25	1.22
	449636	AI656608	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	1.25	3.00
	418406	X73501	Hs.84905	cytokeratin 20	1.24	2.11
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.24	1.14
	436967	AA761729	Hs.136705	ESTs	1.24	2.53
10	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	1.24	2.18
	418414	J04977	Hs.84981	X-ray repair complementing defective rep	1.24	1.35
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidemiolys	1.24	0.92
	421733	AL119871	Hs.1420	fibroblast growth factor receptor 3 (ach	1.24	2.71
	402329			NM_006505*:Homo sapiens poliovirus recep	1.24	1.13
15	447525	AF151031	Hs.300631	hypothetical protein	1.24	1.07
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	1.24	2.23
	421936	AB040884	Hs.109694	KIAA1451 protein	1.24	2.15
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.24	2.15
	426717	N90977	Hs.49690	Homo sapiens mRNA; cDNA DKFZp434D2328 (f	1.24	2.14
20	404751	T70445		ribosomal protein L9	1.24	1.30
	411456	AW847588		gb:IL3-CT0213-161299-038-G09 CT0213 Homo	1.24	2.35
	425417	AF098948	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	1.24	2.88
	434508	AI648501	Hs.118012	ESTs	1.24	2.03
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.24	1.59
25	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.24	2.27
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.24	1.53
	449210	AI635363	Hs.345517	ESTs	1.24	2.18
	439551	W72062	Hs.11112	ESTs	1.24	2.13
	426244	AI064808	Hs.168289	succinate dehydrogenase complex, subunit	1.23	1.06
30	453635	BE148082	Hs.24724	MFH-amplified sequences with leucine-ric	1.23	1.34
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	1.23	2.27
	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	1.23	2.10
	417010	NM_006225	Hs.80776	phospholipase C, delta 1	1.23	1.21
	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.23	1.37
35	434055	AF168712	Hs.3726	x 003 protein	1.23	1.58
	438363	AI886351	Hs.22353	hypothetical protein FLJ21952	1.23	2.44
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	1.23	2.28
	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	1.23	1.44
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	1.23	1.19
40	440112	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	1.22	2.07
	426672	AW270555	Hs.171774	hypothetical protein	1.22	1.16
	404956			C1003210*:gi 6912582 ref NP_035524.1 pe	1.22	2.18
	435088	NM_000481	Hs.102	aminomethyltransferase (glycine cleavage	1.22	1.08
	438588	AW274454	Hs.6318	peroxisomal short-chain alcohol dehydrog	1.22	1.02
45	434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endodig	1.22	1.27
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	1.22	2.52
	428755	D87454	Hs.192968	KIAA0265 protein	1.22	1.16
	420685	AA279362		gb:zs84d04.r1 NCL_CGAP_GCB1 Homo sapiens	1.22	2.75
	458891	AI743502		gb:wf63h12x2 Soares_NFL_T_GBC_S1 Homo s	1.22	2.39
50	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	1.22	1.00
	434023	AI277883	Hs.146141	ESTs	1.22	2.12
	430801	AI580935	Hs.105698	ESTs	1.22	2.53
	414880	AW247305	Hs.119140	eukaryotic translation initiation factor	1.21	1.16
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	1.21	1.04
55	404790			C12001707*:gi 7305215 ref NP_038599.1 k	1.21	2.05
	403943			C5000355:gi 4503225 ref NP_000765.1 cyt	1.21	2.05
	400201			NM_006156*:Homo sapiens neural precursor	1.21	1.35
	421005	AW293089	Hs.33263	ESTs	1.21	2.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.21	1.11
60	400789			C11001367*:gi 1076205 pir J50754 hypoth	1.21	1.06
	412853	M34175	Hs.74625	adaptor-related protein complex 2, beta	1.21	1.24
	449709	BE410692	Hs.23918	hypothetical protein PP5395	1.20	1.27
	413726	AJ278465	Hs.75510	annexin A11	1.20	1.14
	428485	NM_002950	Hs.2280	ribophorin I	1.20	1.24
65	405163			C5000561*:gi 7513700 pir T14151 Inv pro	1.20	1.11
	415887	NM_003375	Hs.78902	voltage-dependent anion channel 2	1.20	1.16
	434468	N29309	Hs.39288	ESTs	1.20	3.20
	446843	AW135925	Hs.98798	hypothetical protein MGC11332	1.20	2.25
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.20	2.18
70	448242	R60646	Hs.20768	HSPC189 protein	1.20	1.22
	415753	U52819	Hs.78781	vascular endothelial growth factor B	1.20	1.05
	442156	AI690586	Hs.29403	hypothetical protein FLJ22060	1.20	1.18
	408824	L80005	Hs.48375	small nuclear ribonucleoprotein polypept	1.20	1.45
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.20	1.03
75	413392	AW021404	Hs.13021	ESTs	1.20	2.07
	401286			Target Exon	1.20	2.08
	415665	AI097276	Hs.274430	surfeit 6	1.20	2.53
	456562	AA306049	Hs.102669	DKFZP434O125 protein	1.20	2.40
	408988	AL119844	Hs.49476	Homo sapiens clone TUAB Cri-du-chat regi	1.20	3.45
	427818	AW511222	Hs.193765	ESTs	1.19	2.99
	406404			NM_002162*:Homo sapiens intercellular ad	1.19	1.17

	400124		Eos Control	1.19	2.12
	416023	AA173029	gbzpp05e01.r1 Stralagene ovarian cancer	1.19	2.45
	427751	AF000152	conserved gene amplified in osteosarcoma	1.19	1.07
5	401204		ENSP00000252232*-Sterol regulatory elama	1.19	2.40
	446771	AA128965	TATA box binding protein (TBP)-associate	1.19	2.03
	429673	AA884407	protein tyrosine phosphatase, non-recept	1.18	2.36
	400130		Eos Control	1.18	2.58
	405365		CX001212*gi 7861932 gb AAF70445.1 (AF2	1.18	2.38
	406181		Target Exon	1.18	2.18
10	422559	AW247696	hypothetical protein MGC12934	1.18	2.13
	409524	AW402151	tumor necrosis factor (ligand) superfam	1.18	1.07
	438446	AW137476	Homo sapiens cDNA FLJ13884 fis, clone TH	1.18	2.11
	447980	AI703397	ESTs	1.18	2.02
15	425503	W92517	actin binding LIM protein 1	1.18	1.29
	411469	T09997	cysteine-rich protein 2	1.18	0.99
	409162	H25530	solute carrier family 22 (organic cation	1.17	1.04
	429986	AF092047	sine oculis homeobox (Drosophila) homolo	1.17	1.00
	420869	X58964	regulatory factor X, 1 (influences HLA c	1.17	2.58
20	425943	H46986	ESTs	1.17	2.25
	415376	R35960	Homo sapiens, Similar to hypothetical pr	1.17	2.13
	420588	AF000982	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.17	2.38
	457205	AI905780	Target CAT	1.17	1.11
	407970	AW403814	BCL2-associated athanogene	1.16	3.60
25	440214	AA247118	hypothetical protein FLJ11305	1.16	2.15
	405646		C12000200:gi 4557225 ref NP_000005.1 al	1.16	1.11
	438438	AA257992	Janus kinase 1 (a protein tyrosine kinas	1.16	1.08
	431427	AK000401	Homo sapiens cDNA FLJ20394 fis, clone KA	1.16	2.08
	419885	AA251551	ESTs	1.16	2.07
30	427679	AA973904	ESTs, Moderately similar to MYPH_HUMAN M	1.16	2.15
	443865	AW296385	hypothetical protein FLJ12610	1.15	2.05
	415511	AI732617	ESTs	1.15	3.44
	417988	AA210878	ESTs, Moderately similar to ALU1_HUMAN A	1.15	2.09
	405058		Target Exon	1.15	1.16
35	446623	AF279865	kinesin family member 13B	1.15	1.21
	419754	H52299	Homo sapiens mRNA; cDNA DKFZp58610523 (I	1.15	1.15
	420003	AA256906	ESTs, Weakly similar to ubiquitous TPR m	1.15	2.06
	422988	AW673847	ESTs	1.15	1.00
	426371	M63967	aldehyde dehydrogenase 1 family, member	1.15	2.31
40	422895	NM_015958	CGI-30 protein	1.15	2.08
	426295	AW367283	zinc finger protein 6 (CMPX1)	1.15	2.13
	448323	AW492298	ESTs	1.14	2.54
	414244	AA287801	ESTs, Moderately similar to Z195_HUMAN Z	1.14	2.23
	442872	AI471987	ESTs	1.14	2.09
45	425318	AJ076845	BCL2/adenovirus E1B 19kD-interacting pro	1.14	2.33
	415667	F11582	developmentally regulated GTP-binding pr	1.14	1.10
	401058		Target Exon	1.14	2.20
	409838	AW502928	gb:U1-HF-BP0p-ahw-e-10-0-U1.r1 NIH_MGC_5	1.14	2.15
50	438493	AI130740	phosphoinositide-3-kinase, regulatory su	1.14	1.00
	404392		C7001450:gi 12667420 gb AAK01436.1 AF332	1.14	2.82
	433220	AI076192	ESTs	1.14	2.78
	405166		Target Exon	1.14	2.23
	401038		C11000425:gi 4507721 ref NP_003310.1 ti	1.14	2.71
55	414052	AW578849	ESTs, Weakly similar to unnamed protein	1.14	2.08
	442043	BE567620	ESTs	1.13	2.17
	419727	AW180796	DKFZP564O243 protein	1.13	1.14
	425206	NM_002153	hydroxysteroid (17-beta) dehydrogenase 2	1.13	2.07
	414682	AL021154	inhibitor of DNA binding 3, dominant neg	1.13	1.47
	402712		C1003562*gi 10047177 db BAB13382.1 (A	1.13	1.18
60	452289	BE568205	mitogen-activated protein kinase kinase	1.12	2.16
	401496		Target Exon	1.12	1.10
	459249	AI970399	ESTs	1.12	2.67
	447495	AW401864	programmed cell death 8 (apoptosis-induc	1.12	2.03
	428422	AI557280	capping protein (actin filament) muscle	1.11	2.60
65	421762	AA297546	gb:EST113074 Fetal brain III Homo sapien	1.11	2.15
	405855		Target Exon	1.11	1.98
	428972	AK001470	cysteine desulfurase	1.11	2.19
	406761	AI241715	ATP synthase, H transporting, mitochondr	1.10	3.33
70	432425	AF070619	Homo sapiens clone 24481 mRNA sequence	1.10	2.30
	446241	AI004677	chromosome 14 open reading frame 4	1.10	2.28
	424454	AB011139	optic atrophy 1 (autosomal dominant)	1.10	2.18
	418242	AW976183	BTB and CNC homology 1, basic leucine zi	1.10	2.07
	437407	AI479332	ESTs	1.10	2.09
	447459	AI380255	ESTs	1.10	2.22
75	426682	AV660038	UDP glycosyltransferase 1 family, polype	1.09	2.33
	403655		NM_003071:Homo sapiens SWI/SNF related,	1.09	2.25
	433156	R59206	Homo sapiens cDNA: FLJ22539 fs, clone H	1.09	2.70
	403826		Target Exon	1.09	1.10

5	433333	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homo	1.09	1.06
	451382	H86180	Hs.221513	ESTs	1.08	2.75
	454717	AW815123		gb:QV4-ST0212-261199-045-b01 ST0212 Homo	1.08	1.98
	422743	BE304678	Hs.119598	ribosomal protein L3	1.08	1.00
	411672	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.08	1.00
10	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	1.08	2.45
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.08	2.15
	447703	AI420277		gb:U06c12.x1 NC1 CGAP_P28 Homo sapiens	1.08	2.05
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.07	2.03
	455234	R41084		gb:Hk7634 Adult heart, Clontech Homo sa	1.07	2.08
15	413945	NM_000591	Hs.75627	CD14 antigen	1.07	0.91
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.07	1.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.07	1.11
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	1.06	2.14
	455424	AW937733		gb:QV3-DT0045-210100-063-d06 DT0045 Homo	1.05	2.03
20	438324	AI792660	Hs.6162	KIAA0771 protein	1.05	2.27
	421604	AW293880	Hs.248367	MEGF11 protein	1.05	2.00
	422614	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.04	2.33
	404058			Target Exon	1.04	2.10
	453085	AW954243		KIAA0251 protein	1.04	2.18
25	417500	H59970		gb:yr16104.r1 Soares fetal liver spleen	1.04	2.40
	408653	AW410189	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	1.04	2.73
	440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	1.04	2.05
	409209	AA460160	Hs.73217	ESTs	1.04	2.73
	456107	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	1.03	2.18
30	415403	F07923	Hs.26744	ESTs	1.02	2.43
	455591	BE008018		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	1.02	2.08
	428491	AF091035	Hs.184627	KIAA0118 protein	1.02	2.81
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	1.02	2.11
	434540	NM_016045	Hs.3945	CGI-107 protein	1.02	2.78
35	442174	AI690080	Hs.128907	ESTs, Weakly similar to ARUX homeodomain	1.02	2.05
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	1.02	1.00
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-tin	1.02	2.25
	454412	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	1.00	2.20
	426955	AA393669	Hs.238094	ESTs	1.00	2.18
40	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	1.00	2.10
	400295	AA305627	Hs.139336	CX000682-gj112741327[ref]XP_008833.2) zi	1.00	2.00
	402001			ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	402812			Target Exon	1.00	1.00
	402892			NM_004930*:Homo sapiens capping protein	1.00	1.00
45	403329			Target Exon	1.00	1.00
	407202	N58172	Hs.109370	Target Exon	1.00	1.00
	408684	R61377	Hs.12727	ESTs	1.00	1.00
	410555	U92649	Hs.64311	hypothetical protein FLJ21610	1.00	1.00
	413573	AI733859	Hs.149089	a disintegrin and metalloproteinase doma	1.00	1.00
50	414343	AL036166	Hs.323378	ESTs	1.00	1.00
	414422	AA147224	Hs.323378	coated vesicle membrane protein	1.00	1.00
	417006	AW673606	Hs.249195	Homeo box A13	1.00	1.00
	421577	BE465451	Hs.80758	aspartyl-tRNA synthetase	1.00	1.00
	423349	AF010258	Hs.105925	single-minded (Drosophila) homolog 1	1.00	1.00
55	424273	W40460	Hs.127428	homeo box A9	1.00	1.00
	424649	BE242035	Hs.144442	phospholipase A2, group X	1.00	1.00
	426827	AW067805	Hs.151461	embryonic ectoderm development	1.00	1.00
	427308	D26087	Hs.172665	methyleneletrahydrofolate dehydrogenase	1.00	1.00
	429597	NM_003816	Hs.174905	KIAA0033 protein	1.00	1.00
60	430261	AA305127	Hs.2442	a disintegrin and metalloproteinase doma	1.00	1.00
	431078	U82827	Hs.237225	hypothetical protein HT023	1.00	1.00
	433222	AW514472	Hs.249195	homeo box A13	1.00	1.00
	434980	AW770553	Hs.238415	dickkopf (Xenopus laevis) homolog 4	1.00	1.00
	435974	U29690	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	1.00
65	443054	AI745185	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	1.00
	443564	AI921685	Hs.8939	yes-associated protein 65 kDa	1.00	1.00
	444542	AI161293	Hs.199713	ESTs	1.00	1.00
	445413	AA151342	Hs.280380	aminopeptidase	1.00	1.00
	448706	AW291095	Hs.12677	CGI-147 protein	1.00	1.00
70	448807	AI571940	Hs.21814	interleukin 20 receptor, alpha	1.00	1.00
	449448	D60730	Hs.7549	ESTs	1.00	1.00
	449517	AW500106	Hs.57471	ESTs	1.00	1.00
	450568	AL050078	Hs.23643	serine/threonine protein kinase MASK	1.00	1.00
	451844	T61430	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	1.00
75	452039	AI922988	Hs.172510	gb:yc06a03.s1 Stralagene lung (937210) H	1.00	1.00
	452795	AW392555	Hs.18878	ESTs	1.00	1.00
	453096	AW294631	Hs.11325	hypothetical protein FLJ21620	1.00	1.00
	453370	AI470523	Hs.139336	ESTs	1.00	1.00
	453966	BE148734	Hs.63325	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	405580			transmembrane protease, serine 4	1.00	1.00
				Target Exon	1.00	1.00

5	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	1.00	1.00
	450377	AB033091	Hs.74313	KIAA1265 protein	1.00	1.00
	433226	AW503733	Hs.9414	KIAA1488 protein	1.00	1.00
	412719	AW016610	Hs.816	ESTs	1.00	1.00
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	1.00	1.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.00	1.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	1.00	1.00
	438817	AI023799	Hs.163242	ESTs	1.00	1.00
10	455474	AW948094		gb:RC0-MT0012-290300-031-c10 MT0012 Homo	0.99	2.00
	420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	0.99	2.33
	428466	AF151063	Hs.184456	hypothetical protein	0.98	2.20
	421594	RA5689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	0.98	3.09
	444654	AV650572	Hs.23440	KIAA1105 protein	0.98	2.00
15	409759	N40285	Hs.81182	histamine N-methyltransferase	0.97	2.20
	401936			Target Exon	0.97	2.39
	403463			Target Exon	0.96	2.58
	434421	AI915927	Hs.34771	ESTs	0.96	2.15
	412636	NM_004415		desmoptakin (DPI, DPII)	0.95	2.01
20	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	0.93	2.55
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	0.93	3.10
	447470	BE618324	Hs.263561	ESTs, Weakly similar to A53531 oncotetral	0.92	2.08
	448369	AW268962	Hs.111335	ESTs	0.91	2.35
	421710	AB007930	Hs.107088	KIAA0461 protein	0.91	2.63
25	406805	AI686003	Hs.296031	ESTs	0.91	2.21
	447475	AI380797	Hs.158992	ESTs	0.90	3.25
	428892	U82828	Hs.194382	ataxia telangiectasia mutaled (includes	0.90	2.02
	450222	U75308	Hs.24644	TATA box binding protein (TBP)-associate	0.89	2.73
	401572			C15001384:gi12737057[refXP_012129.1]	0.88	2.00
30	429226	AA913330	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	0.88	2.37
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	0.87	3.70
	407614	NM_001932	Hs.37144	membrane protein, palmitoylated 3 (MAGUK	0.86	2.02
	417912	R25269	Hs.50547	ESTs	0.86	2.00
	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-A	0.86	2.11
35	403149			NM_001450:Homo sapiens four and a half L	0.86	2.19
	413000	BE046280		gb:dn43c09.x2 NC1_CGAP_RDF2 Homo sapiens	0.85	2.40
	425166	AK001456	Hs.154919	KIAA0625 protein	0.85	2.18
	447371	AA334274	Hs.18368	DKFZP564B0769 protein	0.84	2.13
	452801	AB935587	Hs.34447	ESTs	0.84	2.55
40	400957			Target Exon	0.83	2.15
	426420	BE383808	Hs.322430	NDRC family, member 4	0.83	2.14
	429354	AA451666	Hs.269363	ESTs	0.80	2.25
	417831	H16423	Hs.82685	CD47 antigen (R)-related antigen, integr	0.78	2.43
	443368	BE568891	Hs.199210	ESTs, Moderately similar to bK116F5.2 [H	0.78	2.00
45	441901	AB914445	Hs.128103	ESTs	0.76	2.06
	429462	AB90356	Hs.127804	Homo sapiens, clone IMAGE:3536432, mRNA,	0.76	2.03
	403010			C21000152:gi16226483[sp]Q52118[VM03_ERWS	0.75	2.43
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	0.75	2.42
	448332	AW293110	Hs.171068	ESTs	0.74	2.00
50	421674	T10707	Hs.298355	hypothetical protein FLJ23138	0.71	2.18
	450645	AL117441	Hs.301997	hypothetical protein FLJ13033	0.67	2.06
	448514	AB020626	Hs.301866	KIAA0819 protein	0.67	2.03
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.60	2.54
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	0.60	2.00
55	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	0.57	2.15
	408077	AL133574	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 [f	0.53	2.29

TABLE 9B

60	Key:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
<hr/>		
65	Key	CAT Number
	409345	112147_1
		Accession
		AI949109 AW118631 AI833148 AW117891 R45932 R80970 AA733110 AW269428 T27024 R97693 AI149202 AI475492 H98845 AA609665
		AI125598 AW663742 AI140029 AW103164 AA126862 N68829 W55398 H94509 W65300 R07712 R36955 AA812477 AA609576 AI754304
		Z41075 AA970004 AW274661 AA923584 AI673108 AA070706 AA541812 T90938
	409540	1138613_1
	409806	1155259_1
70	409838	1155987_1
	409844	1156139_1
	409855	1156256_1
	409865	1156518_1
	410600	121108_1
75	410846	1223902_1
	410946	1227589_1
	411456	1246706_1
		Accession
		AW409569 BE297044 BE295828
		AW500960 AW501280 AW500814
		AW502928 AW505606 AW501576 AW501577
		AW502336 AW502339 AW501736 AW501839
		AW502461 AW503000 AW502207 AW501862
		AW502208 AW502366 AW502148
		AW575742 BE549623 AI335824 BE463447 AA729043 AW408712 AW499616 AA086179 AW499617 AA191322
		AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807258 AW807180 AW807331
		AW811502 AW811521 AW811548 AW811471 AW811511 AW811508
		AW847588 AW847716 AW847654 AW847592

5	411609 412210 412383 412560	1251530_1 1283515_1 1292509_1 130601_1	AW993680 AW853769 AW901492 AW947725 AW901448 AW947577 AW947574 AW947576 AW947734 AW947733 AW947732 R24501 R23657 AA194467 AI948584 AI678666 AA194383 AI765219 AA702993 AA813511 AA620965 AI990303 AI624682 AI003925 AI338670 AI004689 AI004690 AI127228 Z25302 F29302 BE044308 F32592 AA112966 T30825 F24958 F18071 C00537 T30841 R24502 AI934786 AI770075 AI144132 AA812597 AW203978 H82735 AI813349 AI142908 C04894 AI208243 AI208044 N89963 AI767866 AI290470 AI865963 H83611 BE463806 AI082639 AA507760
10	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW058840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H01011 AW368529 AW390272 C18457 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700953 AA451923 AI340326 AI590975 T48793 AI568096 AI42882 AA039975 AJ470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AI494069 AI911702 AI494069 AI830049 AI897258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI850584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA951816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T7861 AW850878
30	412998 413000 413611 413709 413804 413895	1343218_1 1343239_1 1380017_1 1384144_1 1390710_1 1397743_1	BE046254 BE045673 BE046253 BE046280 BE046763 BE046576 BE153275 BE153189 BE153329 BE153022 BE153030 BE152974 BE158687 BE158688 T64682 BE168190 BE168256 BE178160 BE177986 BE178330 BE178480
35	415789 416023 416272 417500 419555	1555357_1 156696_1 158407_1 168443_1 165884_1	H01581 H12850 R65905 H13053 AA173029 BE467711 AA176710 AA178882 AA179898 AA178897 H59970 AA203382 R08822 AA244416 AA244401
40	420685 421762 421938 422895	195591_1 206590_1 209376_1 22276_1	AA279362 AA454496 AA584871 AA297545 AA297410 AA297401 AA297465 AA297268 AW966174 AA040581 AA300675 AA412243 AA412383 NM_015958 AF132964 AA088658 N28882 AI197842 AA338679 AA405666 W16871 AA385447 AI928315 AI928318 AW846613 AW960009 AI860587 AI206534 AI961336 T64873 AI735559 H58826 AA857710 AW337576 BE242131 AA339340 AA371380 AA334618 AA316398 R96579 AW771996 AA366110 W07461 H77948 W28514 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI888032 AI823925 AI823566 AW198135 AI287510 AI5655910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479 AI017717 AA349998 AA350286 BE501310 R48207 AI372769 AJ003450 AA915976 AI261513 AI033019 AI222825 AW150983 AA420700 AA420570 AW884784 Z40157 AW182416 AA918195 AA778707 AA927922 AA888718 AA853991 AA609856 AA634398 AF153201 AW888811 AW888810 AW842970 AA383181 F35832 F26805 X78930 AF026094 N83362 AA206766 AW874294 AA284205 AI091885 AA206800 AW370684 AA904608 AA806352 AA894757 AW068376 AA807284 AA311341 AW958314 AW974687 AA649656 AA652145 AA778647 AW070999 R42302 H16902 AA814856 T65225 AI523569 F09869 F04737 AI538427 AI051714 AW172603 F02602 F01437 AI684417 AI801950 F02970 Z39367 F02882 T16704 H14597 AW952332 R52080 H10427 T08175 T31057 AI381431 R60918 R41255 R43059 R39905 H19330 R39988 BE535511 M62098 AA306787 AW891766 AA348998 AA338869 AA344013 AW956561 AW389343 AW403607 L40391 AW408435 AA121738 AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404 AW884390 AA345454 AA303292 AA174174 BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056 AW118940 AA121666 AI832409 AA683475 AI140901 AI623576 AW519064 AW474125 AI953923 AI735349 AW150109 AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166 AA505378 AI041975 AI335355 AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885 AI160934 H79030 AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050 AA907805 AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857 AA296025 AA523155 AA853168 AI696593 AI658482 AI566601 AW072797 AA128047 AA035502 AW243274 AA992517 R43760 AW979062 AA848000 AA847968 AA829138 AA315805 AA376906 BE539395 AW579186 H44349 BE328145 BE041644 AW579187 AW366504 H28241 H25318 W37573 AW600919 AA528775 R75904 AW780125 AA149420 AI672414 AI122760 AA345675 AW172758 AI337912 AI961291 AW090300 AI090244 BE219837 AI623661 BE501576 AI742232 AW887496 BE501734 AI023964 AI288904 AA975373 AA890325 AI458424 AI984583 N32562 AI358102 AW241694 AI038448 AA576391 AI018389 AI672071 AA977874 W37448 AW189392 AA612894 AI373563 H89551 H89365 AI699774 AI277548 W27992 AF056988 BE566411 AL121194 AW976385 AW366882 AI767324 AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010 AI402077 AW747989 W26565
75	442473 442506 445182 447703	543413_1 54405_1 632151_1 733191_1	

448079	74834_1	R76981 AA101801 AA101722 AA122297 AA098802 BE006483 AA343200 AW963375 BE090425 AA213871 BE621402 AA309094 AW960171 AI275045 Z44230 AW243724 AI051487 AI376624 R68631 AW978550 C00116 AI984051 AA122265 AI379941 AW205843 AW205839 AW190219 AW129532 AI954133 AI658859 AI383948 AI537386 AA213788 AI088416 AI360826 AA101802 AI619505 AA101795 AA101723 AW614392 R64287 AA927599 AI251904 AI803003 AI675123 AW023079 AW134959 AI926156 AA831069 AI638324 F29901 R46085 F03383 C17731 R20584 T90131
5	450936 85190_2	AI033745 AI034133 AA844424 AW166024 AI831699 AJ971097 AA011685 H70852 H70851
	451844 888230_1	T61430 AI820546 AI821336
	452900 93691_1	AA626794 AA626779 AA071274 AA928041 AI954235 N71035 N70230 AW674412 AI871136 AI563955 AI954237 AA649543 AI340231 AI368586 AI868721 W44486 T83736 AA126250 AI343619 H94297 T47633 AI672897 AA496355 R23240 AI814680 AA902119 AA644262 N67040 AW074273 AI357512 AA865354 AI027942 R33837 H95828 N63928 AI418701 AI186469 AA693672 AA778429 AA128352 AW954072 C00015 AA861853 AW022016 AI955845 AI753118 AI755095 AA029523 T70086 AA029458 AW675640 N79506 AI659597 AI417119 AI804089 AI383091 AA128493 T83907 T47632 AA094118 AA496405 H94191 AW887759 N98454 AA512988 AI623761 AW028373 AW249740 AI187029 AA991733 AI683085 AI336036 D60550 D60466 D60009 D60248 AW262673 AI524080 AA205843 AI969141 AW674989 AA093704 R81248 R73069 W01019 R23316 C14688 W44485 AA093663 T70157 H57883 R94790 D81287 D81788 AA364340 AA383533 N41706 BE295144 D60973 D81466 D60551 R33836 D60249 AA354560 W01933 T71478 AA515461 F27994 BE084745 W19084 R81247 AI080252 AI382863 AA205642
10		AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306 AA918481 AI183314 D83907 AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767267 W56507 AA847787 AA568692 T10502 AI247870 AA715017 AA643304 AA890233 AA811387 AA897470 AA907729 AI708679 AI078010 AA452830 AW419160 AI783713 N80205 W56778 AA676899 AI888718 N69930 AI338935 AI217580 AA639508 AA575836 BE046852 AI312651 AI038406 AA626649 AA643838 AI493761 AA032024 W38849 AA340178 AA447052 AA452969 W19369 AA296364 H44229 W58767 C05751 C05855 AI741989 N98532 AW102617 AA412583 AI922246 W38495 AA355375 AA928571 C06275 AA352500 N93132
15		AW582568 AW818656 AW818647 AW818655 AW818637 AW818234
	454412 1174764_1	AW807095 AW807022 AW845880 AW807096 AW807461 AW846116 AW807070
	454555 1223870_1	AW815123 AW815138 AW815259
	454717 1230516_1	R41084 AW875856
	455234 1265385_1	AW937733 AW937727 AW937883
	455424 1289247_1	AW948094 AW948118 AW948070 AW948093 AW948084 AW948088 AW948074 AW948079 AW948117 AW948085 AW948081 AW948096
20	455474 1292960_1	AW948102 AW948087 AW948080 AW948061 AW948091 AW948098 AW948089 AW948104 AW948119 AW948089 AW948100 AW948112 AW948121 AW948068 AW948109 AW948105 AW948097 AW948120 AW948108 AW948111 AW948114 AW948115 AW948072 AW948083 AW948095 AW948116 AW948078 AW948077 AW948071 AW948067 AW948107 AW948122 AW948065 AW948064 AW948113 AW948063 AW948062
25		AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181 AW948177 AW948171 AW948183 AW948173
30		BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
35		BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
	455604 1337197_1	BE145837 BE145894
	455842 1374629_1	AW975000 AA658945 AA661558
	457747 397222_1	AI743502 AI807438
40	458991 850804_1	AW176180 AW176212 AI909464 AW176218 AW176171 AW176203 AW176181 AW176213
	459192 923891_1	

TABLE 9C

45	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
50	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400634	8567750	Minus	101102-101223,101886-102018
400750	8119067	Plus	198991-199168,199316-199548
400752	7331445	Minus	36215-36461
400772	8131629	Minus	34896-35021,41078-41197
400773	8131629	Minus	44116-44238,48208-48321
400788	7342055	Plus	184369-184715
400789	8307741	Plus	82281-83693
400835	8954121	Plus	89366-89622
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
400847	9188605	Plus	44543-44835
400957	7705148	Minus	66959-67241
400967	7770682	Minus	32697-32999
401038	7232177	Minus	4277-4469
401041	7232177	Plus	44750-45076
401058	8117654	Minus	45226-45414
401155	9438289	Plus	31381-31526
401177	9438503	Minus	62773-63330
401196	9719673	Plus	33138-33834
401204	9743388	Minus	33694-33872
401286	9801342	Minus	147036-147318
401346	9926605	Minus	12031-13032
401371	9650602	Plus	80901-81283

	401383	6721135	Minus	155543-157381
	401496	7381769	Minus	82790-83002
	401512	7622346	Plus	136399-136557
	401563	8247910	Plus	91395-91763
5	401572	8570271	Minus	78651-78889
	401593	7230957	Plus	10368-10572, 11293-12356
	401600	4388746	Minus	27363-27518, 28727-28891, 29526-29731
	401603	7689953	Minus	116659-116780
	401613	4878062	Plus	22461-22831
10	401654	9097132	Minus	64695-64797
	401660	9100664	Minus	173662-174024
	401720	6468551	Plus	7783-8468
	401784	7249190	Plus	148362-148606, 149453-149535, 149731-149962
	401835	7139700	Plus	142257-142742
15	401886	7229913	Minus	79215-79393
	401936	3808091	Plus	46817-46943
	402001	9501818	Plus	68052-68223
	402087	8117546	Plus	137069-137213, 138678-138828, 138969-139050
20	402138	7704985	Plus	14173-15108
	402144	7242326	Plus	115425-115977
	402190	8576067	Minus	76488-76959
	402191	8576073	Minus	69410-69583
	402329	7798735	Plus	15833-16180, 18419-18715, 22507-22624
25	402368	9558577	Minus	47218-47330, 48052-48203
	402371	9558584	Plus	68736-68956
	402378	9625333	Minus	41312-41468, 48313-48720
	402449	9796674	Plus	59867-60039, 62588-62828, 63465-63623, 64923-65108
	402474	7547175	Minus	53526-53628, 55755-55920, 57530-57757
30	402517	9798106	Plus	17569-17721
	402599	7239666	Plus	5835-5987
	402617	9930797	Minus	69466-69945
	402712	8969253	Minus	10941-11138
	402731	9211639	Minus	117913-118004, 121110-121211, 121327-121457, 125478-125623, 126540-126663
35	402737	9212184	Minus	13358-13552
	402754	9213730	Plus	15345-15852
	402760	9213869	Plus	136829-136952, 137336-137521
	402812	6010110	Plus	25026-25091, 25844-25920
	402845	9369288	Plus	160451-160617, 160788-161009
40	402869	6434843	Minus	138639-139335
	402892	8086844	Minus	194384-194645
	403010	3132346	Plus	78385-79052
	403149	9799833	Plus	25034-25185
	403326	8440025	Minus	110959-111122
45	403329	8516120	Plus	96450-96598
	403342	7233487	Minus	42312-43750
	403349	8569773	Minus	167815-168374
	403381	9438267	Minus	26009-26178
	403463	9929538	Plus	102596-102879
50	403655	8736093	Plus	65668-65859
	403725	7534031	Plus	86737-86843
	403728	7534291	Minus	34481-34671
	403807	8439933	Minus	162963-165773
	403826	9838209	Plus	121197-121358
55	403885	7710403	Minus	53259-53524
	403943	7711864	Plus	100742-100904, 101322-101503
	403988	8575087	Plus	16251-16462
	404029	7671252	Plus	108716-111112
	404058	3548785	Plus	99397-101808
60	404059	3168819	Plus	47310-47450
	404178	7630978	Minus	178075-178383
	404204	3169112	Minus	79868-80321
	404231	8218035	Minus	61077-61322
	404250	9187145	Minus	36099-36212, 37928-38075
65	404273	9885189	Plus	97789-98285, 99601-99855
	404343	9838093	Plus	122664-122931
	404349	7630858	Minus	61006-61187
	404391	3135305	Minus	26030-26173, 27852-27997
	404392	3135305	Minus	29738-29857
70	404397	9558608	Minus	104042-104232
	404438	6984205	Plus	63413-63553
	404439	7139680	Plus	55316-55585
	404530	6479107	Plus	3157-3304
	404596	9958262	Minus	104807-105043
75	404649	9796926	Minus	100027-100399
	404666	7272179	Minus	18677-18993
	404687	9797554	Minus	128456-128565
	404744	9187237	Plus	71776-71852, 72885-73019, 73700-73822, 74692-74850

	404751	7630939	Plus	113799-114252,114393-114715
	404769	8099713	Minus	175801-176823
	404790	7230958	Plus	38611-38761
5	404906	7331453	Minus	100985-101126
	404956	7387343	Plus	55883-56203
	404977	3738341	Minus	43081-43229
	405000	6957544	Minus	88854-89993
	405022	7330304	Plus	217163-217439
10	405053	7651944	Minus	157134-157430
	405068	7655685	Plus	150740-151556
	405155	9966228	Plus	130469-130723
	405163	9966267	Minus	161171-161299
	405165	9966302	Plus	6461-6845
	405166	9966302	Plus	40526-40891
15	405172	9966752	Plus	153027-153262
	405180	7139743	Plus	65438-65740
	405193	7230072	Plus	128187-128383
	405194	7230072	Plus	190465-190645,193346-193610
20	405245	7249293	Minus	57560-58312
	405365	2275192	Minus	119867-120372,120481-120824,121029-121357
	405376	1552533	Plus	28875-29099
	405418	6997292	Plus	51839-51953
	405436	7408068	Minus	55716-55979
25	405443	7408143	Plus	90716-90887,101420-101577
	405474	8439781	Plus	172005-172175
	405602	9211311	Minus	50360-50584
	405580	4512267	Plus	169232-169647
	405595	7159256	Plus	47585-47688
30	405630	4508116	Minus	103218-103291,105858-105993,110051-110126
	405646	4914350	Plus	741-969
	405710	5531256	Minus	66203-66832
	405806	7274891	Minus	224961-226780
	405812	4775630	Minus	29424-29764
35	405855	7652031	Minus	60377-60795
	405879	6758747	Minus	54789-55457
	405891	6758795	Plus	41062-41861
	405902	6758795	Minus	82322-83110
	405932	7767812	Minus	123525-123713
40	406038	8389537	Plus	37764-37877
	406140	9168231	Minus	49887-50219
	406181	5923650	Plus	16586-16855
	406231	7417725	Plus	17206-17641,17772-17968
	406248	7417725	Plus	49711-50227
45	406274	7543787	Plus	932-1123
	406356	7107907	Plus	18761-18973
	406404	9256305	Minus	152569-152874
	406467	9795551	Plus	182212-182958
	406557	7711569	Minus	5446-5574,6170-6352
50	406575	7711679	Plus	142034-142473

TABLE 10A: Genes preferentially expressed in non-invasive bladder tumors

5	Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title R1 80th percentile of T4 tumor Als divided by the 80th percentile of T2-T4 tumor Als			
10	Pkey ExAccn UnigeneID Unigene Title R1			
	421110 AJ250717 Hs.1355 cathepsin E 8.23			
	428651 AF196478 Hs.188401 annexin A10 5.78			
	451668 Z43948 Hs.326444 cartilage acidic protein 1 5.53			
	415511 A1732617 Hs.182362 ESTs 4.72			
15	428336 AA503115 Hs.183752 microseminoprotein, beta- 4.66			
	418026 BE379727 Hs.83213 fatty acid binding protein 4, adipocyte 4.62			
	400752 NM_004293 Hs.239147 NM_003105*:Homo sapiens sortilin-related 3.99			
	430315 guanine deaminase 3.82			
	403010 C21000152:gi 6226483 sp Q52118 YMO3_ERWS 3.56			
	404977 Insulin-like growth factor 2 (somatomedi 3.54			
20	426657 NM_015865 Hs.171731 solute carrier family 14 (urea transport 3.51			
	400409 AF153341 Homo sapiens winged helix/forkhead trans 3.38			
	400844 NM_003105*:Homo sapiens sortilin-related 3.27			
	406081 Target Exon 3.22			
	417275 X63578 Hs.295449 parvalbumin 3.03			
25	402230 Target Exon 2.96			
	454219 X75042 Hs.44313 v-rel avian reticuloendotheliosis viral 2.89			
	403381 ENSP00000231844*:Ecotropic virus Integra 2.87			
	426088 AF038007 Hs.166196 ATPase, Class I, type 8B, member 1 2.86			
30	452286 A1358570 Hs.123933 ESTs, Weakly similar to ZN91_HUMAN ZINC 2.69			
	434061 AW024973 Hs.283675 NP0009 protein 2.68			
	418406 X73501 Hs.84905 cytokeratin 20 2.65			
	418818 AA228899 Hs.101307 Homo sapiens HUT11 protein mRNA, partial 2.59			
	421594 R45689 Hs.21689 Homo sapiens cDNA FLJ12978 fis, clone NT 2.57			
35	403383 Target Exon 2.56			
	435563 AF210317 Hs.95497 solute carrier family 2 (facilitated glu 2.55			
	424800 AL035588 Hs.153203 MyoD family inhibitor 2.54			
	404606 Target Exon 2.53			
	418205 L21715 Hs.83760 troponin I, skeletal, fast 2.53			
40	431912 A1660552 Hs.76549 ESTs, Weakly similar to A56154 Abl subst 2.52			
	413766 AW613780 Hs.13500 ESTs 2.51			
	421100 AW351839 Hs.124660 Homo sapiens cDNA: FLJ21763 fis, clone C 2.50			
	416640 BE262478 Hs.79404 neuron-specific protein 2.50			
	420729 AW964897 Hs.290825 ESTs 2.50			
45	402844 C1000118*:gi 9951913 ref NP_062832.1 pr 2.48			
	401093 C12000586*:gi 6330167 dbj BA486477.1 (A 2.46			
	417720 AA205625 Hs.208067 ESTs 2.45			
	400297 A1127076 Hs.306201 hypothetical protein DKFZp564O1278 2.45			
	403818 Target Exon 2.44			
50	440273 A1805392 Hs.325335 Homo sapiens cDNA: FLJ23523 fis, clone L 2.44			
	418060 AA211589 Hs.208047 ESTs 2.40			
	400843 NM_003105*:Homo sapiens sortilin-related 2.38			
	446006 NM_004403 Hs.13530 deafness, autosomal dominant 5 2.35			
	401512 NM_014080:Homo sapiens dual oxidase-like 2.34			
55	446847 T51454 Hs.82845 Homo sapiens cDNA: FLJ21930 fis, clone H 2.32			
	417094 NM_006895 Hs.81182 histamine N-methyltransferase 2.31			
	436293 A1601188 Hs.120910 ESTs 2.30			
	436246 AW450963 Hs.119991 ESTs 2.30			
	447578 AA912347 Hs.136585 ESTs, Weakly similar to JC5314 CDC28/fdc 2.29			
	417381 AF164142 Hs.82042 solute carrier family 23 (nucleobase tra 2.28			
60	426028 NM_001110 Hs.172028 a disintegrin and metalloproteinase doma 2.27			
	431448 AL137517 Hs.306201 hypothetical protein DKFZp564O1278 2.26			
	437181 A1306615 Hs.125343 ESTs, Weakly similar to KIAA0758 protein 2.23			
	415025 AW207091 Hs.72307 ESTs 2.18			
65	412610 X90908 Hs.74126 fatty acid binding protein 6, ileal (gas 2.04			
	424099 AF071202 Hs.139336 ATP-binding cassette, sub-family C (CFTR 2.03			
	433078 AW015188 Hs.121575 Homo sapiens cDNA FLJ12231 fis, clone MA 2.01			
	416225 AA577730 Hs.186684 ESTs, Weakly similar to PC4259 ferritin 2.00			
	411880 AW872477 gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens 1.99			
70	452316 AA298464 Hs.61265 ESTs, Moderately similar to G786_HUMAN P 1.89			
	413804 T64682 gb:yc48b02.r1 Stratagene liver (937224) 1.88			
	432306 Y18207 Hs.303090 protein phosphatase 1, regulatory (inhib 1.76			
	405364 ENSP00000239138*:Guanine nucleotide-bind 1.60			
	414320 U13616 Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) 1.52			
	401929 C17001690:gi 6005701 ref NP_009099.1 AT 1.00			

TABLE 10B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5

Pkey	CAT Number	Accession
411880	1263110_1	AW872477 BE088101 T05990
413804	1390710_1	T64662 BE168190 BE168256

10

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

20

Pkey	Ref	Strand	Nt_position
400752	7331445	Minus	36215-36461
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
401093	8516137	Minus	22335-23166
401512	7622346	Plus	136399-136557
401929	3810670	Minus	3167-3286,4216-4310
402230	9966312	Minus	29782-29932
402844	9369286	Plus	54958-55313
403010	3132346	Plus	78385-79052
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403818	8962065	Minus	138360-138512,144656-144796
404606	9212936	Minus	22310-23269
404977	3738341	Minus	43081-43229
405364	2281075	Minus	48325-48491,49136-49252
406081	9123861	Minus	38115-38691

35

TABLE 11A: Genes preferentially expressed in muscle-invasive bladder tumors

5	Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigenes number Unigene Title: Unigene gene title R1 80th percentile of T2-T4 tumor AIs divided by the 80th percentile of Ta tumor AIs			
	Pkey	ExAccn	UnigenelD	Unigene Title
10	423961	D13666	Hs.136348	periostin (OSF-2os)
	421948	L42583	Hs.334309	keratin 6A
	401780			NM_005557*:Homo sapiens keratin 16 (foca
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
15	439926	AW014875	Hs.137007	ESTs
	408243	Y00787	Hs.624	Interleukin 8
	414183	AW957446	Hs.301711	ESTs
	411573	AB029000	Hs.70823	KIAA1077 protein
	414522	AW518944	Hs.76325	step II splicing factor SLU7
20	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (tus
	401781			Target Exon
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous
30	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
35	406663	U24683	Hs.293441	immunoglobulin heavy constant mu
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous
40	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy
	433470	AW960564		transmembrane 4 superfamily member 1
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom
45	413324	V00571	Hs.75294	corticotropin releasing hormone
	436729	BE621807		transmembrane 4 superfamily member 1
	450455	AL117424	Hs.25035	chloride intracellular channel 4
	413731	BE243845	Hs.75511	connective tissue growth factor
	412429	AV650262	Hs.75765	GRO2 oncogene
50	418283	S79895	Hs.83942	cathepsin K (pseudosarcosis)
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CATC RAT COL
55	413441	AJ929374	Hs.75367	Src-like-adaptor
	404854			Target Exon
	431319	AA873350	Hs.302232	ESTs
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fls, clone H
60	429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
	408380	AF123050	Hs.44532	diubiquitin
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac
	422545	X02761	Hs.287820	fibronectin 1
	418203	X54942	Hs.83758	CDC28 protein kinase 2
65	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a
	406687	M31126		matrix metalloproteinase 11 (stromelysin
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers
	417497	AW402482	Hs.82212	CD53 antigen
70	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3
	445033	AV652402	Hs.72901	mucln 13, epithelial transmembrane
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo
	427527	AI808057	Hs.293441	immunoglobulin heavy constant mu
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso
75	453331	AJ240665		ESTs
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR
	417366	BE185289	Hs.1076	small proline-rich protein 1B (corniflin)

5	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	3.07
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.02
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	2.77
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.75
	406755	N80129	Hs.94360	metallothionein 1L	2.75
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.67
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.65
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.64
10	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	2.51
	410204	AJ243425	Hs.326035	early growth response 1	2.46
	438973	AW959503	Hs.60440	ESTs, Weakly similar to serin protease w	2.46
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.44
	422626	AA344932	Hs.118786	metallothionein 2A	2.44
15	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.43
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	2.42
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.42
	407207	T03651	Hs.336780	tubulin, beta polypeptide	2.30
	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.29
20	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20
	424909	S78187	Hs.153752	cell division cycle 25B	2.18
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	2.17
	416819	U77735	Hs.80205	p1m-2 oncogene	2.11
	422582	AI962060	Hs.118397	AE-binding protein 1	2.07
25	414081	AW969976	Hs.279009	matrix Gla protein	2.07
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.03
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.01
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.94
	414420	AA043424	Hs.76095	Immediate early response 3	1.90
30	415149	X12451	Hs.78056	cathepsin L	1.72
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.70
	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.69
	452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.64
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.64
35	415198	AW009480	Hs.943	natural killer cell transcript 4	1.60
	424390	AW815557	Hs.182241	interferon induced transmembrane protein	1.59
	426825	AL133415	Hs.297753	vimentin	1.51
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.46
	407694	U77594	Hs.37682	retinoic acid receptor responder (Iazaro	1.44

TABLE 11B

Pkey: Unique Eos probe/identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428036	28620_1	<p>AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M64110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875 AI868636 AA864291 AI685060 AW088029 AI924908 AW466328 AI093800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330 AL046953 AA852666 AW391995 W30846 AW662928 W25261 AA042863 R99045 H97060 W03910 H94687 TB8984 AL048165 T29632 N31556 N36484 AI798679 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047816 R24137 R63433 AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370721 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594 AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA808425 R63380 AA384736 AA384738 AA852352 AI073645 AA527960 AA525036 AA044414 AI752450 AA703064 R01216 AA897183 AI751996 TB1078 H95047 AA573642 D58348 N20953 AA437143 N95439 AA579540 AW857056 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020 AW994984 H20896 AW964438 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309 AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813 AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 AW608407 R05674 H16712 N85426 N42354 H85516 BE147991 T28113 R32662 AA384578 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409 AA042828 AA363555 AJ223812 AA344709 BE149590 R70995 W46881 W90778 N71242 AA534826 AL040676 R23797 H96450 AA062957 D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343690 AW888731 AI751527 AA937490 AA937505 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046506 AW384981 AA043908 AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821 AI626043 N37087 AI624140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022 AW069069 AW069454 AA342989 AI077712 AI311467 AI087381 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356670 AA873156 AI004219 AI189685 AA478018 AA076063 AI445222 AI753124 AI521569 AI925026 AI022368 AI475993 H20846 AI223234 AI635123 AA579170 N30442 AW117889 AA807935 AA558975 AI306636 AA888963 AI952591 AI935835 AI445293 H16713 AW139833 AA622122 AA972051 AI280828 H09543 AI453725 AW069613 AI865615 AI753921 AI368782 AI633208 AA46651 W46961 N22201 H82276 C16555 AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N67873 AW023948 C15861 C16601 AI251465 AW079187 BE045090 AI273006 C16390 C16503 AI620823 F13661 N68864 Z21311 C16103 C16089 C16400 AA758273 AI287781 AI6487 N29477 AW608074 AW385583 AI589944 AA655817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C16255 AW029046 C16202 AW189997 AI370492 C16471 AA652809 AA936687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662 T94414 AI567041 AI619654 AW008488 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA669781 AA026678 AW132002 AW263919 C18562 AA759137 AA693351 Z40779 C16577 AA885045 AW073763 R45484 AI520895 U54708 T49285 AI568126 AW005589 AI093317 AL119781 T61046 AI053563 H51958 AF114144 AA305739 AW950394 AW793928 AW793910 AL047737 AV659047 AV659632 AI750389 AA092053 AA092798 H85367 T61597 R23745 Z20418 T78485 AI751528 AW068121 AA853188 AI752459 AA853711 AW950653 R78964 R36359 R21626 R21522</p>

433470	3672_1	AW950564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176446 AA304671 AW583735 T61714 AA316968 AI446515 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873 AA180483 AA159546 F00242 AI940609 AI940602 AI189753 T97663 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510 AW629109 AW513200 AA921353 AI677934 AI148699 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AW733014 AI591384 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682684 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300 BE621807 AI445461 AI346835 AI453743 AI564644 AI928364 AW984527 BE156214 AI694111 AI591358 C17504 C17476 C17963 C18304 AW071625 AI678712 C17732 D57559 H61762 AI720939 AI262930 H27252 AA479712 AI927769 AA291465 AA155661 AI963432 AI567995 AA421678 AI925607 AA292956 AA192448 AW192593 AI865838 AI696905 AI871950 AI911921 BE619741 BE439796 AI161312 AI597801 AI424384 AI093510 AI240988 AW820230 AI92554 BE044033 AW262737 AW008570 AA043216 AW629505 AA136645 AA037772 AA706057 AA088439 AW806193 AW806183 AA479834 BE501957 AA129574 R38114 AA649494 AA524526 BE327120 AW572531 BE219784 BE349186 AW015724 AA043217 AW772000 AI799814 AI671727 AW779725 AA502832 AI470033 AA129575 W38161 AI972739 AA404570 AA627686 AA723200 AA147228 AA903050 AI990245 AI075878 T32487 C06123 AA157944 AI800106 W60075 AI859160 AA478328 AW673152 AA182640 AI990827 AW275048 AW103470 AI298935 AW471421 R79190 AW085158 W45410 AI333170 AW300456 AA662517 T55840 AI823466 AI692845 AA962397 AW191997 AA136658 AI251817 BE044134 AW339104 AW517762 AA724739 R79933 AA411100 AA191349 AA037696 AA190966 AA757735 AW772283 AA010631 H80983 AI769516 H64985 AI061065 AI950693 AA085492 AI245632 H28594 AW088968 BE156360 AI349390 AI621320 AI738844 AW194272 AA148284 AA953883 C06365 AA487893 AI927217 AI918523 AI453453 AI798502 AI189366 AI261359 AI032569 AW338678 AI972899 AI500576 AI872628 AI693030 Z28771 AI985583 AI363829 AW339301 AA581093 AI650338 W60032 AA603586 AI686240 AW242958 AA719173 AI745717 AW675302 AI582462 AI244845 AI565439 F09579 AI918453 AA035576 AI472527 AW351556 AA191414 AW674145 D57558 AI446740 D57845 AI589264 C05782 AA722206 AI432033 R21752 BE157510 AI829640 AI468237 AW384233 AA989662 AI865912 AW197954 AI344941 X75684 AI344943 AW583310 AA988297 AI334860 AI348877 AI798415 D11921 AI377596 AI983655 AI744233 C06111 AI248307 AA948565 AI224807 AI240655 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410588 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25871 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
--------	--------	---

TABLE 11C

35

Pkey:
Ref:

Strand:
Nt_position:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
404854	7143420	Plus	14260-14537

45

TABLE 12A: Genes preferentially expressed in muscle-invasive bladder tumors

	Key:	Unique Eos probe set identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence Identification Number linking Information in Table 12A to sequences in Table 13			
10	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	Seq ID No. 1 & 2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	Seq ID No. 3 & 4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. 5 & 6
15	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. 7 & 8
	406964	M21305		FGENES predicted novel secreted protein	Seq ID No. 9 & 10
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seq ID No. 11 & 12
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	Seq ID No. 13 & 14
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savigny)	Seq ID No. 15 & 16
20	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. 17 & 18
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	Seq ID No. 19 & 20
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	Seq ID No. 21 & 22
	415511	AI732617	Hs.182362	ESTs	Seq ID No. 23 - 25
	452461	N78223	Hs.108106	transcription factor	Seq ID No. 26 & 27
25	413324	V00571	Hs.75294	corticotropin releasing hormone	Seq ID No. 28 & 29
	443211	AJ128388	Hs.143655	ESTs	Seq ID No. 30
	439926	AW014875	Hs.137007	ESTs	Seq ID No. 31 & 32
	432222	AJ204995		gb:an03c03.x1 Stralagene schizo brain S1	Seq ID No. 33
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. 34 & 35
30	443171	BE281128	Hs.9030	TONDU	Seq ID No. 36 & 37
	432829	W60377	Hs.57772	ESTs	Seq ID No. 38 & 39
	410553	AW016824	Hs.272068	hypothetical protein MGC14128	Seq ID No. 40 & 41
	419183	U60669	Hs.89563	cytochrome P450, subfamily XXIV (vitamin	Seq ID No. 42 & 43
	425721	AC002115	Hs.159309	uroplakin 1A	Seq ID No. 44 & 45
35	420370	Y13645	Hs.97234	uroplakin 2	Seq ID No. 46 & 47
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s]	Seq ID No. 48 & 49
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	Seq ID No. 50 & 51
	456034	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCL_CGAP_Su	Seq ID No. 52
40	421110	AJ250717	Hs.1355	cathepsin E	Seq ID No. 53 & 54
	451668	Z43948	Hs.326444	cartilage acidic protein 1	Seq ID No. 55 - 60
	408243	Y00787	Hs.624	interleukin 8	Seq ID No. 61 & 62
	440304	BE159984	Hs.125395	ESTs	Seq ID No. 63 & 64
	414918	AJ219207	Hs.72222	hypothetical protein FLJ13459	Seq ID No. 65 & 66
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	Seq ID No. 67 & 68
45	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. 69 & 70
	405033			C1002652*.gij544327[sp]Q04799[FM05_RABIT	Seq ID No. 71 & 72
	422282	AF019225	Hs.114309	apolipoprotein L	Seq ID No. 73 & 74
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	Seq ID No. 75 & 76
50	400844			NM_003105*:Homo sapiens sortilin-related	Seq ID No. 77 & 78
	404875			NM_022819*:Homo sapiens phospholipase A2	Seq ID No. 79 & 80
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	Seq ID No. 81 & 82
	431347	AJ133461	Hs.251664	insulin-like growth factor 2 (somatomedi	Seq ID No. 83 & 84
	413804	T64682		gb:yc48b02.r1 Stralagene liver (937224)	Seq ID No. 85 & 86
	444163	AJ126098		FGFESH predicted RNaseH domain-containl	Seq ID No. 87 - 89
55	444444	AJ149332	Hs.14855	ESTs	Seq ID No. 90 & 91
	427747	AW411425	Hs.180655	serine/threonine kinase 12	Seq ID No. 92 & 93
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. 94 & 95
	420281	AI623693	Hs.323494	Predicted cation efflux pump	Seq ID No. 96 & 97
	402305			C19000735*.gij4508027[ra]NP_003414.1 [z	Seq ID No. 98 - 100
60	436608	AA628980		down syndrome critical region protein DS	Seq ID No. 101 & 102
	427239	BE270447		ubiquitin carrier protein	Seq ID No. 103 & 104
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	Seq ID No. 105 & 106
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	Seq ID No. 107 & 108
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	Seq ID No. 109 & 110
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. 111 & 112
65	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	Seq ID No. 113 & 114
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	Seq ID No. 115 & 116
	401093			C12000586*.gij6330167[kib]BAAB6477.1 [A	Seq ID No. 117 - 119
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	Seq ID No. 120 & 121
70	449722	BE280074	Hs.23960	cyclin B1	Seq ID No. 122 & 123
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. 124 & 125
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	Seq ID No. 126 - 133
	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. 134 & 135
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. 136 & 137
75	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No. 138 - 141
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	Seq ID No. 142 & 143
	427335	AA448542	Hs.251677	G antigen 7B	Seq ID No. 144 & 145
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kafni	Seq ID No. 146 & 147

404440			NM_021048:Homo sapiens melanoma antigen,	Seq ID No. 148 & 149
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	Seq ID No. 150 & 151
408380	AF123050	Hs.44532	diubiquitin	Seq ID No. 152 & 153
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	Seq ID No. 154 & 155
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No. 156 & 157
438817	AI023799		ESTs	Seq ID No. 158
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	Seq ID No. 159 & 160
431515	NM_012152	Hs.258583	EDG-7 (endothelial differentiation, lys	Seq ID No. 161 & 162
433159	AB035898	Hs.150587	kinesin-like protein 2	Seq ID No. 163 & 164
432441	AW292425	Hs.163484	ESTs	Seq ID No. 165
425726	AF085808	Hs.159330	uroplakin 3	Seq ID No. 166 & 167
448045	AJ297436	Hs.20166	prostate stem cell antigen	Seq ID No. 168 & 169
431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. 170 & 171
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	Seq ID No. 172 & 173
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	Seq ID No. 174 & 175
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	Seq ID No. 176 & 177
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	Seq ID No. 178 & 179
400297	AJ127076	Hs.306201	hypothetical protein DKFZp564O1278	Seq ID No. 180 & 181
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. 182 & 183
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. 184 & 185
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	Seq ID No. 186 & 187
445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	Seq ID No. 188 & 189
423961	D13666	Hs.136348	periostin (OSF-2os)	Seq ID No. 190 & 191
417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	Seq ID No. 192 & 193
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	Seq ID No. 194 & 195
430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	Seq ID No. 196 & 197
425650	NM_001944	Hs.1925	desmoglein 3 (permpiguis vulgaris antigen)	Seq ID No. 198 & 199
409103	AF251237	Hs.112208	XAGE-1 protein	Seq ID No. 200 & 201
129404	AI267700		ESTs	Seq ID No. 202
403047			NM_005656*:Homo sapiens transmembrane protease	Seq ID No. 203 & 204
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmem	Seq ID No. 205 & 206

TABLE 12B

35	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

40	Pkey	CAT Number	Accession
	413804	1390710_1	T64682 BE168190 BE168256
	427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
45			BE269715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248261 AW250313 T19021 AA355115 AA316879
			BE269633 BE621936 AA290724 AA380031 AA993616 BE301331 W79220 H73020 AW797850 BE274611 BE314315 BE542407 BE562063
			BE312868 BE278817 BE252503 AA426470 M91670 NM_014501 BE264533 AI884863 AI884942 AI678077 AA829937 AI869333 AW273060
			AA906924 AI571293 AW172642 AA582906 AW674596 AW300936 AW615753 AW615587 AW665495 AI859298 AA594105 AA928110
			AI038859 AI589898 AA828316 AA938955 AA283711 AW170665 BE047759 AW732128 AI015067 AW070748 AW248955 AA975490
			AA211097 AI826097 AA826730 AA994072 AI367867 W74508 AI086474 AA827720 AI922589 AW000868 W58033 AA991461 BE048131
50			M91218 AA876186 AA661759 AI123879 AI089508 AW272915 AI566244 AW245061 AA688299 AW250988 AI953468 AI891144 AW089131
			AJ471577 AA293354 AA464019 BE044549 T29587 AW956171 BE537716 BE269400 AA918328 AI538087 AA969243 AW075033 BE139361
			AI340589 AI250128 AI247038 BE138953 AW075177 AI307208 BE049086 AW302327 AI054335 AI345565 AI334881 AI252075 AI254494
			AW075006 AW302733 AW302738 AI054057 AI054217 AI054172 AI054302 AI053722 AI054060 AI054079 AW075181 AI307473 AI312145
			AI340734 AI334909 AW071374 BE138502 AW074809 AW301901 AI251662 AI307559 BE139228 AI254764 AW073049 AI251264 AI802837
			AW271867 AI307442 AW075100 AW073456 AW072496 AI270787 AW271039 AW071307 AI610913 AW071289 AI251232 AI251262
55			AW073656 AW072901 AI307493 AI255068 AI251289 AI252160 AI271495 AI252427 AW073469 AW071420 AI270156 AI252926 AI252839
			AI252868 AW072520 AW073433 AI340643 AI802854 AI334733 AI583896 AW071311 AI802853 AI289711 AI345035 AW072513 AI348921
			AI307478 AI305762 BE139315 AW271034 AI334886 AI340619 AW470476 BE139260 BE138965 AW302085 BE041872 AW268964
	432222	343347_1	AI204995 AW827539 AW969308 AW440776 AA528756
60	436608	42361_3	AA628980 AI126603 BE504035
	438817	465592_1	AI023799 AA826307 AI683094 AI307373 AI870547 AW979007
	444163	593658_1	AI126098 AI184745 AI148521
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 12C

70	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24745-24872,25035-25204
	401093	8516137	Minus	22335-23166

402305	7328724	Plus	40832-41362
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
405033	7107731	Minus	142358-142546

5

Table 13
Seq ID NO: 1 DNA sequence:
Nucleic Acid Accession #: NM_002205
Coding sequence: 24..3173

5

	1	11	21	31	41	51	
10	CAGGACAGGG	AAGAGCGGGC	GCTATGGGGA	GCCGGACGCC	AGAGTCCCTT	CTCCACGCCG	60
	TGCAGCTGCG	CTGGGGCCCC	CGGGCGCGAC	CCCCGCTCGT	GCCGCTGCTG	TTGCTGCTCG	120
	TGCGCGCGCC	ACCCAGGGTC	GGGGGCTTCA	ACTTAGACGC	GGAGGCCCA	GCAGTACTCT	180
	CGGGGCCCCC	GGGCTCCTTC	TTCCGATTCT	CAGTGGAGTT	TTACCGGCCG	GGACACAGCG	240
	GGGTCAAGT	GCTGGTGGGA	GCACCCAGG	CTAATACCAG	CCAGCCAGGA	GTGCTGCAGG	300
	GTGGTCTGT	CTACCTCTGT	CCTTGGGGTG	CCAGCCCCAC	ACAGTGCACC	CCCAATTGAAT	360
15	TTGACAGCAA	AGGCTCTCGG	CTCCTGGAGT	CCTCACTGTC	CAGCTCAGAG	GGAGAGGAGC	420
	CTGTGGAGTA	CAAGTCTCTG	CAGTGGTTTG	GGGCAACAGT	TCGAGCCCAT	GGCTCTCTCA	480
	TCCTGGCATG	CGCTCCACTG	TACAGCTGGC	GCACAGAGAA	GGAGCCAATG	AGCGACCCCG	540
	TGGGCACCTG	CTACCTCTCC	ACAGATAACT	TCACCCGAAT	TCTGGAGTAT	GCACCTTGCC	600
	GCTCAGATTT	CAGCTGGGCA	GCAGGACAGG	GTTACTGCCA	AGGAGGCTTC	AGTGGCGAGT	660
20	TCACCAAGAC	TGGCCGTGTG	GTTTATGGTG	GACCAGGAAG	CTATTTCTGG	CAAGGCCAGA	720
	TCCTGTCTGC	CACCTCAGGAG	CAGATTGCAG	AATCTTATTA	CCCCGAGTAC	CTGATCAACC	780
	TGGTTCAAGG	GCATCTGCAG	ACTCGCCAGG	CCAGTTCCTT	CTATGATGAC	AGCTACCTAG	840
	GATACTCTGT	GGCTGTGGT	GAATTCAGTG	GTGATGACAC	AGAAGACTTT	GTGCTGGTGG	900
	TGCCCAAAGG	GAACCTCACT	TACGGCTATG	TCACCATCCT	TAATGGCTCA	GACATTGGAT	960
25	CCCTCTACAA	CTTCTCAGGG	GAACAGATGG	CCTCCTACTT	TGGCTATGCA	GTGGCCGCCA	1020
	CAGACCTCAA	TGGGGACGGG	CTGGATGACT	TGCTGGTGGG	GGCACCCTTG	CTCATGGATC	1080
	GGACCCCTGA	CGGGCGGCGT	CAGGAGGTGG	GCAGGGTCTA	CGTCTACCTG	CAGCACCCAG	1140
	CCGGCATAGA	GCCCCACGCC	ACCCTTACCC	TCACCTGGCA	TGATGAGTTT	GGCCGATTTG	1200
	GCAGCTCCTT	GACCCCTCTG	GGGGACCTGG	ACCAGGATGG	CTACAATGAT	GTGGCCATCG	1260
30	GGGCTCCCTT	TGGTGGGGAG	ACCCAGCAGG	GAGTAGTGTG	TGTATTTCTT	GGGGGCCCAG	1320
	GAGGGCTGGG	CTCTAAGCCT	TCCAGGTTTC	TGCAGCCCTT	GTGGGCGAGC	AGCCACACCC	1380
	CAGACTCTCT	TGGCTCTGCC	CTTCGAGGAG	GCCGAGACCT	GGATGGCAAT	GGATATCCTG	1440
	ATCTGATTGT	GGGTCTCTTT	GGTGTGGACA	AGGCTGTGGT	ATACAGGGGC	CGCCCATCG	1500
	TGTCGCTAG	TGCCTCCCTC	ACCATCTTCC	CCGCCATGTT	CAACCCAGAG	GAGCGGAGCT	1560
35	GCAGCTTAGA	GGGAACCCCT	GTGGCCTGCA	TCAACCTTAG	CTTCTGCCTC	AATGCTTCTG	1620
	GAAACACAGT	TGCTGACTCC	ATTGGTTTCA	CAGTGGAACT	TCAGCTGGAG	TGGCAGAAGC	1680
	AGAAAGGAGG	GGTACGGCGG	GCACGTGTTC	TGGCCTCCAG	GCAGGCCAACC	CTGACCCAGA	1740
	CCCTGCTCAT	CCAGAATGGG	GCTCGAGAGG	ATTGCAGAGA	GATGAAGATC	TACCTCAGGA	1800
	ACGAGTCAGA	ATTTCCGAGAC	AAACTCTCGC	CGATTACAT	CGCTCTCAAC	TTCTCCTTGG	1860
40	ACCCCAAGC	CCCAAGTGAC	AGCCACGGCC	TCAGGCCAGC	CCTACATTAT	CAGAGCAAGA	1920
	GCCGGATAGA	GGACAAGGCT	CAGATCTTGC	TGGACTGTGG	AGAAGACAAC	ATCTGTGTGC	1980
	CTGACCTGCA	GCTGGAAGTG	TTTGGGGAGC	AGAACCATGT	GTACCTGGGT	GACAAGAATG	2040
	CCCTGAACCT	CACITTTCCAT	GCCCCAGAATG	TGGGTGAGGG	TGGCCCTTAT	GAGGCTGAGC	2100
	TTGGGCTCAC	CGCCCTTCCA	GAGGCTGAGT	ACTCAGGACT	CGTCAGACAC	CCAGGGAACCT	2160
45	TCTCCAGCCT	GAGCTGTGAC	TACTTTGCCG	TGAACCAAGG	CCGCTGTGCT	GTGTGTGACC	2220
	TGGGCAACCC	CATGAAGGCA	GGAGCCAGTC	TGTGGGGTGG	CCTTCGGTTT	ACAGTCCCTC	2280
	ATCTCCGGGA	CACATAAGAA	ACCATCCAGT	TTGACTTCCA	GATCCTCAGC	AAGAATCTCA	2340
	ACAACCTCGA	AAGCGAGCTG	GTTTCTCTTC	GGCTCTCCGT	GGAGGCTCAG	GCCCAGGTCA	2400
	CCCTGAACGG	TGTCTCCAAG	CCTGAGGCG	TGCTATTCCC	AGTAAGCGAC	TGGCATCCCC	2460
50	GAGACCAAGC	TCAGTAGGAG	GAGGACCTGG	GACCTGCTGT	CCACCATGTC	TATGAGCTCA	2520
	TCAACCAAGG	CCCCAGCTCC	ATTAGCCAGG	GTGTGTGGGA	ACTCAGCTGT	CCCCAGGCTC	2580
	TGGAAGGTCA	GCAGCTCCTA	TATGTGACCA	GAGTTACGGG	ACTCAACTGC	ACCACCAATC	2640
	ACCCCATTA	CCCAAGGGCG	CTGGAGTTGG	ATCCCGAGGG	TTCCCTGCAC	CACCAAGCAA	2700
	AAAGCGGAAG	TCCAAGCCGC	AGCTCTGCTT	CCTCGGGACC	TCAGATCCCT	AAATGCCCGG	2760
55	AGGCTGAGTG	TTTCAGGCTG	CGCTGTGAGC	TCGGGCCCCC	GCACCAACAA	GAGAGCCAAA	2820
	GTCTGCAGTT	GCAATTCCGA	GTCTGGGCCA	AGACTTTCTT	GCAGCGGGAG	CACCAAGCAT	2880
	TTAGCTGCA	GTGTGAGGCT	GTGTACAAAG	CCCTGAAGAT	GCCCTACCGA	ATCCTGCCTC	2940
	GGCAGCTGCC	CCAAAAGAGG	CGTCAGGTGG	CCACAGCTGT	GCAATGGACC	AAGCGAGAAG	3000
	GCAGCTATGG	CGTCCCACCT	TGGATCATCA	TCCTAGCCAT	CCTGTTTGCC	CTCCTGCTCC	3060
60	TAGGTCTACT	CATCTACATC	CTCTACAAGC	TTGGATTCTT	CAAAAGCTCC	CTCCCATATG	3120
	GCACCGCCAT	GGAAAAGCT	CAGCTCAAGC	CTCCAGCCAC	CTCTGATGCC	TGAGTCTCTC	3180
	CAATTTCAGA	CTCCCATTTCC	TGAAGAACCA	GTCCCCCCAC	CCTCATTCTA	CTGAAAAGGA	3240
	GGGGTCTGGG	TACTTCTTGA	AGGTGCTGAC	GGCCAGGGAG	AAGCTCCTCT	CCCCAGCCCA	3300
	GAGACATACT	TGAAGGGCCA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3360
65	GCACTGTGAA	GGACCTTGT	TTACACATAC	CCTCTTCATG	GATGGGGGAA	CTCAGATCCA	3420
	GGGACAGAGG	CCGACCTTCC	CTGAAGCCTT	TGCATTTTGG	AGAGTTTCTT	GAAACAACTG	3480
	GAAAGATAAC	TAGGAATATC	ATTACAGATT	CTTTGGGCCA	GACATGCCAC	AAGGACTTCC	3540
	TGTCCAGCTC	CAACCTGCAA	AGATCTGTCC	TCAGCCTTGC	CAGAGATCCA	AAAGAGCCCC	3600
	CCAGTAAGAA	CCTGGAACCT	GGGGAGTTAA	GACCTGGCAG	CTCTGGACAG	CCCCACCTTG	3660
70	GTGGGCCAAC	AAAGAACAAT	AACTATGCAT	GGTGCCCCAG	GACCAAGCTCA	GGACAGATGC	3720
	CACAAGGATA	GATGCTGGCC	CAGGGCCAGA	GCCAGCTTCC	AAGGGGAATC	AGAACTCAA	3780
	TGGGGCCAGA	TCCAGGCTGG	GGTCTGGAGT	TGATCTGGAA	CCCAAGCTCA	GACATTGGCA	3840
	CCRAATCCAG	CAGATCCAGG	ACTATATTTG	GGCCTGTCTC	AGACCTGATC	CTGGAGGCCC	3900
	AGTTCAACCT	GATTTAGGAG	AAGCCAGGAA	TTTCCCAAGG	CCTGAAGGGG	CCATGATGGC	3960
75	AACAGATCTG	GAACCTCAGC	CTGGCCAGAC	ACAGGCCCTC	CCTGTTCCCC	AGAGAAAGGG	4020
	GAGCCCACTG	TCTTGGGCTC	GCAGAAATTT	GGTCTGCTCT	GCCAGCTGCA	CTGATGCTGC	4080
	CCCTCATCTC	TCTGCCCAAC	CCTTCCCTCA	CCTTGGCACC	AGACACCCAG	GACTTATTTA	4140
	AACCTCTGTT	CAAGTGCAAT	AAATCTGACC	CAGTGCCCCC	ACTGACCAGA	ACTAGAAAAA	4200

AAAA

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_002196.1

5
10
15
20
25
1 11 21 31 41 51
MGSRTPEPSP HAVQLRWGPR RRPPLVPLLL LLVPPPPFRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQGLQLT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPEKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDGFG RFGSSLTPLG DLDQDGYNDV AIGAPPGET 420
QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YFDLIVGSFG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GPTVELQLDW QKQKGVVRR LFLASROATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNMF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHYVYLG KNALNLTFHA QNVGEGGAYE AELRVTAPPE ABYSGLVRHP GNFSLSLSDY 720
FAVNSRRLLV CDLGNPMKAG ASLWGLGRPT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QOKREAPSR 900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
YKLGFFKRLS PYGTAMEKAQ LKPPATSDA

Seq ID NO: 3 DNA sequence:
Nucleic Acid Accession #: NM_002425
Coding sequence: 23..1453

35
40
45
50
55
60
65
1 11 21 31 41 51
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTGTGTCGTG TGTGTCGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCACGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAATAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTGCGCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGAAGC 720
TTTGATGTAC CCACCTTACA ACTCATTAC AGAGCTCGCC CAGTTCCGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCAACA AAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTITTC TACTTCTTCA GTGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTITTTAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGTCATG TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCAATGA GAATGTTTCT GGAATCTTCT 1620
ACTTGTCTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_002416

70
75
1 11 21 31 41 51
MMHLAFLVLL CLPVC SAYPL SGAKEEDSN KDLAQQYLEK YYNLEKDVQK FRRKDSNLIV 60
KKIQGMQKFL GLEVTKGLDT DTLEVMRKPR CGVPDVGHFS SPPGMPKWRK THLTIRIVNY 120
TFDPLRDAVD SAIEKALKVW EVTPTLTFSR LYEGEADIMI SFAVKEHGDF YSPDGPGLSL 180
AHAYPPGPGY YGDHFDDE KWTEDASGTN LFLVAHELQ HSLGLFHSAN TEALMYPLYN 240
SFTELAQFRL SQDDVNGIQS LYGPFPASTE EPLVPTKSVS SGSEMPAKCD PALSFDAIST 300
LRGEYLFPPK RYFWRSHWN PEPEPHLISA FWP9LPSYLD AAYEVNSRDT VFIFKGNEFW 360
AIRGNEVQAG YPRGIHTLGF PPTIRKIDAA VSDKEKKKTY FFAADKYWRF DENQSMEQG 420

FPRLIADDFP GVEPKVDAVL QAFGFFYFFS GSSQFEFDPN ARMVTHILKS NSWLHC

Seq ID NO: 5 DNA sequence:
Nucleic Acid Accession #: NM_002421
Coding sequence: 72..1481

5
10
15
20
25
30
35
40
45

1	11	21	31	41	51	
GGGATATTGG	AGTAGCAAGA	GGCTGGGAAG	CCATCACTTA	CCTTGCACTG	AGAAAGAAGA	60
CAAAGGCCAG	TATGCACAGC	TTTCCTCCAC	TGCTGCTGCT	GCTGTCTCGG	GGTGTGTTGT	120
CTCAGAGCTT	CCCAGCGACT	CTAGAAACAC	AAGAGCAAGA	TGTGGACTTA	GTCCAGAAAT	180
ACCTGGAAAA	ATACTACAAC	CTGAAGAATG	ATGGGAGGCA	AGTTGAAAAG	CGGAGAAAAT	240
GTGGCCCACT	GGTTGAAAAA	TTGAAGCAAA	TGCAGGAATT	CTTTGGGCTG	AAAGTGAAGT	300
GGAAACGAGA	TGCTGAAACC	CTGAAGGTGA	TGAAGCAGCC	CAGATGTGGA	GTGCCTGATG	360
TGGCTCAGTT	TGTCCTCACT	GAGGGGAACC	CTCGCTGGGA	GCAAAACACAT	CTGACCTACA	420
GGATTGAAAA	TTACACGCCA	GATTTGCCAA	GAGCAGATGT	GGACCATGCC	ATTGAGAAAG	480
CCTTCCAACT	CTGGAATTAAT	GTCAACCTCT	TGACATTAC	CAAGGTCTCT	GAGGGTCAAG	540
CAGACATCAT	GATATCTTTT	GTGAGGGGAG	ATCATCGGGA	CAACTCTCCT	TTTGATGGAC	600
CTGGAGGAAA	TCTTGCTCAT	GCTTTTCAAC	CAGGCCCAGG	TATTGGAGGG	GATGCTCATT	660
TTGATGAAGA	TGAAAGGTGG	ACCAACAATT	TCAGAGAGTA	CAACTTACAT	CGTGTTCGGG	720
CTCATGAAGT	CGGCCATTCT	CTTGGACTCT	CCCATTCTAC	TGATATCGGG	GCTTTGATGT	780
ACCTTAGCTA	CACCTTCACT	GGTGATGTTC	AGCTAGCTCA	GGATGACATT	GATGGCATCC	840
AAGCCATATA	TGGACGTTCC	CAAAATCCTG	TCCAGCCCAT	CGGCCACAA	ACCCCAAAAG	900
CGTGTGACAG	TAAGCTAAAC	TTTGATGCTA	TAACTACGAT	TCGGGGAGAA	GTGATGTTCT	960
TTAAAGCAGAG	ATTCTACATG	CGCAAAATC	CCTTCTACCC	GGAAAGTTGAG	CTCAATTICA	1020
TTTCTGTTTT	CTGGCCACAA	CTGCCAAATG	GGCTTGAAGC	TGCTTACGAA	TTTGCCGACA	1080
GAGATGAAGT	CCGTTTTTTC	AAAGGGAATA	AGTACTGGGC	TGTTACAGGA	CAGAAATGTGC	1140
TACACGGATA	CCCCAAGGAC	ATCTACAGCT	CCTTTGGCCT	CCCTAGAACT	GTGAAGCATA	1200
TCGATGCTGC	TCTTCTGAG	GAAACCACTG	GAAAAACCTA	CTTCTTTGTT	GCTAACAAAT	1260
ACTGGAGGTA	TGATGAATAT	AAACGATCTA	TGGATCCAGG	TTATCCCAAA	ATGATAGCAC	1320
ATGACTTTCC	TGGAATTGGC	CACAAAGTTG	ATGCAGTTTT	CATGAAAGAT	GGATTTTCTT	1380
ATTTCTTTCA	TGGAACAAGA	CAATACAAAT	TTGATCCTAA	AACGAAGAGA	ATTTTGACTC	1440
TCCAGAAAAG	TAATAGCTGG	TTCACCTGCA	GGAAAAATTG	AACATTACTA	ATTTGAATGG	1500
AAAACACATG	GTGTGAGTCC	AAAGAAGGTG	TTTTCTTGAA	GAACGTGCTA	TTTTCTCAGT	1560
CATTTTTAAC	CTCTAGAGTC	ACTGATACAC	AGAATATAAT	CTTATTTATA	CCTCAGTTTG	1620
CATATTTTTT	TACTATTTAG	AATGTAGCCC	TTTTTGTAAT	GATATAATTT	AGTTCCACAA	1680
ATGGTGGGTA	CAAAAAGTCA	AGTTTGTGGC	TTATGGATTC	ATATAGGCCA	GAGTTGCAAA	1740
GATCTTTTCC	AGAGTATGCA	ACTCTGACGT	TGATCCCAGA	GAGCAGCTTC	AGTGACAAAC	1800
ATATCTTTTC	AAGACAGAAA	GAGACAGGAG	ACATGAGTCT	TGCGCGAGG	AAAAGCAGCT	1860
CAAGAACACA	TGTGCAGTCA	CTGGTGTGAC	CCTGGATAGG	CAAGGGGATA	CTCTCTAAC	1920
ACAAAATAAG	TGTTTTATGT	TTGGAATAAA	GTCAACCTTG	TTTCTACTGT	TTT	

Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002412

50
55
60

1	11	21	31	41	51	
MHSFPPLLLL	LFNGVVSHSF	PATLETOEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPFV	60
VEKLQKMQEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNPRWE	QTHLYTRIEN	120
YTPDLPRADV	DHAIEKAPQL	WSNVTPLTFT	KVSEQQADIM	ISFVRGDHRD	NSPFDGPGGN	180
LAHAFQPGPG	IGGDAHPDED	ERWTNNFREY	NLHRVAAREL	GHSGLSLHST	DIGALMYPST	240
TFSGDVQLAQ	DDIDGIQAIY	GRSQNFVQPI	GPQTPKACDS	KLPDAITTI	RGEVMFFKDR	300
FYMRNPFYFP	EVELNFIQVP	WPQLPNGLEA	AYEFADRDEV	RFFKGNKYNA	VQGNVNLHGY	360
PKDIYSSPGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YPRMIADDFP	420
GIGHKVDVAF	MKGDFYFFFH	GTRQYKFDPK	TKRILTLQKA	NSWFCNCKN		

Seq ID NO: 7 DNA sequence:
Nucleic Acid Accession #: NM_014331
Coding sequence: 1..1506

65
70
75

1	11	21	31	41	51	
ATGGTCAGAA	AGCCTGTTGT	GTCCACCATC	TCCAAGGAG	GTTACCTGCA	GGGAAATGTT	60
AACGGGAGGC	TGCTTCCCTT	GGGCAACAAG	GAGCCACCTG	GCGCAGGAGAA	AGTGCAGCTG	120
AAGAGGAAAG	TCACTTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
GGAACTCTCA	TCTCTCCTAA	GGGCGTGCTC	CAGAACACGG	GCGACGTGGG	CATGCTCTCTG	240
ACCATCTGGA	CGGTGTGTGG	GGTCCTGTCA	CTATTGGAGG	CTTTGTCTTA	TGCTGAATTG	300
GGAACTAATA	TAAAGAAATC	TGAGGTCAT	TACACATATA	TTTGGGAAGT	CTTTGGTCCA	360
TTACCACTTT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
GTGATATCCC	TGGCATTGGG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCCTAAAT	540
AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACTTTTGT	CAAGCTCACA	600
GCAATTCTGA	TAATTTATAGT	CCCTGGAGTT	ATGCAGCTAA	TAAAGGTCA	AACGCAGAAC	660
TTTAAAGACG	CGTTTTCAGG	AAGAGATTCA	AGTATTACCG	GTTGCCACT	GGCTTTTAT	720

5
10
15
20
25
30
35
40

TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780
AACCOCTGAAA AAACCATTC CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATTTGGC 840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA 900
AATSCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960
ATCTTTGTGT CCCTCTCCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020
TTATTCTATG TTGCGTCTCG AGAGGGTCCAC CTTCAGAGAA TCCTCTCCAT GATTCAATGTC 1080
CGCAAGCACA CTCTCTACCC AGCTGTTATT GTTTTGCAACC CTTTGACAAT GATAATGCTC 1140
TTCTCTGGAG ACCTCGACAG TCTTTTGAAT TTCCTCAGTT TTGCCAGGTG GCTTTTATT 1200
GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCGCAGATAT GCATCGTCTC 1260
TTCAAGGTGC CACTGTTTAT CCCAGCTTTG TTTTCTTCA CATGCTCTT CATGGTTGCC 1320
CTTTCCCTCT ATTCGGACCC ATTTAGTACA GGGATTGGCT TCGTCATCAC TCTGACTGGA 1380
GTCCTCGCTT ATTTATCTCT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440
TCAGAGAAAA TAACCAAGAA ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500
TTATGAACATA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGAGACAC AAAATAGGGA 1560
TTTTTACTTC ATTTTCTGAA AGTCTAGAGA ATTACAACCT TGGTGATAAA CAAAGGAGT 1620
CAGTTATTTT TATTCAATATA TTTTAGCATA TTCGAACTAA TTCTAAGAA ATTTAGTTAT 1680
AACTCTATGT AGTTTAGAAA AGTGAATATG CAGTTATCTT ATGAGTCGCA CAATTCCTGA 1740
GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAGACTA GACAATTACT ATGTGGTCAT 1800
TCTCTACAAC ATATGTTAGC ACGCAAAAGA ACCTTCAAAT TGAAGACTGA GATTTTCTG 1860
TATATATGGG TTTTGTAAGG ATGGTTTAC ACCTACAGA TGTCTTACT GTGAAAAGTG 1920
TTTTCAATTC TGAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTACATT GACATTGCTT TGCTTCCCTT TAGATACCAA TTTAGATAAC AAACACTCAT 2040
GCTTTAATGG ATTTATACCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100
TTAAAGAAGA GTTCTTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAAT 2160
AAAAATCCTT GAGAATTTAT TATGTCAGAT GTTTTTCAT TCATTATCAG GAAGTTTATG 2220
TTATCTGTCA TTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGATAAC CACATCTTAG 2280
AGCAAGAGTT AGTTTGTAT TAAATCCTCA TTAGAACCAAC CACCTGTTTC ACTAATAACT 2340
TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAAGCC TTCAAATTAC ATTATCAACA 2400
TGAGAGAAAT AACCAACAAA GAAGATGTTT AAAATAATAG TCCCATATCT GTAATCATAT 2460
CTACATGCAA TGTAGTAAT TCTGAAGTTT TTTAAATTTA TGGCTATTTT TACACGATGA 2520
TGAATTTTGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTTCTTCTG TAAATAICT 2580
CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAAACATA AAAATTGCAA 2640
AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAAATT CCACTTCTAT 2700
ATCTAGGCTT TGTCAATAT TTCCACACCT TAATTATCAT TCAACTTGCA AAGAGACAA 2760
CTGATAAGAA GAAATTTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTT AGAAGATGTT 2820
GTTTGGCCAG TATTAGAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAAATCCCA 2880
GCACCTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCCG GAGTTCTAGA CCAGCCTGAC 2940
CAACATGGAG AAACCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCAGAT 3000
GCTGTGTAAT TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGAGGCG 3060
GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
CCATCTCCAA AAAAAAAAAA AAAA

Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_055146

50
55
60

1 11 21 31 41 51
MVRKPVVSTI SKGGYLGQNV NGRLPSLGNK EPPGQEKVQL KRKVTLLRGV SIIGTIIGA 60
GIFISPKGVL QNTGVSQMSL TIHTVCGVLS LFGALSYAEL GTTIKSSGGH YTYILEVFGP 120
LPAPFVRVWE LLIIIRPAATA VISLAFGRYI LEFFFIQCEI PELAIKLITA VGITVVMVLN 180
SMSVSWNSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTON FKDAFSGRDS SITRLPLAFY 240
YGMAYAGWF YLNFVTEVEE NPEKTIPLAI CISMAIVTIG YVLTNVAYPT TINAEELLS 300
NAVAVTFSEF LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
RKHTPLPAVI VLHPLTMIML FSGDLSLLN FLSFARWLF GLAVAGLIYL RYKCPDMHRP 420
FKVPLPIPAL PSPTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480
SEKITRTLQI ILSEVVPEEDK L

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..546

65
70
75

1 11 21 31 41 51
ATGGCCTTGG GCAGCTCCGC CCCTGTGGCT TTGCAGGGTA ATGCCCACTT CCTGCTGCT 60
TTCATGGCTG GCATTAAAGT TCTGTGGCTT TTCCAGGTAG TCCCCCTGGG GCTCCCCGAG 120
TTGGTGCAAA GGCTCTCTGG TGGAGCTCGA ACTGAAACTC GCTTTGTGCC CGCAGCCCTG 180
CAGCTCGCGG GTGCCCCTGA CCTGCCCGCT GGGTCTCTGT CCTTTGAAGA GAGCACTTGC 240
GGCTTTGACT CCGTGTGGC CTCTCTGCCG TGGATTTTAA ATGAGGAAGG CCAGCAACCT 300
TTCGTGCTCT CAGGAGACAT GTCTGACTGG GACTACTGGG TTGGCTGGCG GAAGTTAATT 360
CATTTCTCTC TGAGCACTCC AGGGTGGAGC AGGCAGGTTA GGCTCCAGTT GTTCCAGCTT 420
CAGTTTGTCA AAGGCCAGAA CTTGGACGTA ACAGTGTACT GCAGGCTCCA GGGCAGTGAG 480
AAACCCCTTG AAACCTGGTC CATGGTTCCA TTCACCTTCA TGTACTGGAT CCACCATGGA 540
AAGTAG

Seq ID NO: 10 Protein Sequence
Protein Accession #: FGENESH

	1	11	21	31	41	51	
5	MALGSSAPVA	LQNAHFPA	FMAGIKLWL	FOVPLGLPE	LVQRLGGA	TETRFVPAAL	60
	QLAGALDLPA	GSCAFESTC	GFDSVLASLP	WILNEEQQP	FWSSGDMSDW	DYVWGWKRLI	120
	HSPLSTPGWS	RQVRLQLFQL	QFVKGNLDV	TVYCRLQGSE	KPFETGSMVP	FTFMYWIHHG	180
	K						
10	Seq ID NO: 11 DNA sequence						
	Nucleic Acid Accession #: EOS sequence						
	Coding sequence: 461-3286						
	1	11	21	31	41	51	
15	GCGGCCCTTG	AGCAGCCTCG	CCTTCGCTTC	CCGCGTTTCC	TGCGGTCCGC	CCTCCCCCGG	60
	CCGAGCTCCA	GGGGCTGCCG	CCTAGCAGCT	CCCGCGGGGA	GAGCGGTTCA	GAGCGCGCAC	120
	GGGGGCGGGC	GGAGGCGGCC	CGGTGCGGGG	CGGCCGCGCT	GGAGAGAGGC	GCGCGCGGAG	180
	ACGCGCGCCC	CCCTCTCCGC	GTTTGCTCGC	TTGCTCCCGC	CCTCCGCGAC	TCCGCTCGCT	240
	CCCACCCCTT	CCCGGCGTGA	TTGATCGGTC	ACGGGCGCCG	CCGCTGCCGC	CGCGGCGGCC	300
20	GCGGCGGTTT	TGAGCCGAGC	CGGAACCTTA	GCCCGAGACG	GAGCCGGGGC	CGGGGCGGGC	360
	GCCATTGCGC	GGGCGCGCGC	GGAGACCTTT	GGCGCGGGGC	GGCGGGCCGG	GCCAGGCCAT	420
	GCGGGCGGAG	TGAGCGGGCG	CCCGCAGCCC	CGCGCGCGGC	ATGGCTTCCC	CGCGGAGCTC	480
	CGGGCAGCCC	GGGCGCGCGC	CGCGCGCGCC	ACCGCGCGCC	GCGCGCTGCG	TACTGCTACT	540
	GCTGCTGCGC	CTGCTGCTGC	CTCTGGCGCC	CGGGCGCTGG	GGCTGGCGGC	GGGGCGCCCC	600
25	CGGGCGCGCC	CGCAGCAGCC	CGCGCTCTCT	CATCATGGGC	CTCATGCGGC	TCACCAAGGA	660
	GGTGGCCAA	GAGCAGCATC	GGCGGGTGT	GCTCCCGGCC	GTGGAATCGG	CCATCGAGCA	720
	GATCGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCGAC	CTCGGCTCT	ATGACACGGA	780
	GTGCGCAAC	GCAAAAGGGT	TGAAAGCCTT	CTACGATGCA	ATAAAATACG	GGCTTAACCA	840
	CTTGATGGTG	TTTGAGGCGG	TCTGTCCATC	CGTCACATCC	ATCATTGCGG	AGTCCCTCCA	900
30	AGGCTGGAAT	CTGGTGCAAG	TTTCTTTTTC	TGCAACCAAG	CCTGTCTAG	CCGATAAGAA	960
	AAAATACCTT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	GCGGTGAATC	CAGCCATTCT	1020
	GAAGTTGCTC	AAGCACTACT	AGTGAAGCG	CGTGGGCAAG	CTGACGCAAG	ACGTTACAGG	1080
	GTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	GGCGAGGACA	TTGAGATTTC	1140
	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAAGTGC	AAAAAGCTGA	AGGGGAATGA	1200
35	TGTGCGGATC	ATCCTTGACC	AGTTTGACCA	GAATATGGCA	GCAAAAGTGT	TCTGTGTGTC	1260
	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCACTGGATC	ATTCGGGGCT	GGTACGAGCC	1320
	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAACTCATCC	CGCTGCTTCC	GGAAGAATCT	1380
	GCTTGTCTGC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	CCCTGAGCT	CCAAGCAGAT	1440
	CAAGACCATC	TCAGGAAAGA	CTCCACGACA	GTATGAGAGA	GAGTACAACA	ACAAGCGGTC	1500
40	AGGCGTGGGG	CCCAGCAAGT	TCCACGGGTA	CGCTACGAT	GGCATCTGGG	TCATCGCCAA	1560
	GACACTGCGG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	CGGCACCGAG	GGATCCAGGA	1620
	CTTCAACTAC	ACGGAACCA	CGCTGGGCAG	GATCATCTTC	AATGCCATGA	ACGAGACCAA	1680
	CTTCTTGGGG	GTACAGGGTC	AAGTTGTATT	CCGGAATGGG	GAGAGAATGG	GGACCATTA	1740
	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	GAGTACAACG	CTGTGGCCGA	1800
45	CACACTGGATC	ATCATCAATG	ACACCATCAG	GTTCGAAGGA	TCCGAACCA	CAAAAGACAA	1860
	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	CTCTACAGCA	TCCTCTCTGC	1920
	CCTCACCATC	CTCGGATGTA	TGATGGCCAG	TGCTTTTCTC	TTCTTCAACA	TCAAGAACCG	1980
	GAATCAGAA	TCATAAAGA	GTGCGAGTCC	ATACATGAAC	AACCTTATCA	TCCTTGGAGG	2040
	GATGCTCTCC	TATGCTTCCA	TATTTCTCTT	TGGCTTGTAT	GGATCCTTTG	TCTCTGAAAA	2100
50	GACCTTTGAA	ACACTTTGCA	CCGTGAGGAC	CTGGATTCTC	ACCGTGGGCT	ACAGACCCGC	2160
	TTTTTGGGGC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	ATCTTCAAAA	ATGTGAAAA	2220
	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	GTGGGGGGCA	TGCTGCTGAT	2280
	CGACCTGTGT	ATCTGTAGCT	GCTGGCAGGC	TGTGGACCCC	CTGCGAAGGA	CAGTGGAGAA	2340
55	GTACAGCATG	GAGCGGAGCC	CAGCAGGAGC	GGATATCTCC	ATCCGCGCTC	TCTTGGAGCA	2400
	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	TATGCCCTACA	AGGGACTTCT	2460
	CATGTTGTTC	GGTGTGTTCT	TAGCTTGGGA	GACCGCAAC	GTACGATCC	CCGCACTCAA	2520
	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	ATCATGTGCA	TCATCGGGGC	2580
	CGCTGTCTCC	TTCTTGACCC	GGGACCAAGC	CAATGTGCGG	TTCTGATCG	TGGCTCTGGT	2640
	CATCATCTTC	TGCAGCACCA	TCACCTCTTG	CCTGGTATTC	GTGCGGAAGC	TCATCACCTT	2700
60	GAGAACAAAC	CCAGATGCGG	CAACGCAAGG	CAGGCGATTG	CAGTTCACCT	AGAATCAGAA	2760
	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCAAGTGT	AACCAAGCCA	GCAATCCCG	2820
	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	AAGATCACAG	AGCTGGATAA	2880
	AGACTTGGAA	GAGGTCAACA	TGCAGCTGCA	GGACACACCA	GAAAGACCA	CCTACATTAA	2940
	ACAGAACCA	TACCAAGAGC	TCAATGACAT	CCTCAACCTG	GGAAACTTCA	CTGAGAGCAC	3000
65	AGATGGAGGA	AAGGCCATT	TAAAAAATCA	CCTCGATCAA	AATCCCCAGC	TACAGTGGAA	3060
	CACAAAGAG	CCCTCTGGAA	CATGCAAGAA	TCCTATAGAA	GATATAAACT	CTCCAGAACCA	3120
	CATCCAGGCT	CGGCTGTCCC	TCCAGCTCCC	CATCTCCAC	CACGCTTACC	TCCCATCCAT	3180
	CGGAGGCGTG	GACGCGAGCT	GTGTGAGCCC	CTGCGTCAGC	CCCAACCGCA	GCCCCCGCCA	3240
70	CAGACATGTG	CCACCTCTCT	TCCGAGTCAT	GGTCTCGGGC	CTGTAAGGGT	GGGAGGCTTG	3300
	GGCCCGGGGC	CTCCCCCGTG	ACAGAACCA	ACTGGGCGAG	GGGGTCTGCT	GCAGAAACAC	3360
	TGTGCGCTCT	GGCTGCGGAG	AAGCTGGGCA	CCATGCGTGG	CCTCTCAGGA	CCAATCGGAT	3420
	GGCACTCAGG	TGGACAGGAC	GGGGCAGGGG	GAGACTTGGC	ACCTGACCTC	GAGCCTTATT	3480
	TGTGAAGTCC	TTATTCTTCT	ACAAAGAAGA	GGAACGGA	TGGGACGTCT	TCCTTAACAT	3540
	CTGCAACAA	GGAGGCGCTG	GGATATCAAA	CTTGCAAAAA	AAAAAATAAA	AAAAAATAAA	3600
75	CAAAAAAATC	AGAGCAAGGAG	AGAGGCACTA	GAACTCCAGC	TGGAAGTCAC	GGAGTGGCTC	3660
	GAGCAGCCTT	GGGAGAGGCG	AAGGAGCTTC	TGAAGAAACT	GCCTCTGCAC	ACACATCACT	3720
	GGCTGTGACC	CCTCAGGCTA	GCCCTTCTCC	ACTCTGGGGG	AGGAGGTGGG	AAGGGCCACC	3780
	AGGCCCCAG	CTGCCAGGCC	AGCTGACCCC	AGCCTTCTCT	GAACAGGAG	TCTGACGAG	3840

CGCAGACAGG CACAGCCCTG GAGCAGGCAG GCCGAGGGCT GCGSCACTGG AGCAGGCTGA 3900
 CTTACATGCT CCACATGGGA CCTGTGTAC CCAATGAGAT GTTTGTTACT CTGGTAAATG 3960
 CCACACGTGA ACACAAATAC ACCCATTCCT GGGACCGTGG GGATTAGGG CACGTCACTG 4020
 CAGACACGCT CTGCAGCATT CACCGACAGT CTGTCAATGCA CCCACCACTG TGGCCATGTC 4080
 5 CTGTGTGTTCC TATCGGATGC TCCAGTAAC CAGGGGGACC ACCCGAGCTA ATCATGGAAT 4140
 GTCTGTTCCT AGCAACACAG ATAAAGAAAG ATTGTGCACT TTAACCTCTC TCATCAGGGC 4200
 CCAGGGCTG GCTGGGATTG TTTTCTTTT TTTCCCACTA ACTTGTGTTT TGACCAAAAGT 4260
 GAATTGGAGG CACTCTGCTA AAAGACATCC CCGTAGACAT AGGGGAGAGA GTTGTGGGCT 4320
 GAGGGCTTCC CTGTGGCTCC AGAAGGCAGC CTTCCATCCA GACAAGCCAG TGAGCTCTCC 4380
 10 CCTTGGGATC ACTGGGGTGA TCAGTCAGCA GATTGATTCT CATTCTAAG ATCATTCCTC 4440
 CCTTTAAAT GAGCCCTTAA GAGCACTGGC CTGGGAGTCA GACAGACCTG GGTTCAGTTC 4500
 CTCAGTCCCC TGCCCACTCC CTACGTGACT TTGATCAGGT CACTAGTGTCT TCTCTGAGCC 4560
 TCAGTTTCCC CTCTGTAATC TGGGGTTGAA CTAAACACCC TGTCCTGCTC ACCTCACAG 4620
 GTCACCTGTA GGATTGAAC TTGATCTTGT CCAGGAAAGC TTTGTACCA ACAGTGAAGC 4680
 15 GCCTCTGATC CAGTGGGTAT GAGTATGACT CTGACCTTCA GCCCTCCCTA CAGCCGGGGG 4740
 TGTGGCCAG AGAAGCTTCC AGCAGACCCC TCTACCCAGA ACATCCGGGC TGGAGGGAGG 4800
 CTCCAGTGA CTCTTCTGAC ATTCCTAGAC AGGTTCATT TTTGCTCAAG AAAGGCGCTGA 4860
 ATGACAATGT CCAGGATGTC TGCACAACCT AGCAGCTCGC TCACTCCCTA AAGAAACCTA 4920
 TTGGCAGCTT CAACAGGCAG GCAATATCT CTTCCAGAA CCACTGCAGT CAGGAATAAA 4980
 20 CTGTTTCTC CACCAAGGCT TGACAAAAGG GCCCACAGGA ATCTTACCA TGCCCAACATT 5040
 TCAAAGCACC CTATTTCAG TAGCATAGCT TTCTGCTCCC CTTCCCAAA GAGAGGTTAT 5100
 GGAGGTACTG GTATCTTTAG GAAAGAAAAA ATGTTAACAC ATCAGAGTCT AAGTTGAAGT 5160
 CATTCTCTGT TTAGGCACTA AAAATCGGTG TTGTCACCTA CTGTGTATTA CCAGTATTTA 5220
 CTGTCTTCT TGATTTTACC AAAACCAAA TTAATTTAAA GGACCACTT AATTTTCAA 5280
 25 AGGGAAGAG ACAATTAAT GTACATAATG TATACACACA CACAAAAAAA AATACCTGTA 5340
 GAAATATTAT TCCAGCATAG CAGGAAAAA AACAAAAGTA TTGACTGTCT GGAGGTGAGC 5400
 CTGTGCTCTG GTAACTCTT GTGACTCTG AGCGTGCCT GTCTTCTAGG TTAACCTCAG 5460
 AAGTACATTC TCTGTCTTAC TGATACTGTA GGTTCAACCA TTTTCTTTA ATTTCTCTGC 5520
 AAATAACAAG ACCCAGAGAA GTGACTCTAG CTACTTAATG GTTCTGTCTT TTTATATGCA 5580
 30 GCAACACAC MEGYIGVDPE PLSSKQIKTI SGKTPOQYER EYNNKRSVG PSKFHGYAYD 5640
 GTGCACAAA CGCTTTAAAT TAGACTGGAA CTGCCAGAA CAAATGTAAA TGAGGAATTT 5700
 CTCGTACCCC TACTGCATGG TATCGATTTT TAATAAATG TTGCAAAATT GTTTTATGA 5760
 ATAAAGGAA AAAACCTGTC GTCTTT

Seq ID NO: 12 Protein sequence:
 Protein Accession #: EOS sequence

1 11 21 31 41 51
 MASPRSSGQP GPPPPPPPPP ARLLLLLLLL LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60
 40 LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPFYFLD LRLYDTECDN AKGLKAPYDA 120
 IKYGNHLMV FGVCPSVTS IIAESLQGNW LVQLSFAATT PVLADKKKYP YFFRTVPSDN 180
 AVNPAILKLL KHYQKRVGT LTQDVQRPSE VRNDLTGVLY GEDISIDTE SPSNDPCTSV 240
 45 KKLKGNLVRI ILGQFDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWV EQVHTEANSS 300
 RCLRNLLAA MEGYIGVDPE PLSSKQIKTI SGKTPOQYER EYNNKRSVG PSKFHGYAYD 360
 GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTGQVVFVRNG 420
 ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRPOG SEPPKDKTII LEQLRKISLP 480
 LYSILSALTI LGMIMASAPL FPNIKNRNQG LIKMSSPYMN NLIILGGLMS YASIFLPLGLD 540
 50 GSFVSEKTFE TLCTVTRTIL TVGYTTAFGA MFAKTWRVHA IFKNVKKKKK IIKDQKLLVI 600
 VGGMLLDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGI 660
 YAYKGLMLF GCFLAWETRN VSPALNDSK YIGMSVYVNG IMCIIGAAVS FLTRDQPNVQ 720
 FCIVALVIF CSTITLCLVP VPKLITLRTN PDAATQNRFF QPTONQKKED SKTSTSVTSV 780
 NQASTSRLEG LQSENHRLRM KITELDKOLE EVTMQLQDTP ERTTYIKQNH YQELNDILNL 840
 55 GNFTSTDDG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPLIH 900
 HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67-363

1 11 21 31 41 51
 GAGACATTC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
 AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTCTGAC TCTAAGTGGC 120
 65 ATTCAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 CGTGTGAGA TCATTGCTAT AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 70 TAAACCCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCTA CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTC TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 GGTAAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAA TATTCCCTC 660
 75 ACCTTTCCCA TCTTCAAGG GTACTAAGG ATCTTCTGCT TTTGGGTTT ATCAGAATTC 720
 TCAGAACTCT AAATAACTAA AAGGTATGCA ATCAAACTG CTTTAAAGG AATGCTCTTT 780
 ACTTCATGGA CTCTCACTGC CATCTCCCA AGGGGCCCAA ATCTTTCAG TGGCTACCTA 840
 CATACAATTC CAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
 CTTATTTAAT GAAAGACTGT ACAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960

TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAAATA AAAATGAGGT ACTCTCTGG AAATATTAAG

5 Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
 10 MNQTAILICC LIFLTLGSIQ GVPLSRTVRC TCISISNQPV NPSLEKLEI IPASQFCPRV 60
 EIIATMKKKG EKRLCLNPESK AIKNLLKAVS KEMSKRSP

15 Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 241..1272

1 11 21 31 41 51
 20 GCGCAGAGCG CCCAGCCCCC CACCGCCCCC AAAGGGGCGA GCGACGCCAA GCTCTGCGCT 60
 CTCTACAAAG AGGCGAGCT GCGCCTGAAG GGCAGCAGCA ACACCAAGCA GTGTGTTCCT 120
 GTGCCACCT CCGAGCAGT GGCAGAGATC GTGGGCGAGC AAGGCTGCAA GATTAAGGCC 180
 TTGAGGGCCA AGACCAACAC CTACATCAAG ACACCGGTGA GGGGCGAGGA ACCAGTGTTC 240
 ATGGTGACAG GGCAGCGGA GACGTGGCC ACAGCCCGGC GGGAAATCAT CTCAGCAGCG 300
 GAGCACTTCT CCATGATCCG TGCCCTCCGC AACAGTCAG GCGCCGCTT TGGTGTGGCT 360
 25 CCGCTCTGCG CGGCGCAGGT GACCATCCGT GTGCGGGTGC CCTACCGGT GGTGGGGCTG 420
 GTGGTGGGCC CCAAGGGGCG AACCATCAAG CGCATCCAGC AGCAAAACAA CACATACATT 480
 ATCACACCAA GCCGTGACCG CGACCCCGTG TTCGAGATCA CGGTGTCCCG AGGCAACGTG 540
 GAGCGTGGCG GCGAGGAGAT CGAGACGCAC ATCGCGGTGC GCACTGGCAA GATCTCGAG 600
 TACAACATG AAAACGACTT CTTGGCGGG AGCCCGGACG CAGCAATCGA TAGCCGCTAC 660
 30 TCCGACGCT GCGCGGTGCA CCAGCCCGCG TCGAAGCCCC TCTCCACCT CCGGCAGAAC 720
 AGCCTGGGCT GCATCGGCGA GTGCGGAGTG GACTCTGGCT TTGAGGCCCC ACCTCTGGGT 780
 GAGCAGGGCG GGGACTTTGG CTACGCGGGG TACCTCTTTC CGGCTATGG CGTGGGCAAG 840
 CAGGATGTGT ACTACGGCGT GGCAGAGACT AGCCCCCGCG TGTGGGCGGG CCAGGAGAAC 900
 35 GCCACGCCCA CTTCCGTGCT CTTCTCTCT GCCTCCTCT CTTCTCTCT TTCCGCCAAG 960
 GCGCGCGCTG GCGCGCGGG CGCACACCGC TCCCTTGCCA CTTCCGCGGG ACCCGAGCTG 1020
 GCGCGACTCC CGAGCGCGCC CCGCGGAGAG CCGCTCCAGG GCTTCTCTAA ACTTGGTGGG 1080
 GGCGGCTGCG GGAGCCCCCG CGCGGGCGCG GATTGCATGG TCTGCTTGA GAGCGAAGTG 1140
 ACTGCGCGCC TTGTGCGCTG CGACACAAAC CTGTTCTGCA TGGAGTGTGC AGTACGCATC 1200
 40 TCGGAGAGCA CGGACCCAGA GTGTCCCGTC TGCCACATCA CAGCCACGCA AGCCATCCGA 1260
 ATATTCTCT AGAGCCCGTG CCCCATGCCT CCGGGGCCCA CTCACCTGG CCCACCTGG 1320
 ACCTGTTTTC CACTAAAGCC TTTTGGAAAG CGGTGATTG AGGGGCAAGG TGCTTAGAGA 1380
 TACTCGCTCG CTGGGGAAGG GGGGAGGAG GCAGTGGTGG CTGGAGGGTG CGCCACTTTC 1440
 45 AGAGCCTCTG GTCAACCTGT CTTGGAAGA TTGGGAGGGG GCCAGACTGA AAATTTTACT 1500
 AGAGTTACAA CTCTGATACC TCAACACACC CTTAAATCTG GAAGCAGTGA AGAGAACTT 1560
 TGTGTTTGGC AGAGGTGGCC ACTAAGGCAT TCTGACGCCC TCTGCCACCC TCCCGCTG 1620
 TGTGTCACTC CACCCCTTCT TCGAGGAGG GGGTGGGTAA AAGGAGAGAG GAGAATTACC 1680
 ACCTGTATCT AGAGGTGCTC TTTGCAATCC CCCATATCTT GTTTGGGAAA CTGTACCCAG 1800
 50 CTAACATGAC CCTTTACCTC CCACCCACC CCAATATCTT GTTTGGGAAA CTGTACCCAG 1860
 TTTCCAGCAG TGTAAGGAGG TTGGAGTCTT ATCAGAAGTT GCATAGATCT TCTAGGGGTT 1920
 GGGGAGAGAA GCATGTCAAT CGTTTCTGTG GCTGAAAGGC TCGAAGCCCA TCTGTCCCA 1980
 CAAAGCTGGG CTAGAGGAAT CTGAGAGGGA GTCTCTCTCT CTGCCCCGT CCGCTGCAGT 2040
 GTTTCCTTTC ACTCTCTCG CTTATCTTCC CTTCTTTGG GATCTTCCCT TTCCTCACT 2100
 55 CTTTCTTTC CTTCTCTTTC TTTGCTTGG TGGCTGTGAC TCCAGCTCT 2160
 GTCTTGTTC TTGCTTTGT CTTTCTTCC TTTCCCTGCG CCGTGCCTCT ACCAGCCAG 2220
 CTTTGGGAC ACCATCCTTC TGGGAGAAAG TAGGGGAGG AATATTGGA TGGTCCCTCC 2280
 ATTCTCTTC AGGCATCTGG AGGCCCTCT CCCCCTCTT CCAAGAAAC ATCTCAAAT 2340
 ATTGATGGAA TGTATCCCCA TTCTCAGTGA AAATGTGAGG AGGGGACTAA TACTGGGGTA 2400
 60 AAGGGTCAAA CCCCCACCTT CATCACTATG GGCATTATAT TTAGGGAGTA GTTCTTGGG 2460
 TGGATTCTCT GGTGTGGAAG GTGGGGGCGC CAGAGTAGTG TGTCTGTAT TTAAGGAGC 2520
 AGGAAAGGCG GTGAGGCGAG AGGAGAGACT GGTGGAGGGA AGAGCTGCTC CTCCATGCA 2580
 GTGCCCGACT CCGTGCACCC CTCTCAACCT GACCTGAACC TTTATTGAAT CCTTATTAGC 2640
 TTGAATCCTT ATTAGCTTGA ATCTCTCATG CAAATCATGG AGTCTGTGTC CCACCTGATG 2700
 TGGTTGAGGA GAAGCCAGGT CTTCAAAGAG GGTTCAGCTT GGGGCAAGC AGGACTGGG 2760
 65 GGAGGTGGG AGCAGGGGCT ATTCTGAGAA TCACATATTT TTACAGGCCT TGCACCCCT 2820
 TTGCTGCTTC CTTCTGCTC ATTTGGGGCT GCCACCACT CTTCCACCTC CTGGTTCCG 2880
 TGGCCGGGCC AAGAGAGGAT GGAGGGATGG GAGTCCCAGG AGATCCTTGT AAATAGTGG 2940
 GTGGGACTGT TCTGAGTAT CACCCGAGCA CTTAAAGCT CAGAGTCCCA TTCTTCTGG 3000
 70 ATGGAGCAGG TGGAGGTGCA GAGGGGATTT CCTCTCTCC TTTCTCTCT CGAGAATTAA 3060
 CACCTCTCCA CAGCCTTCCC CTCCAGAAAC CCAGCCAGGG AGGGGTGGGG AAGGAGGTCA 3120
 CAGCAAGAA AACTGGCCTG TGAAGACTTC CCTCTTCCC GCCTATGTGA GGCATCTGA 3180
 GATGTCTGTA CAATAGAAAC CAAACCAAT GGGCACCCCT GGTGGCCGG GGGCAGGTGG 3240
 GGAGGGGGGT GGGAGAAAGG GATGTCTGTC TGTCTTCCC CTCCCTCTC CCACCTTTA 3300
 75 CCCAAGAGG CAGAAGACTG TTACACTAGG GGGCTCAGCA AATTCAATCC CACCTTACC 3360
 AATTGAGCCA AACTAGAAAC CAAACACAAA ACACGAATAG TGAGAGACAA AATAGAGGAG 3420
 AGAAGAGAG CATGAGAGGG AGCAGTCTTT TATAATTAA TATTCTATT TAATAAGGC 3480
 TAGCAAAAAA AAAAAAAGG AGCAGTCTTT TATAATTAA TATTCTATT TAATAAGGC 3540
 GTTATTATCC ATATAATGT AGCAAGAAC CTGGGCTAAT ATGAAAAAA AAGACTTTTT 3600
 ATTAGGTAAT TTATTATATG AAAAGGATAT TTTATTTTAT GATAAAGTGA TCCTTAAAAA

5
10
15
20
25
30
35
40

AATAAAAAA CTTTGAAGG TTTAGAATAT ATGTAGGGAG AGAAGAAGAA AAAAATACAT 3660
TTGTATTACAG AGTTAAATCT TAAAAAATAA AAGTGTITTT AATATATGTT TGGGTTTACG 3720
TTGCTTTTTT CCCCCACTTT TTTTITGGGG AGGAATGTCA TTTGCTTTTC TTTGGGGAGC 3780
ATCCCGGGGG TGAATGGTGG AGAGAGGAGC TGGGGGAACC CGGTCCCTCC TGGGACCCCT 3840
CCAGTAGATT GGATTTCACT CCATGGACTC CTCCTCCCTC CTCCCTCCCT CCCCAGGGG 3900
AGCCGCGAGA GCCAAACAAA GAAAGGGATT AACAAGAAAG GAAGAAGCTG TAGGACTAAG 3960
GACTAGGAT CCTGGGGTGT CCCCACCCAC TTTCCCTGCG CCTGTCGAG GGGCAAGTGA 4020
GGAGGGGGA TCCAGAAATTA AGGCCTAGCA GGCCTATAGG AACCTCAGA GATGTGTGAG 4080
ATTAAAGAGA TCTAGATTTT TTTTAAACCA AAAACAAGAG AGAAAGAGAA GAAAAAGAGA 4140
AACCGAGGGG TTTAAAGAA AAGAATACTA CAAAAATAA ATTATTAATA ATAATAATTC 4200
AAATTTAATT CATATAATCC TAGAGAGAGA AAGAAACAAT TACTAGTTAC TAGTAGACA 4260
ATATTAAGAT AGCTTAAAGT TTAGTAGCAT TGAGGGCCCC TGGGTCCAGT AGAATGTATA 4320
AAAGTTGTAA GGAAAGATA AATAGAGGAG GGAAGTGGCT GAGTCCACCC TGAGTTGCC 4380
AATCTTCAGA TACCAGGGT GGATCAGGTT GCTAGTTTAA GATTGGGAGC TTCCAGTCTG 4440
CTGGGGTTGA TTCTGAGAAT CCTTGGATT TTAATTTGTA GGACAAAGAA ATGAGGGGTT 4500
CATTTCCAGG GGTCTTGGAA AGGATGCACA CTGATCATCT CAATAAGACA GGGGCTGGGT 4560
TGGGGCGAG AGAGGAGGCC AAGCACATTC ACCTGCACCC CTAGTACCTG GGCAGCCCAT 4620
ACTCCAATGT GGTATGTCCC CTCCTGGGGC TCCAGCTCA AACCTCCCA TGCTGTCTC 4680
CCCCAGGCT AACTGAGGAA GTCCTTCTTG AAGTGTGACC TCGGTCCACT TCTCTACAGA 4740
TTGATTTAAG AGCCTGGGAA GTCATTCCAC AAACAGACAC ACATGCACAC ACGCTTCTCA 4800
CCTTCAGAGC TTCAAGAGCA CTGAGGCGAT CAGTCCCCTA CCCCCTGTCC CATCCAGCTT 4860
TCCACTTAGC TTTGACCTCC ATGGCAGCAG TAGCAGTAAC AATCTCAGTA ATTGTTCTTT 4920
AAAGCTGACT CGTTCCTCAC CTACTTGCAA AGTGTCTTCT TGTCTCTATA AAGTTAGATT 4980
CCAAGAAGGA CTTCACCGG AGTGGAGTGG AAACACTGTC CTTGAAGGCC TGGAGAAAG 5040
GCATCCCCAT GGGCACAGAG GCTGGGGAAG GGACAGGGA CTTTGGGTGA CCTAACCCCT 5100
GACCTCTGCG TCCAGTTTAC CTCATCTAT ATGTGTTTCA GTAGGGGTCA TCTACTGTAC 5160
CCTGGGCTGG GAACACATTC CCCCCTCCAC ACAAAAGTGG AGGGCTTGGC TTCTGCGTGT 5220
GAGAAATCAA CATTTTTTAA GCACTTGCCCT TCTACCAACC CCAGCTTGCA ATCACTGGGC 5280
CTTCCCCTCC TATCCAAGGG GTTGGAGGGG CCCCTTGCT CTCTTTTGG CAGGAGGAGC 5340
CTGCTTCATT ACACCAATGA CTCTGCCATC CCCCCTCCCTG GGCCTAGACC CCAACACAT 5400
CTCCCTCTAC CCAATTTACT CTCTCGCCC CACCTAGGGA CAGATTCCCC CTGCTCTTTT 5460
TGCTCTAGAA ACCCCGCTAG TTTGGGATGG TAGCGTCTGG GGTGGGAGG GCTTCCCCTT 5520
CCCCACTCGA GGGTGGGGT GGGGAAGGG GGTGGGTGG AGACAGCCCT GGGGAGGGA 5580
GGATGGTCTC TCCACTGTAG AAGTAGAGT AGGATTGTGG TCAGACTTAA TTTGAGGCAT 5640
CTAGTGAAGA CACGTACAAA TCCACCAAGG AAAAAAGATT CAAAGCAAA ATAAAAGCGG 5700
GAAATAAAC AGACCCAGA ATAATCAAGT CAAAGTGATG TTGCACAAA TGACAGAGAA 5760
CCAAGAAGGG GGAGGGTTAA TGTATTAAT GTGCTATTAA GAACTTAATT TTATTAAGG 5820
TACTATTACT TAAGGCTC

Seq ID NO: 16 Protein Sequence
Protein Accession #: XP_044166

45
50

1 11 21 31 41 51
| | | | | |
MVTGRREDVA TARREIISAA EHFSMIRASR NKSGAAGFVA PALPGQVTR VRVPIRVVGL 60
VVGPRGATIK RIQQQNTYI ITPSRDRDPV FEITGAPGNV ERAREEIEHT IAVRTGKILE 120
YNNENDFLAG SPDAAIDSRV SDAWRVHQPG CKPLSTFRQN SLGCIPEGCV DSGFEAPRLG 180
EQGDFGYGG YLFPYGVGK QDVYVGAET SPPLWAGQEN ATPTSVLFPSS ASSSSSSSAK 240
ARAGPPGAHR SPATSAGPEL AGLPRRPGE PLQGFSLGG GGLRSPGGGR DCMVCFESEV 300
TAALVPCGHN LFCMECAVRI CERTDPECFV CHITATQAIR IFS 343

55

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23-1489

60
65
70
75

1 11 21 31 41 51
| | | | | |
AAGCCAGCA GCCCGGGGCG GATGGCTCC GCGCGCTGG CTCGCGAGCG CGGCCGGGCG 60
CGCCCTCCTG CCCCAGATGC TGCTGCTGCT GCTCCAGCCG CCGCGCTGCG TGGCCCGGGC 120
TCTGCGCGCG GAGTCCACCC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACCGAG GAAGCCCCCG GGCCTGCCAG 240
CAGCCTCAGG CTTCCCGCTG GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCGCCAA 300
CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
GATCCTTCGG TTCCCATGCG AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC 480
TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGAC GACCTGCGGT TTGATGGGCC 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACACGGGC ACAGACCTGC TGCAGGTGGC 660
AGCCCATGAA TTTGGCCAGC TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
TCAACACCTA TATGGCCAGC CCTGGCCAC TGTCACTCC AGGACCCCGC CCCTGGGCCC 840
CCAGGCTGGG ATGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900
CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TTTTCAAAGC 960
GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC 1020
TGGGCACTGG CAGGAGCTGC CCAGCCCTGT GGAAGCTGCC TTCGAGGATG CCGAGGGGCA 1080
CATTGTGTTT TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTGGG 1140

5 CCCCCCACC CTCACCGAGC TGGGCCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCCC 1260
 CAGCACCCGG CGGTAGACAC GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCGCGGCCG 1380
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440
 GGGTCTCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAAACACT TTCCTCTGAC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTCTGAC CCTGTCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGCTCTCTGC AGGGGGATGG 1620
 10 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCTGT GTCACCTGCC 1680
 AGCGACTGTG TCAGACTGGG CAGGGAGGCT TTGCGATGAC TTAAGAGGAA GGGCAGTCTT 1740
 GGGACCCGCT ATCAGGTGCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCTCAGG 1800
 GTAGACCAT GGCAGGACTG GGGGAACTGG AGTGTCTTGG CTGTATCCCT GTTGTGAGGT 1860
 TCCTCCAGG GGCCTGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCT CAGCCCTGGC 1920
 TGAGCAACTG GGCCTGAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
 15 ATCTGTCTGC CTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
 GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCCTGAA GCCCTTTTTC CAGCACTGCT 2160
 ATCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 20 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT

Seq ID NO: 18 Protein sequence:
 Protein Accession #: NP_005931.1

25 1 11 21 31 41 51
 MAPAAWLRS AARALLPPL LLLQLPPPL ARALPPDVH LHAERRGPQ WHAALPSSPA 60
 PAPATQEA PR PASSLRPPRC GVPDPDGLS ARNRQKRFVL SGRWEKTDL TYRILRFPWQ 120
 LVQEQVQRTM AEALKVHSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DPGGILAHA 180
 FFPKTHREGD VHFDDYDETWT IGDDQGTDL QVAHEPHGV LGLQHTTAAK ALMSAFYTFR 240
 30 YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAPEDA QGHINFPQGA 360
 QWVYDGEKF VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420
 FVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFPD VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL

Seq ID NO: 19 DNA sequence
 Nucleic Acid Accession #: NM_005794.1
 Coding sequence: 434-1276

40 1 11 21 31 41 51
 GGTTCCTTC CACGCTGTGA AGCTTTGTTC TTTTGGTCTT CATGATAAAT CTTGCTGCTG 60
 CTCACCTCGT GGGTCCGTGC CACCTTTAAG AGCTGTAAAC CTCACCGCGA AGTCTGCAA 120
 45 CTTCACTCCT GGGGCCAGCA AGACCACGAA TGCACCGAGA GGAATGAACA ACTCTGACA 180
 CACCATCTTT AAGAACCGTA ATACTCACCG CAAGGCTCTG CAACCTCATT CTTGAAGTCA 240
 GTGAGGCCAA GAACCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTACCC 300
 TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360
 CACCAAGCGG TGAGACTATC ACCTATCGCC AAGTGGCCTG ATTGAGCAGG AAGCATCTCA 420
 GACACCAACC ACTATGCTGT CAGCAGTTGC CCGGGGCTAC CAGGCTGGT TTCTCCCTG 480
 50 TGCTAGGCTT TCTGTGAGGA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA 540
 CCGGTGAGCC GTGGTCAGCG GGTCCACCAAG TGGGATCGGC TTTGCCATGG CCCGACGTCT 600
 GCGCCCGGAC GGGGCCACG TGGTCATCAG CAGCCGGAAG CAGCAGAACG TGGACCGGCG 660
 CATGGCCAA GTCAGGGGG AGGGGCTGAG TGTGGCGGGC ATTGTGTGCC ACGTGGGGAA 720
 GCGCTGAGGAC CGGGAGCAGC TGGTGGCCAA GGCCTGGAG CACTGTGGGG GCGTGGACTT 780
 55 CCGTGGTGTG AGCGCAGGGG TCAACCTCT GGTAGGGAGC ACTCTGGGGA CCGATGAGCA 840
 GATCTGGGAC AAGATCCTAA GTGTGAACGT GAAGTCCCA GCCCTGCTCT TGAGCCAGTT 900
 GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTATCCTG GTCTCTTCCA TTGACGTTA 960
 TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTACGCAAG ACAGCGCTCG TGGTCTCAC 1020
 TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCCG GTAAACTGCG TGGTCCAGG 1080
 60 AATTATAAAA ACTGACTTCA GCAAAGTGTT TCATGGGAAT GAGTCTCTCT GGAAGAACTT 1140
 CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGCGG GAATCGTGTG 1200
 CTTCTGTGTC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA 1260
 CTCACCTCGG CTCTGAGAGG AGTGGGGGGC GCTGCGTAGC TGTGGTCCA GCCCAGGAGC 1320
 CTGAGGGGGT GTCTAGGTGA TCATTTGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT 1380
 65 AGCAATTTGG GGGCTTACTC ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGGCATTCT 1440
 CC

Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_005785.1

70 1 11 21 31 41 51
 MLASAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLRDQ 60
 AHVVISRRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGVDPLVCS 120
 75 AGVNPVVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM ENRRGAVILV SSIAAYNPVV 180
 ALGVYVNSKT ALLGLRTRTLA LELAPKDIRV NCVVPGIIKT DPSKVPHGNE SLWKNFKEHH 240
 QLQRIGESED CAGIVSPLCS PDASYVNGEN IAVAGYSTR

5	1	11	21	31	41	51	
	GC	GC	CAG	CT	CT	AG	60
	AT	GT	GC	CT	CAG	CT	120
10	GG	GT	AC	CA	GC	AG	180
	CA	AAT	TT	AC	TC	GT	240
	GT	TC	GT	TA	CT	TT	300
	AAT	GT	AT	TG	GC	TT	360
	TG	TG	TG	GC	TT	GC	420
15	AA	CG	GG	CA	GT	TC	480
	TA	TC	TA	CA	TC	TA	540
	AG	AC	TC	GC	TG	TG	600
	TAT	CT	GC	AA	GC	CA	660
	CC	TG	CT	CA	TC	GC	720
20	CA	TG	TG	CT	TC	TC	780
	CT	TG	CT	CA	TC	TC	840
	CT	TC	CT	CA	TC	TC	900
	CT	TC	CT	CA	TC	TC	960
25	TG	TC	TC	TC	TC	TC	1020
	CT	TC	TC	TC	TC	TC	1080
	CT	TC	TC	TC	TC	TC	1140
	CT	TC	TC	TC	TC	TC	1200
	AG	TC	TC	TC	TC	TC	1260
	TG	TC	TC	TC	TC	TC	1320
30	AA	TC	TC	TC	TC	TC	1380
	CT	TC	TC	TC	TC	TC	1440
	TA	TC	TC	TC	TC	TC	1500
	CT	TC	TC	TC	TC	TC	1560
	TG	TC	TC	TC	TC	TC	1620
35	GA	TC	TC	TC	TC	TC	1680
	TA	TC	TC	TC	TC	TC	1740
	GAG	TC	TC	TC	TC	TC	1800
	GAG	TC	TC	TC	TC	TC	1860
	AC	TC	TC	TC	TC	TC	1920
40	CT	TC	TC	TC	TC	TC	1980
	GAG	TC	TC	TC	TC	TC	2040
	GT	TC	TC	TC	TC	TC	2100
	AT	TC	TC	TC	TC	TC	2160
	CA	TC	TC	TC	TC	TC	2220
45	CA	TC	TC	TC	TC	TC	2280
	AAT	TC	TC	TC	TC	TC	2340
	TC	TC	TC	TC	TC	TC	2400
	AC	TC	TC	TC	TC	TC	2460
	AG	TC	TC	TC	TC	TC	2520
50	AG	TC	TC	TC	TC	TC	2580
	AG	TC	TC	TC	TC	TC	2640
	GT	TC	TC	TC	TC	TC	2700
	GT	TC	TC	TC	TC	TC	2760
	TA	TC	TC	TC	TC	TC	2820
55	TA	TC	TC	TC	TC	TC	2880
	AT	TC	TC	TC	TC	TC	2940
	AT	TC	TC	TC	TC	TC	3000
	CT	TC	TC	TC	TC	TC	3060
	CT	TC	TC	TC	TC	TC	3120
60	CT	TC	TC	TC	TC	TC	3180
	GT	TC	TC	TC	TC	TC	3240
	TG	TC	TC	TC	TC	TC	3300
	TA	TC	TC	TC	TC	TC	3360
	TA	TC	TC	TC	TC	TC	3420
65	TA	TC	TC	TC	TC	TC	3480
	AG	TC	TC	TC	TC	TC	3540
	TT	TC	TC	TC	TC	TC	3600
	AG	TC	TC	TC	TC	TC	3660
	AAT	TC	TC	TC	TC	TC	3720
70	TT	TC	TC	TC	TC	TC	3780
	AA	TC	TC	TC	TC	TC	3840
	AG	TC	TC	TC	TC	TC	3900
	TA	TC	TC	TC	TC	TC	3960
	TA	TC	TC	TC	TC	TC	4020
75	AC	TC	TC	TC	TC	TC	4080
	TG	TC	TC	TC	TC	TC	4140
	TC	TC	TC	TC	TC	TC	4200

Seq ID NO: 22 Protein sequence:
Protein Accession #: E0S sequence

```

5  1      11      21      31      41      51
   |      |      |      |      |      |
MGAPHWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF   60
NSGIYLIWTL LVVVGIGSVY FHATLSFLGQ MDELAVLWV LMCALAMWPP RRYLPKIFRN   120
DRGRPKVWVS VLSAVTTCLA FVKPAINNIS LMTLGVFCTA LLIAELKRCO NMRVFKLGLF   180
SGLWTLALF CWISDRAFCE LLSSFNFPYL HCMWHILICL AAYLGCVCTA YFDAASEIPE   240
10 QGPVIKFWPN EKWAFIGVPY VSLLCANKKS SVKIT

```

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: CAT cluster

```

15  1      11      21      31      41      51
   |      |      |      |      |      |
TGAAGTATCT CTGTTTAATG TCATATATCT GAGATGTTCT GTGGAGCCAG AATTCAAAAC   60
CCAGATACCC AGGAGGACAC ATCTCTGATC GGTATTTTAT TCTATTATT TTATTAGTTC   120
CAATCCTTAT GACTCTGTTT AAAATGAGTA TCTGCATTAT TGTGCAACA CTCTGAGAT   180
CTCATCACAT ACCTGATCCC ATTTAACTTC AGTCTATCCC TCCATTACTT TTTGTGGAAA   240
GTGCTATCTA AGTTGGAGGT TCTGCTTGAG TATTCTTAAT TTTTCTTCTT TTTAATGCAT   300
ACGGTGGTCA AAGTAAATAG CTAACATATT GGCATCAAAC CATTGCCTAT TGAAGCAAGC   360
TTTGAATGAA ATTGGTTTGT CATTGACCAC TGTAAAGAAC TCATTGTGTA AGATAATACT   420
GAAAAACATC CTGACTCTTA TGTATGCTTG CCTGTCTCTG AACTCCACT CTATCAGCAT   480
ACTCAATACA TTGCCTCTTT CCAACATTTA TCTCCTATTT CAGGAGAAAG TTTTGTGGGA   540
CGCTCTACCA CGTTGCAAGG ATTCAACATT TCTCTTAAAA ATAGAGGTTT CTTTGTAGATA   600
TAAGCAATGA AATTTCAGC AACAATATTA CTCTCTCAT GTCCCTTGCT TTTTAAAGAT   660
CTGAACCTCA AGATTCAAAT GGATTTTCAT TGAATTCAC CACGATCCCC TCTGCAGCTG   720
TGGTCTGAAA GTACCATTTT TGCATTTATT TTAGCCCATG GAATACTGT GCTGAGAAAC   780
CACAGAGTCA ATCAGATTCA AAATGTTAAA ATCCTTCCTG CTTGAGGTTT TCCGCTTCA   840
CATCAAGCA TTTTCATGCC GTACGCAACT TTTTAATGCA TTTGCTCATG GTTTGCAGAA   900
TTTCATTTA AAGACTTTC TTGGCTGACT TCTCTGATGA GGTTCCTGC TTGCCTC

```

Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: E0S sequence

```

35  1      11      21      31      41      51
   |      |      |      |      |      |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGGACG CTGTCCAAGG   60
AGTAGGCTCA GTAGCAGCAA CTGCAAAATAC TTGAGAAGGG AAAAGTTCAG CCTTGTGCTG   120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA   180
ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAA TGGTGCTAAT AATAGCACCC   240
ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC   300
CTGTTCCTGG TAAGTCTCTG GAAAGAAGTC TATGGATTAT ACTCAACCTA CACTCCAGTT   360
AAAGGAACAT CTACACACAG AGGAAATGAA TAACATGAAG TGAAGTCTTC ATCTCCATTG   420
CCAACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAATATCAG TTTATTTTCC   480
CCTGCTGCAA AGAACAGTCG TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG   540
GTCTCTCGGA AAAGGAGCGT GAAGCCCCCT TTGTAATTTT TGCATTAGCG TGCTCTCCTG   600
GCAAGCAGGA AACCTCATCA GAGAAGTCAG CCAAGGAAAG TCTTTAAATG GAAATTGTGC   660
AAACGAGGAG CAAATGCATT AAAAAAGTTG TGACGGGCAT GAAATGCTTT GATGTGAAGA   720
CGGAAACTC CRAAGCAGGA GGATTTTAACT ATTTTGAATC TGATTGACTC TGTGGTTTCT   780
CAGCACAGTT ATTCCATGGG CTAAAATAAA TGCAGAAATG GTACTTTTCA ACCACAGCTG   840
CAGAGGGGAT CGTGGTGAAT TTCAATGAAA ATCCATTGTA ATCTTGAGGT TCAGATCTTA   900
AAAAAGCAAA GGACATGAGA GAAGTAATAT TGTGTCTTGA AATTTCATTG CTTATATCTA   960
AAAGAACTC CTATTTTAA GAGAAATGTT GAATCTTTGC AACGTGGTAG ACCTGCCAC   1020
AAACTTTCT CTTGAAATAG GAGATAAATG TTGGAAGAG GCAATGTATT GAGTATGCTG   1080
ATAGAGGTGG AGTTCAGAGA CAGGCAAGCA TACATAAGAG TCAGGATGTT TTTCACTATT   1140
ATCTTTACAA ATGAGTTTCT TACAGTGGTC AATGACAAAC CAATTTCAAT CAAAGCTTGC   1200
TTCAATAGGC AATGGTTTGA TGCCAATATG TTAGCTATT ACTTTGACCA CGGTATGCAT   1260
TAAAAAGAG AAAAATTAA GATACTCAAG CAGAACCTCC AACTTAGATA GCACTTTCCA   1320
CAAAAAGTAA TGGAGGGATG GACTGAAGTT AAATGGGATC AGGTATGTGA TGAGATCTCA   1380
GAAGTGTGTT CACAATAATG CAGATACTCA TTTTAAACAG AGTCATAAGG ATTGGAACCTA   1440
ATAAAATAA TAGAATAAAA TACCGATCAA GAATGTGTCC TCCTGGTAT CTGGGTTTGT   1500
AATTCTGGCT CCACAGAACT TGTGAGATAT ATGACATTAA AC

```

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: E0S sequence

```

70  1      11      21      31      41      51
   |      |      |      |      |      |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGGACG CTGTCCAAGG   60
AGTAGGCTCA GTAGCAGCAA CTGCAAAATAC TTGAGAAGGG AAAAGTTCAG CCTTGTGCTG   120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA   180
ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAA TGGTGCTAAT AATAGCACCC   240
ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC   300
CTGTTCCTGG TAAGGAAATG AATAACATGA AGTGAAGTCT TCATCTCCAT TCCCAACAGT   360
CCCCATTCTA CTTGCAGAAA GGTGCTTAC ACTGAAATC AGTTTATTTT CCCTGCTGTC   420
AAAGAACAGT CGTTTCTCCA AAAGTGAAGC TGGAAATAT CTGAATATC AGGTCTCTCC   480

```

5 GAAAAGGGAC GTGAAGCCCC CTTTGTAAAT TCTGCATTAG CGTGCTCTCC TGGCAAGCAG 540
 GAAACCTCAT CAGAGAAGTC AGCCAAGGAA AGTCTTTAAA TGGAAATTGT GCAAAOCAGG 600
 AGCAAATGCA TTAAGAAAGT GCTGACGGGC ATGAAATGCT TTGATGTGAA GACGGAAAAAC 660
 TCCAAGCAGG AAGGATTTTA ACATTTTGAA TCTGATTGAC TCTGTGGTTT CTCAGCACAG 720
 TTATTCCATG GGCTAAAAATA AATGCAGAAA TGGTACTTTC AGACCACAGC TGCAGAGGGG 780
 ATCGTGGTGA ATTTCAATGA AAATCCATTT GAATCTTGAG GTTCAGATCT TAAAAAGCA 840
 AAGGACATGA GAGAAGTAAT ATTGTGCTT GAAATTTCAT TGCTTATATC TAAAAAGAAC 900
 TCCTATTTTT AAGAGAAATG TTGAATCTTT GCAACGTGGT AGACGCTCCC AAAAACTTT 960
 CTCCTGAAAT AGGAGATAAA TGTGGGAAAG AGGCAATGTA TTGAGTATGC TGATAGAGGT 1020
 GGAGTTCAGA GACAGGCAAG CATACTAAG AGTCAGGATG TTTTTCAGTA TTATCTTTAC 1080
 AAATGAGTTT CTTACAGTGG TCAATGACAA ACCAATTTC TCAAAAGCTT GCTTCAATAG 1140
 GCAATGGTTT GATGCCAATA TGTAGCTAT TTACTTTGAC CACCGTATGC ATTAAAAAGA 1200
 AGAAAAATTA AGAATACTCA AGCAGAACCT CCAACTTAGA TAGCACTTTC CACAAAAAGT 1260
 AATGGAGGGA TAGACTGAAG TTAATGGGA TCAGGTATGT GATGAGATCT CAGAAAGTGT 1320
 15 TGCACATAAA TGCAGATACT CATTTTAAAC AGAGTCATAA GGATTTGGAAC TAATAAAAAAT 1380
 AATAGATAAA AATACCGATC AAGAAATGTG CTCTCTGCGT ATCTGGGTTT TGAATTCTGG 1440
 CTCCACAGAA CTGTGCAGAT ATATGACATT AAAC

20 Seq ID NO: 26 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

25 1 11 21 31 41 51
 CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60
 GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTT GACCATGGA CGGGAGGCAG 120
 ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC 180
 CAGGAGCTGT TCCAGTGGGA GCCAGGCCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
 30 GAGGAGCGCC ATACCTCTTT CGACTACGAG GTCCGCTGTA ATGACACCAT CCAGCTCCTG 300
 GTCCGCGAGA GCCTCGTGTG CCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC 360
 ACCGACTCCG GCTGCTGCT GGGCCAGAGT GAGTCAGACA AGTCTCCAC CCACGGCGAG 420
 GCGGCCCGCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480
 GGGCTGTACA AGGTCAATGA GTACGTGAT GCTCGGGACA CGAATCATGG GCGTGGTTT 540
 GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCTCTCCC GGGACGAGCC CTGCACTCC 600
 35 ACGTCCAGGC CCGCGCTGGA GGAGGACGTC ATTTACCACG TGAATACGA CGACTACCG 660
 GAGAACGGGG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CCGCGCGCCG CACCATCATC 720
 AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780
 AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGGG 840
 CGGGAACTCT ACGCAACGCT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC 900
 40 TTGCTGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCCAT GGTGACAAC 960
 CCCATGAGAC GGAAGAGCGG GCGCTCTGCG AAGCACTGCA AGGACGAGT GAACAGACTC 1020
 TGCCGGGTCT GCGCTGCGCA CTGTGCGGG GGCCTGAGG ACCCGACAA GCAGCTCATG 1080
 TGCGATGAGT GGCACATGCG CTTCCACATC TACTGCTGG ACCCGCCCT CAGCAGTGT 1140
 45 CCCAGCGAGG ACGAGTGGTA CTGCCCTGAG TGCCGGAATG ATGCCAGCA GGTGGTACTG 1200
 GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCTCTGG CACATCGTCC 1260
 TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC 1320
 GTCCCGTCCA ACCATACGG ACCCATCCCG GGGATCCCG TGGGCACCAT GTGGCGTTT 1380
 CGAGTCCAGG TCAGCGAGTC GGGTGTCCAT CGGCCCCAG TGGTGGCAT ACACGGCGGG 1440
 50 AGCAACGACG GAGCGTACTC CTTAGTCTGT GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
 GGGAAATTTT TCACATACAC GGGTAGTGGT GTTCGAGATC TTTCCGGCAA CAAGAGGACC 1560
 GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTCG 1620
 TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG 1680
 GTCAGGGTGG TCGCAATGT CAAGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
 AACCGCTACG ATGGCATCTA CAAGGTGTGT AAATACTGGC CCGAGAAGGG GAAGTCCGGG 1800
 55 TTTCTCGTGT GCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
 GAGGGGAAGG ACCGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920
 GAAGCCCTGG CCAACGAGA GCGAGAGAAG GAGAACAGCA AGAGGGAGGA GGAGGAGCAG 1980
 CAGGAGGGGG GCTTCGCTG CCCCAGGACG GGCAGGGGCA AGTGAAGCG GAAGTCGGCA 2040
 60 GGAGGTGGCC CGAGCAGGGC CGGGTCCCCG CGCCGACAT CCAAGAAAAC CAAGTGGAG 2100
 CCTACAGTCT TCACGCCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG 2160
 CTGTGGAATG AGGTCTGGC GTCACTCAAG GACCGGCCG CGAGCGGCAG CCCGTCCAG 2220
 TTGTTCTGTA GTAAAGTGA GGAGACGTTT CAGTGTATCT GCTGTGAGGA GCTGGTGTTC 2280
 CGGCCCATCA CGCCGTGTG CAGCACAAC GTGTGCAAGG ACTGCTGGA CAGATCCTTT 2340
 65 CCGGCACAGG TGTTCAGCTG CCTGCTGCTG CGCTACGACC TGGGCGCGAG CTATGCCATG 2400
 CAGGTGAACC AGCTCTGCA GACCGTCTCT TTTTGTGAA AACGTGTGG AGGGCTCGTT 2460
 CGGTGATCTC CAAGCACTT TCGACAGGCG TTTTGTGAA AACGTGTGG AGGGCTCGTT 2520
 CATCGGCACT GATTTGTGTT TTAGTGGGCT TAACCTAAAC AGGTAGTGT TCCTCGGTT 2580
 CCTAAAAAGG TTTGTCTTCC TTTTTFTTTA TTTTATTTT TCAATCTAT ACATTTTCAG 2640
 70 GAATTTATGT ATTCTGGCTA AAGTTGGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAA 2700
 CATAAAGGCC TGCAATTTCT GCACAAAAACA ACACAAGATT TTTTAAAGAT GGAATCAGAA 2760
 ACTACGTGCT GTGGAGGCTG TTGATGTTTC TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC 2820
 CAACCTTTTA AGAAGGCGAC AGGATCAGTC CTTCTTAGG GTTCTGGCCC CCAAGGTCAG 2880
 TGGCCCGTGG CAGCCGTGG CATGGCGTGG CTCAGCTGTC TGTGAAGTT GTTGAAGGA 2940
 75 AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTTGCTTC AAAGCCATCC CCCACAGAC 3000
 TGCTTAGCGT CTGAGATCCG CGTGAAAAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC 3060
 CACGCGAGAA TGGCCTCAAG GGGACTCTGC TCCAGTGGG GCCAGGCGTG TGAATGACGC 3120
 TGTCCGACGA AGGGGGCCAC GGACGAGCAG CAGCACAGCA AGTCACGTGC AAGTGCCTTT 3180

5
10
GATTGCTGCC TTCTTCTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAA 3300
GTCAACCAGA TTCTAGAAAC TGCGGTCAAT CAGTCTCTCC TGACACCGGA TGGGTGCTTG 3360
GGAACCGTT GAGCCTTATA GATCATTTAC ATTCAATTT TTTAACTCAG CAAGTGAGAA 3420
CTTACAAGAG GGTTTTITTT TAATTTTTTT TTCTCTAAT GAACACATTT TCTAAATGAA 3480
TTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TGGTGTGTT 3540
TTGTTTTGT ATTTTTTTC TTTTGAAGG GTTTGTAAAT TTTTCTAAT TTACCAAAGT 3600
TTGCAGCCTA TACCTCAATA AAACAGGGAT ATTTTAAAT ACATACCTGC AGACAACTG 3660
GAGCAATGTT ATTTTAAAG GGTTTTTTC ACCTCCTAT TCTTAGATTA TTAATGTATT 3720
AGGGAAGAA GAGACAATT TGTGTAGGCT TTTCTAAAG TCCAGTACT TGTCCAGATT 3780
TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAA AAAAAAA 3828

Seq ID NO: 27 Protein Sequence
Protein Accession #: NP_037414.2

15
20
25
30
1 11 21 31 41 51
MWIQVRTMDG RQHTVDSLS RLTKVEELRR KIQLFHVPE GLQLRFYRGK QMEDGHTLFD 60
YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAEITDSR 120
PAEDMWDTE ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMLNYPND NPKBRGFWDY 240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGESEPMV DNPMRKSGP 300
SCKHCKDDVN RLCRVACACH CGRQDPDXQ LMCDECDMAF HIYCLDPPLS SVPSSEDEWYC 360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQDWDGK MACVGRTEKC TIVPSNHYGP 420
IPGIPVGTMW RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFFTYTG 480
SGGRDLSGNK RTABEQSCDQK LNTNRLALAL NCFAPINDQE GAEAKDWRSG KPRVVRNVK 540
GGNRSKYAPA EGNRYDGIYK VVKYWPKEGK SGFLVWRYLL RRDDDEPGPW TKEGDKRIKK 600
LGLTMQYPEG YLEALANRER EKENSKEEB EQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
TFQCICQDEL VFRPITTVCC HNVCKDCLDR SFRAQVFSCP ACRYDLGRSY AMQVNQPLQT 780
VLNQLFFGYG NGR

Seq ID NO: 28 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence:186..776

35
40
45
50
55
60
1 11 21 31 41 51
AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
TCTCTGAGAG GAGGCGGCGC CACCCGCGCT ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC 180
CTAACATGCG GCTGCGCGTG CTTGTGTCCG CGGAGTCTCT GCTGGTGGCT CTCTGCCCC 240
GCCCCGCAAT CAGGCGCGCT CTGAGCGCGG GCGCGGTCCC GGGAGCTCGG CAGGCGCGCG 300
AGCACCTTCA GCCCTTGGAT TTCTCCAGC CGCGCGCGCA GTCCGAGCAG CCCAGCAGC 360
CGCAGGCTCG GCCGCTCTG CTCCGCGATG GAGAGGAGTA CTCTCTCCGC CTGGGGAACC 420
TCAACAAGAG CCGGCGCGCT CCCCTTTCGC CGGCTCTCTC GCTCTCTCGC GGAGGCGAGC 480
GCAGCGCGCC TTGCGCGGAA CAGGCGAGCG CCAACTTTT CCGCGTGTTC CTGCAGCAGC 540
TGCTGCTGCC TCGGCGCTCG CTGACAGCC CCGCGGTCTC CGCGGAGCGC GCGCTAGGA 600
ATGCCCTCGG CGGCCACGAG GAGGCACCG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCCTGGA TCTCACCTTC CACCTCTCTC GGGAGTCTT GGAATGGGCC AGGGCCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTTAAAAA AATACAGTAT 840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA 960
GCAGCAACAC AATGTTATTG GTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAAATG AGACCTGTGA GAAAACGTTT TGTTTGAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACITTTCTCT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAAGGT

Seq ID NO: 29 Protein Sequence
Protein Accession #: NP_000747.1

65
70
1 11 21 31 41 51
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SSLLAGSGS RPSPEQATAN FFRVLLQQLL 120
LPRRSLDSPA ALAERGARNA LGGHQEAPEP ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180
AQQAHNRRL MEITGK

Seq ID NO: 30 DNA sequence
Nucleic Acid Accession #: CAT cluster

75
1 11 21 31 41 51
ATTTCTTGAG ATGGCTCTCT TTGGAATAT GCATCTCTCC TGATACTTGG ATGCTTTTCC 60
TCTGACTGAT GAAGATCCTG AATACCAAAG AGGGCCGCTG AAAGGCTCTC AGGAGTACAC 120

5
10
15
20
25
30
35
40
45
50
55
60
65

```

CTTCTAGGAA CCCTAAGCCA GAGAGAGGCT TCACTACATC ATGCTTCTCG ACATCTCTCC 180
CTTTGAAGAG CAGTCAGACT CCTGCTTTGC TCTTCAGACT TAATTTGGGG GTTTAACAGG 240
TGAGGTTGCT GGGGGAACCT TTTTACAACA TCTCTCTGAA AGAATCCGGG CTGCCAGTTT 300
CATTTGGTTT GGGTGTCACT AGCATGATGG AAAGACAAAA AAACACAAC TGACATCTGC 360
AGAAATGGGT TCAAAATTTA CCTGCAACTC ACCAATTCTG TGGCCTTGGT TCAGCAATTA 420
AACTCCCTAA AATTCACTTT TTTCTTTGTA AAATGGGGTT ATGAACAGTA CCTACTTCAA 480
AATGTGTTTG TGAAGATTAA AAAAGTTAAC ATAAAGAGTT TAGAAGAGTG TCTGGCATAT 540
TGTGCTCAAT AAGTGTTTAT TTATTTATTG CTGAATAAAC CAGTAATTTA ATTAGTAT

```

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 134..1917

15
20
25
30
35
40
45
50
55
60
65

```

1      11      21      31      41      51
|      |      |      |      |      |
CACCTCAGCC CCAACCCCAA CCCCAGCCGC ATCCCCTGCC CCAGCTGACG GGTCAAAGCC 60
TCAGGAGAGT GTGGCTCTCC CCAGGCGCTA CCAGGAGGGG CAGGCTCTAG CCAGCTGGGG 120
AAACCTTATT GCATGGTTC TTAGAAGCCA CCCCTTCCCC AGGCAAGACA GGCCCAAGG 180
GAGTGTCCCG AGGCGCGTTC CTTCACTGAG GACAGTCATA GGGACAGSTA CAGGGGGGCT 240
GGACAGACAC GGGCCCTCTT CTTCACTGAG GACAGTCATA GGGACAGSTA CAGGGGGGCT 300
GGTTGAGGCT GGAGGTGAG CACAGCCAAG AAGCTCCGAG ACCAACGGAT CGCCAGAGCC 360
AGACCTCTCC CAGAGCCCTAA GAGGAGAGGG AACCAGGGAG AAAAGTCTAG ACCCGCTGCC 420
CCAGCCCGCG ATGCCAGGGG GCCCAGCACA GCCCAGCGCG CAGAGGCCGC CTGGCCCGCG 480
GGCTCTCTCC TCTGCSAGGC GCTCACAGCC GGTACCCAG CTACGGAAAC GCAGCAGGTG 540
CGAATTCGCC CGAGCTCGG AGCAGGAGGT CAGGCGGGCC GCCTCGGGGG ACCCTCAAAG 600
GGAGGCGCGG GGGGAGGGGG GCAGCCCTGC CGCCCGCAGC GGGGCGCTCA CGGAAAGCA 660
GGAGGAGGCC CGGAAGCTCA TGGTGTCTT GCAGAGGCCG GGGGTTGGG GGTGTGTGGA 720
GGGGCCCGCG AAGCCAGACT CCGGGGCCCT GGAGCCCGCC ACGGCGGCG CCCTCGGGCG 780
GCGGCTGGAC CTGGSCAGTT GCCTGGACGT GCTGGCCTTT GCCCAGCAGC ACGGAGAGCC 840
CGGCTGGCGG CAGGAGACCT ACGCGCTGAT GAGCGACAAC CTGCTCGGAG TGCTGGGAGA 900
CCGCTGCCCT TACCGCCGGC TGAGCGCGGC CGACCGCGAG CGCATCTCTA GCCTCGGGAC 960
CGGCGGGGGC CGGCGGTGCG TGGGCGTCTT CGTACTGCCG AGCCTCTACC AGGGGGGGCG 1020
CTCAGGCGTC CCGAGGGGCC CTGCTGGCGA GGAGCCTCTT CGGCGGGCCC CTGTGTCCCT 1080
GCCTCTACCT GCGCACCTGC ATGTGTTCAA CCCCAGGGAG AACACCTGGC GGGCCCTGAC 1140
CCAGGTGCCC GAGGAGGGCC CGCTTCGGGG CTGCGGTCTC TGCAACATGC ACAACTACCT 1200
GTTTCTGGCG GGGGSCATCC GTGGCTCCGG TGCCAAAGGC GTCTGTCTCA ACGAGGTCTT 1260
CTGCTACACC CTTCTGACCA ACATCTGGAG CCAAGTTCCG CCATGCGAGC AGGCCCGAGC 1320
CCAGCTCAAG CTGCTGGGCC TGAACGGGCT GCTCTATGCC ATCGGTGGCG AATGCCCTGA 1380
CAGCATGGAG TGCTACGACC CGCGAACAGA CGCCTGGACC CCAGCGCGC CACTCCCGCG 1440
AGGCACCTTC CTTGTGGGCC ACGAGGCTGT GGCCTGCCGT GGGGACATCT ACGTCACCGG 1500
GGGTACCTCT TTCTACCGCC TGCTCAGGTA CAGCCCGCGT AAGGATGCTT GGGACGAGTG 1560
CCCATACAGT GCCAGCCACC GCGGTTCCAG CGACATCGTG GCACTGGGGG GCTTCTGTGA 1620
CGGCTTCGAC CTGCTGGCGG GCGTGGGCGC CGCCGTGATG CGCTACACA CAGTGACCGG 1680
CTCCTGGAGC AGGGCTGGCT CCGTGGCCCT GCCCAGCCCC GCCCACCTGC ACTGCACCAC 1740
CCTGGGCAAC ACCATTACT GCCTCAACCC CCAGGTCACT CCAGCTCTCA CGGTCTCTGG 1800
GGGGTCTGCC CAGTTCAGG CCAAGGAGCT GAGCCCTTTC CCCTTGGGGA GCACCGGGGT 1860
CCTCAGTCCA CTTCTCTGA CTCTGCCCCC TGAGGACCGG CTGCAGACCT CACTCTGAGT 1920
GGCAGGCAGA GAACCAAAGC TGCTTGGCTG CTCTCCAGGG AGACCTCTCT GGGATGGGCC 1980
TGAGAGGCGG GGGCTCAGGG AAGGGGCTGG GATCGGAAC TCTGCTCTTT GTTCTGGAC 2040
AACTTTCCCC TTCTGCTTTA AAGTTTGTG ATTATTTTGA AGCCAGACT CCCTCAGCCT 2100
CTTTCTGCC CTCACTCCAC ACCCAGACTG TTTCTGACT CAATTCGTA CCTACTTACA 2160
GACCCTCTCA GCTTGTCTAG ACCCCCTGT CTGTGGGACT CCCTATTCCC TAGAGCCAGG 2220
GACTGATGCG TCTCCACAGA CAAGGACTTG GCTCGTGGG GCTCTGCTGA GCCGAGAGAG 2280
GAGGGGATAG AAAACATTCA CACTTCTAT GCTCTGTGAG CAGGACAGG AGCAAAAAG 2340
TCCCCAGGCA ACGCCCTCG CTCTGGGACT TTCTGCGTGT CCTAAGGCCT CCCAGGTAC 2400
CAACCCCGTA GCTATCTGGG TCTGTTTGGC ACTGTGGATT CTCAAGGGCC TAGAACCCCT 2460
GCCTCTGAAA CTGCTCCGCT GGTGCAGCCC TGCTGTCTGC AGCTCCTGCC CATACCCCCA 2520
GCCACACCA GCCCAGGGCC ACTCCGGGCT CACCAACCTC TGACGCTTG TGGGGCTCTC 2580
CCAGCCCTC CAGAAGCCCA CCCCACTTCT CGCCAACCTC CGATCTCTAA ATGAGGCTG 2640
AGCGTCAACC TAGTTCTGCC CTTTCTTAGC TGTGTAGACT TGGACGAGAC ATTTGACTTC 2700
CCTTCTCCT TGTCTATAA ATGTGGACAG TGGACGCTG TCACCAAGA GAGTGTGGG 2760
AGACAGATC ACAGCTATGA GCACCTCGCA CGGTGTCCAG GATGCACAGC ACAATCCATG 2820
ATGGGTTTTC TCCCTTACG CACTTTGAAA CCCATGCTAG AAAAGTGAAT ACATCTGACT 2880
GTGCTCCACT CCAACCTCCA GCCTGGATGT CCCTGTCTGG GCCCTTTTTC TGTTTTAT 2940
TCTATGTTCA GCACCACTG CACCAAATAC ATTTTAATTC ACCGAAAGCA

```

Seq ID NO: 32 Protein Sequence
Protein Accession #: XP_054631.1

70
75

```

1      11      21      31      41      51
|      |      |      |      |      |
MPRGPAQPPA QRPFGPAASS SARRSQPVVQ LRKRSRCEIA PSSEQEVVPA ASGDPQGEAP 60
GEGGSPAGRS GALTEKQBEA RKLWVFLQRP GGMVGVVEGR KPSRRALEPA TAAALRRRLD 120
LGSCLDLVLP AQHGEPGLA QETALMSDN LLRLVLDPLC YRRLSAADRE RILSLRTGRG 180
RAVLGLVLPL SLVQGGRRSL PRGPRGSEPP AAAPVSLPLP AHLHVFNP RE NTWRPLTQVP 240
EEAPLRGCGL CTMNYLFLA GGIRGSGAKA VCSNEVFCYN PLTNISQVR PMQARAQLK 300
LVALDGLLYA IGGECLYSME CYDPRDAWT PRAPLPAGTF PVAHEAVACR GDIVYTGHL 360
FYRLRLRSPV KDAWDECPYS ASHRRSSDIV ALGGFLYRFD LLRGVGAAMV RYNTVTGSWS 420

```

RAASLPLPAP APLHCTTLGN TIYCLNPQVT ATFTVSGGTA QFQAKELQPF PLGSTGVLSF 480
FILTLPPEDR LQTSL

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
CCTCTGTCTA ACCTTACATG AAAAAACCG TTTCCAACGA AGGCCTCTAA AAGCCAAGA 60
AATCCCCCTG CAGACTTTAC AAACAGAGTG TTTCCCTAACT GCTCTATGAA CAGAAAGGTT 120
AAACTCTGTG AGTTGAACCA ACACATCACA ACGCAGTTTG TGGGAATGAT TCTGTCTAGT 180
TTTGAAACGA AGATATTTC TTTCTGCGG TTGACCTTAA AGCGCTTGAA ATCTACACTT 240
GCAAAATTGCA CAAATAGAGT GTTTCAAATC TGCTCTGTCT AAGGGAACGT TCAACTCTGT 300
GAGTTGAATG CACACAACAC AAGGAAGTTA CTGGGAATTC TTCTGTCTAG CCTTACATGA 360
AAGAAAACCC GTTTCACACG AAGGCCTCTA AGTGGTCAAA ATATCCACGT GCAGACTTTA 420
CAACAGAGAG GTTTCACAAAC TGCTGAATGA AAAGAAAAGT AAACCTCTAG AGTTGAACGC 480
ACACATCGCA GAGCAGTTTC TGAGAATGAT TCTGTCTAGT TTTTATACGA AGATATTTC 540
TTTTCTGCCT TTGGCCTCAA AGCGCTTGAA ATCTCCACTT GCAAAATCCA CAAAAGAGGT 600
GTTTCAAAATC TGCTCTGTCT AAAGGAAGGT TCAACTCTGT GAGTTGAATA CACACAACAC 660
AAAGAAGTTA CTGAGAATTC TTCTGTCTAG CATTATATGA AGAAATCCCG TTTCCAACGA 720
AGGCATCTAA GAGGTCCAAA TATCCACTTG CAGACTTTAC AAACAGAGGG TTTCCAGAAT 780
GGCTGTATGA AAGAAAAGGT TAAACTCTGT GAGTTAAACA CACA

Seq ID NO: 34 DNA sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

1 11 21 31 41 51
GGAAGACTTG GGTCTCTGGG TCGCAGGTGG GAGCCGACGG GTGGGTAGAC CGTGGGGGAT 60
ATCTCAGTGG CGGACGAGGA CGGCGGGGAC AAGGGGCGGC TGCTCGGAGT GCGCGAGCGT 120
CAAGTCCCCT GTCCGTTCTCT CCGTCCCCTGA GTGTCTCTGG CGCTGCCTTG TGCCCGCCCA 180
GCGCCTTTGC ATCCGCTCCT GGGCACCAGG GCGCCCTGTA GGATACTGCT TGTACTTAT 240
TACAGCTAGA GGCATCATGG ACCGATCTAA AGAAAACTGC ATTTCAAGAC CTGTTAAGGC 300
TACAGCTCCA GTTGGAGGTC CAAAACGTGT TCTCGTGAAT CAGCAAAATC CTGTGTCAGAA 360
TCCATTACCT GTAATATAGT GCCAGGCTCA GCGGGTCTTG TGTCTCTCAA ATTCTTCCA 420
GCGGTCTCCT TTGCAAGCAC AAAAGCTTGT CTCCAGTCAC AAGCCGGTTC AGAATCAGAA 480
GCAGAAGCAA TTGCAAGCAA CCAAGTGTACC TCATCCTGTC TCCAGGCCAC TGAATAACAC 540
CCAAAAGAGC AAGCAGCCCC TGCCATCGGC ACCTGAAAAA AATCCTGAGG AGGAACCTGGC 600
ATCAAAACAG AAAAATGAAG AATCAAAAAA GAGGCAGTGG GCTTTGGAAG ACTTTGAAAT 660
TGCTCGCCCT CTGGGTAAAG GAAAGTTTGG TAATGTTTAT TTGGCAAGAG AAAAGCAAAG 720
CAAGTTTATT CTGGCTCTTA AAGTGTATT TAAAGCTCAG CTGGAGAAAG CCGGAGTGA 780
GCATCAGCTC AGAAGAGAAG TAGAAATACA GTCCACCTT CCGCATCCTA ATATTCTTAG 840
ACTGTATGGT TATTTCCATG ATGCTACCAG AGTCTACCTA ATCTGGAAT ATGCACCACT 900
TGGAACAGTT TATAGAGAAC TTCAGAAACT TTCAAAGTTT GATGAGCAGA GAACTGCTAC 960
TTATATAACA GAATTTGGCA ATGCCCTGTC TTACTGTCTA TCGAAGAGAG TTATTGATAG 1020
AGACATTAAAG CCAGAGAACT TACTTCTTGG ATCAGCTGGA GAGCTTAAAA TTGCAGATTT 1080
TGGTGGTCA GTACATGCTC CATCTTCCAG GAGGACCACT CTCTGTGGCA CCGTGGACTA 1140
CCTGCCCCCT GAAATGATTG AAGTCTGGAT GCATGATGAG AAGGTGGATC TCTGGAGCCT 1200
TGGAGTTCTT TGCTATGAAT TTTTAGTTGG GAAGCTCTCT TTTGAGGCAA ACACATACCA 1260
AGAGACCTAC AAAAGAATAT CACGGTGTGA ATTCACATTC CCTGACTTTG TAACAGAGGG 1320
AGCCAGGGAG CTCAATTCAA GACTGTGTA GCATAATCCC AGCCAGAGGC CAATGCTCAG 1380
AGAAGTACTT GAACACCCCT GGATCACAGC AAATTCATCA AAACCATCAA ATTGCCAAAA 1440
CAAAGAATCA GCTAGCAAAC AGTCTTAGGA ATCGTCAGG GGGAGAAATC CTTGAGCCAG 1500
GGCTGCCATA TAACCTGACA GGAACATGCT ACTGAAGTTT ATTTTACCAT TGAATGCTGC 1560
CCTCAATCTA GAACGCTACA CAAGAAATAT TTGTTTTACT CAGCAGGTGT GCCTTAACT 1620
CCCTATTGAG AAAGCTCCAC ATCAATAAAC ATGACACTCT GAAGTGAAAG TAGCCACGAG 1680
AATTGTGCTA CTTATACTGG TTCAATATCT GGAGGCAAGG TTCAGATGCA GCCGCCCCGT 1740
CAGCCTGTGC TAGGCATGGT GTCTTCACAG GAGGCAAAATC CAGAGCTTGG CTGTGGGGA 1800
AGTGACCACT CTGCCCTGAC CCGATCAGT TAAGGAGCTG TGCAATAACC TTCTAGTAC 1860
CTGAGTGAGT GTGTAATCTA TTGGGTTGGC GAAGCCTGGT AAAGCTGTTG GAATGAGTAT 1920
GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGATATT TTTCTCTGGT 1980
GGCATTCTCT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCTGT ATTGGGTTTC 2040
TAGTCTCTCT TAACCACTTA TCTCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT 2100
ACCTCCATTT AGGGATTTCG TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTTAAG 2160
GGCTTATTTT TTTAAACAT TGGAGTCATA GCATGTGTGT AAACCTTAAA TATGCAATA 2220
AATAAGTATC TATGTCTAAA AAAAAAAAAA AAA

Seq ID NO: 35 Protein Sequence
Protein Accession #: AAC63902.1

1 11 21 31 41 51
MDSKENCIS GPKVATAPVG GPKRVLVTQO IPCQNPLFVN SGQAQRVLCF SNSSQVRVPLQ 60
AQKLVSSEHKP VQNKQKQLQ ATSVPHVPSR PLNNTQKSKQ PLPSAPENNP EEELASKQKN 120
EESKKRWAL EDPEIGRPLG KKGKFGNVYLA REKQSKFILA LKVLFPKALE KAGVEHQLR 180
EVEIQSHLRH FNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSRFDL QRTATYITEL 240
ANALSYCHSK RVIHRIKPB NLLGSGAGEL KIADEFGSVH APSSRRRTLC GTLDYLPFEM 300

IEGRMHDEKV DLNLSGLVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI 360
 SRLLLGNFSQ RPNMLREVLEH PWITANSSKP SNCQNKESAS KQS

Seq ID NO: 36 DNA sequence
 Nucleic Acid Accession #: NM_016267
 Coding sequence: 67..843

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACGAGG ACAGAATCAG GTGATGGTCC AGAATTAAGA GCTGTCACTT GTGTCAATTCA 60
    CTCACAATGG AAGAAATGAA GAAGACTGCC ATCCGGCTGC CCAAAGGCCA ACAGAAGCCT 120
    ATAAAGACGG AATGGAATTC CCGGTGTGTC CTTTTCACCT ACTTCCAAGG GGACATCAGC 180
    AGCGTAGTGG ATGAACACTT CTCCAGAGCT CTGAGCAATA TCAAGAGCCC CCAGGAATTG 240
    ACCCCCTCGA GTCAGAGTGA AGGTGTGATG CTGAAAAACG ATGATAGCAT GTCTCCAAAT 300
15 CAGTGGCGTT ACTCGTCTCC ATGGACAAAG CCACAACCAG AAGTACCTGT CACAAACCGT 360
    GCGGCCAACT GCAACTTGCA TGTGCTTGGT CCCATGGCTG TGAATCAGTT CTCACCGTCC 420
    CTGGCTAGGA GGGCCTCTGT TCGGCTGGG GAGCTGTGGC ATTTCTCTCT CCTGGCGGGC 480
    ACCAGCTCCT TAGAGCTCTG CTACTCTCAT CCCTTCCCG CTGGCCACCT GGTTCAGAG 540
    CCCAGCCTG ATGGGAAACG TGAGCCTCTC CTAAGTCTCC TCAGCAAGA CAGATGCCTA 600
20 GCCCGTCTCT AGGAATCTGC CGCCAGGGAG AATGGCAACC CTGGCCAGAT AGCTGGAAGC 660
    ACAGGGTGGC TCTTCAACCT GCCTCCCGGC TCAGTTCACT ATAAGAACT ATATGTATCT 720
    CGTGGATCTG CCAGTACCAAG CCTTCCAAAT GAAACTCTTT CAGAGTTAGA GACACCTGGG 780
    AAATACCTAC TTACACCAAC AAACCACTGG GGCCACCCAC ATCGATACCT GCAGCATCTT 840
    TAGTCAAGTT GGAGGAGAAA GACAACACTT GGTCTAAGAC ACGGCAGCAA GACATCCCTG 900
25 CATATTGTTT CAGATAAAAA TGAAAGCTGC TCACACCCAC TTGCTCTCCC AATCTGTTAA 960
    ACAGCTTCGT GTCTAGTATG AGCTCAGTAC TTGCTCTGTG AAAATCCAG AAGCCCCGCG 1020
    TGTCAATGTT CCCCATCCAC ACCCTGCTTG CTCCTGTGTA ACAGCTCAGA TGATGAATAA 1080
    TAATAAAACT GTACTTTTTT GGAAAAAATA AAAAAAATA AAAAAA
  
```

Seq ID NO: 37 Protein Sequence
 Protein Accession #: NP_057351.1

```

1      11      21      31      41      51
|      |      |      |      |      |
35 MEEMKKTAIR LPKGKQKPIK TEWNSRCVLF TYPQGDISSV VDEHFSRALS NIKSPQELTP 60
    PSSQSEGVML KNDDSMSPNQ WRYSSPWTKP QEVPVFNRA ANCNLHVPGP MAVNQFSPSL 120
    AARRASVRPG ELWHFSSLAG TSSLEPGYSH PFPARHLVPE PQPDGKREPL LSLLQDQRCL 180
    ARRPQESAAR ENGNFGQIAG STGLLPNLPP GSVHYKLYV SRGSASTSLP NETLSELETP 240
40 GKYYSLTPPN HWGHPHYLQ HL
  
```

Seq ID NO: 38 DNA sequence
 Nucleic Acid Accession #: AK058088.1
 Coding sequence: 252..1772

```

45 1      11      21      31      41      51
    |      |      |      |      |      |
    AGGAAACCAA GGCAAGCTCC CCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
    GCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGCGCGCCCC AGCTCTCCTG 120
    TAATCAGAG GCCAGTGTGA TGGAGTTCC TCCACTCAGC ACACTTCCCC TGTAAACACG 180
50 CCTGTGTGG GCAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTC 240
    CACTTTCAAT CATGATAATG TCGAACACGC ACAAGCTCG GCTGGAACGC CGGGTCACTG 300
    GCTCAACCAA CCGGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGACCTG CTCTCACTTT 360
    CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
    TATGCATTC ACAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480
55 GTGGGAAGC AGATGTGATT CTCGAGTCCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
    GGCTTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600
    CACACCCCTT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCACCCTAG AAGACCAAAG 660
    AAAAATCCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
    AAGTGCCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780
60 AAGACCTACT GGGAGTGTG GCTTCCGCC ACATCTCCCA GTTCAGTGGC CTGTTTCAAA 840
    GGTGCGTGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
    CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960
    ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACTGTCTCC 1020
    ACAAAGTGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080
65 TGCTTTTGTG GGTCTTCTTG CAACTGAAT ACAAGATTCA GGCAATTCCG ACTTATGAAA 1140
    CGTGATGAC ATTTTAAAG AGCTTTCCTG AGAAGTGTG CTCTCTGGAC CGGACATAG 1200
    GACGGAGCTT GAGGCGCTC TTCTCTGCT TGCGTCTGCA CGGCATCACC AAAGGCAAGG 1260
    ATCTGGAGGT GCTGCGGCAC CTTAACTTCT TCCAGAGTC ATGGCTCGAC CAGGTACAG 1320
    TCAACCATTA CCACGACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380
70 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAATTAT TCGAAAAACA 1440
    TGCTCTATA TGGATTCTTC TTTAAGATAA AGGAGTCAA ACATGATACT ACCTCTTATA 1500
    GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCTCTGCG GTCTACGAGC 1560
    ACAACCACT CAGCCTGCGA GCGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
    TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACAGAT CAAGCAGAAG TTTGGGTGA 1680
75 CCACGTATC CTGCAAAAGC CATACCTTGA AAATCCAAC TGTGGGATCT CCAATCTATG 1740
    TAAGTTTTCG ATTCACTTTC CCAGCATCTT GACAGTTTCC AGAAGATCT ATGGGATTTT 1800
    CCCCCACTG GTCTGCATAA AAGAAATAA AATGACATAA AAGGGAGC
  
```


Seq ID NO: 39 Protein Sequence
Protein Accession #: BAB71658.1

```
5 1 11 21 31 41 51
| | | | |
MIMSNTHKAR LERRVTGSTN RWRLPKQPPS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS 60
QIQKFFNFEN KNKDIQSGEA DVILECLGPK NELHQPRLFO SETLAKLYLK ALAQGTTTHPL 120
RELEELLRAQ SPKTKYKESP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180
GVLASAHILQ FSQLPQRCVD VMIA RLKPST IKKPYEAGCK YKEEQLTGCG EKWLEMLNVP 240
10 LGGTQIHLHK IPQDLLHKVL KSPRLFTFSE FHLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
FFKSFPFENC FLDRDIGRSL RPLFLCLRHL GITKGDLELV LRHLNFFPES WLDQVTVNHY 360
HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTTSYSFYM 420
QRIKHTDLES PSAVYEHNVH SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFGLTSS 480
15 CKSHTLKIQT VGPIYVSFA FIFPAS
```

Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_032899.1
Coding sequence: 186..1070

```
20 1 11 21 31 41 51
| | | | |
GGCACGAGGA TTGCTCAGGA CAGCGGTAAA TCACTTCTTG GAGGTGCCCT GCACGCCGGT 60
CCTGGGAGCA GCGGCGCTCC CGGGGGTGCG GGAGCCCCAC TCCTCCGTGG TGTGTTCCAT 120
TTGCTTCCCA CATCTGGAGG AGCTGACGTG CCAGCCTCCC CCAGCACCA CAGGGACGCG 180
25 GAGGCATGAG CCGGTCAAGG CACTGGGCA AAATCCGGAA GCGTCTGGAA GATGTCAAGA 240
CCGAGTGGGT CCGGCCAGCC AGGGCTGACT TTAGTGACAA CGAGAGTGCC CGGCTGGCCA 300
CGSACGCCCT CTTGATGGG GGTCTGAAG CCTACTGGCG GGTGCTCAGC CAGGAAGGCG 360
AGGTGGACTT CTGTCTCTCG GTGGAGGCC AGTACATCCA GGCCAGGCC AGGGAGCCCC 420
CGTGTCCCCC AGACACCTCT GAGGGGGCGG AAGCAGGCC TAAGGGACTG GACTCCAGCT 480
30 CCTACAGTC CGCACCTAC TTCCCTGTGG CCTCAGAGGG CAGCGAGCCG GCCCTACTGC 540
ACAGCTGGGC CTAGCTGAG AAGCCCTACC TGAAGGAAAA ATCCAGGCC ACTGTGTACT 600
TCCAGACCGT CAGACCAAC AACATCAGAG ACCTCGTCCG CCGCTGCATC ACCCGGACTA 660
GCCAAGACAT TTCCATCCCG AGTGTGGAAG GAGAGATATA CTGTGCCAAG TCAGGCAGGA 720
AATTCACCTG CCAATCCCG GAGAAGTTCA TCATCTCGGA CTGGAGATT GTCTGTCTG 780
35 GATCTTACAG CTTCACCTGG CTCTGCGGAC ACGTGACCGG GAACATCCTC TCCAAGTTCA 840
CAGGCCAGGC GGTGGAGCTG TTGACGAGG AGTTCCGCCA CCTCTACGCC TCCTCCAAGC 900
CTGTGATGGG CTGAAGTCC CCGCGCTGG TCGCCCCCGT CCGGCCCGGA GCAGCCCCGG 960
CCAATGGCCG CCTTAGCAGC AGCAGTGGCT CCGCCAGTGA CCGCACGTCC TCCAACCCCT 1020
40 TCAGCGGCCG CTCGGCAGGC AGCCACCCCG GTACCCGAAC TGACGGGTGA GATGAGGTTA 1080
GAATGACTGG GCGCGGCTGA ACATTCCAAA TTGGATTTC AATCTGTCTG AGAAAGTTA 1140
AGGAAGCAAA AGCTTGCCAG GTACAGAAAG CTCCTAAGCC CAGCTTTCCA AAGGCTCAG 1200
CCTGTGCGCTG TGTCGAGCTC AGTCTGCGGA GATAGGGGAG AACCTGCAGG CAGGAACAAG 1260
45 GGTAGTCTGG GGTGAGCTC CTCCATCAGC AGTCTCCCT CCGTGGTCTG CTCTGTGAG 1320
CCCCCTACT CTGACCAACC CTCCATCAGC AGTCTCCCT CCGTGGTCTG CTCTGTGAG 1380
AAAGGTGCGA TTTCTCTCT CTCTGGGCACC TGTAACATGT GATGCGGTGC CTGCTGTGAG 1440
GTTAGTCTGG GGTGAGCTC GCGAGTGGAG CATGAGCAGA ACCGCGAGG GTCACTTCTG 1500
GGCAGAGCTC TTGAGAGCTT GGTGAGCTC TGCCACATAG AAGCAGCTCT CCAGTTGAAA 1560
CCCTCTCTG CCAGCTCTGG GTCTTAAGCG ATGAGCAGAA TCCCCACTC CCACCCCAAC 1620
50 AAAAAAAA
```

Seq ID NO: 41 Protein Sequence
Protein Accession #: NP_116288.1

```
55 1 11 21 31 41 51
| | | | |
MSRSRHLGKI RKRLEDVKSQ WVRPARADFS DNESARLATD ALLDGGSEAY WRVLSQGEV 60
DFLSSVEAQY IQAQAREPPC PPDTLGGAEA GPKGLDSSSL QSGTYFFVAS EGSEPALHLS 120
WASAEKPYLK EKSSATVYFQ TVKHNINRDL VRRCITRTSQ NISIRSVEGE IYCAKSGRKF 180
60 TGQIREKPII SDWRPVLSSG YSPTNLCGHV HRNLSKFTG QAVELFDEEF RHLVASSKPV 240
MGLKSPRLVA PVPFGAAPAN GRLSSSSGSA SDRTSSNPFS GRSAGSHPGT RTDG
```

Seq ID NO: 42 DNA sequence
Nucleic Acid Accession #: NM_000782.2
Coding sequence: 405..1946

```
65 1 11 21 31 41 51
| | | | |
TGGAGAGGGA CAGGAGGAAA CGCAGCGCCA GCAGCATCTC ATCTACCCCT CTTGACACCT 60
CCCGGTGGCT CCAGCAAGCC CTAGAGGTCA GCCTTGCGGA CCAACAGGAG GACTCCAGC 120
70 TTTCCCTTTT CAAGAGGTAC CCGAGACACC GGCCACCCCT TTCCAGCCCC TGCGGCCAGT 180
GCAAGGAGGC ACCAATGCTC TGAGGCTGTC GCGTGTGTGA GCGTCGAGCA TCCTCGCGCA 240
GTCTCTCTGC TGCTGTCTCC AGCCCCGACT CCACTAGTCA CCTGTATCA ACCTCGCCCC 300
TCTTTTCCC AGAATGTTA AGCCCCGACT CCACTAGTCA CCTGTATCA ACCTCGCCCC 360
ACCCATCTCT CTGCTCTTCC CGCGCTCCGG TGTCCCCCGC TGCCATGAGC TCCCCATCA 420
75 GCAAGAGCGG CTGCTTGGCC GCCTTCTGCG AGCAGCTGCG CAGTCCGAGG CAGCCCCGA 480
GACTGTGTAC ATCTACGGCG TACAAGTCCC CTCAGCGCGG AAGAGGTGCA GTCTGCCCCG 540
TGACAGCTGG TGCGGAGACT CAGAACGCGG CCGCCCTGCC GGGCCCCACC AGCTGGCCAC 600
TGCTGGCGAG CCTGCTGCAG ATTCTCTGGA AAGGGGGTCT CAGAAACAG CACGACACCC 660
```

5 TGGTGGAGTA CCACAAGAAG TATGGCAAGA TTTCCGCGAT GAAAGTTGGGT TCCTTTGAGT 720
 CGGTGCACCT GGGCTCGCCA TGCCTGCTGG AAGCGCTGTA CCGCACOGAG AGCGTACCCC 780
 AGCGGCTGGA GATCAAAACCG TGGAAAGGCT ATCGCGACTA CCGCAAAGAA GGCTACGGGC 840
 TGCTGATCCT GGAAGGGGAA GACTGGCAGC GGGTCCGGAG TGCTTTCAA AAGAACTAA 900
 TGAACCAGG GGAAGTGATG AAGCTGGACA ACAAATCAA TGAGGTCTTG GCCGATTTTA 960
 TGGGCAGAAT AGATGAGCTC TGTGATGAAA GAGCCACGT CGAAGACTTG TACAGCGAAC 1020
 TGAAACAAATG GTCGTTTGAA AGTATCTGCC TCGTGTGTA TGAGAAGAGA TTTGGGCTTC 1080
 TCCAGAAAGAA TGCAGGGGAT GAAGCTGTGA ACTTCATCAT GGCCATCAAA ACAATGATGA 1140
 GCACGTTTGG GAGGATGATG GTCACTCCAG TCGAGCTGCA CAAGAGCCTC AACACCAAGG 1200
 10 TCTGCGAGGG ACACACTCTG GCCTGGGACA CCATTTTCAA ATCAGTCAAA GCTTGTATCG 1260
 ACAACCGGTT AGAGAAGTAT TCTCAGCAGC CTAGTGCGAA TTTCCCTTGT GACATTTATC 1320
 ACCAGAATCG GCTTTCAAAG AAGAATTGT ATGCTGCTGT CACAGAGCTC CAGCTGGCTG 1380
 CGGTGGAAC GACAGCAAC AGTCTAATGT GGATCTCTA CAATTTATCC CGTAATCCCC 1440
 AAGTGCACCA AAGCTTCTT AAGGAAATTC AAGTGTATT ACCTGAGAAT CAGAGGCCAC 1500
 15 GGGAGGAAGA TTTGAGGAAT ATGCGGTATT TAAAGCCCTG TCTGAAAGAA TCTATGAGGC 1560
 TTACCCGGGG TGTACCATTT ACAACTCGGA CTCTTGACAA GGCAACAGTT CTGGGTGAAT 1620
 ATGCTTTACC CAAAGGAACA GTGCTCATGC TAAATACCCA GGTGTTGGGA TCCAGTGAAG 1680
 ACAATTTTGA AGATTCAAGT CAGTTTAGAC CTGAACGTTG GCTTCAGGAG AAGGAAAAAA 1740
 TTAATCCTTT TGCGCATCTT CCATTTGGCG TTGGAAGAA AATGTGCATT GGTGCGCGAT 1800
 20 TAGCAGAGCT TCAACTGCAT TTGGCTCTTT GTTGGATTGT CCGCAAATAC GACATCCAGG 1860
 CCACAGACAA TGAGCTGTGT GAGATGCTAC ACTCAGGCAC CCTGGTGCCC AGCCGGGAAC 1920
 TCCCATCGC GTTTTGCCAG CGATAATACG CCTCAGATGG TGGTATTTCG TAACATCATA 1980
 TCCAACCTAG GGAAGCGGAC TGAGTGCTGG GATCCAAGGC ATTCTACAGG GTTCACTGCT 2040
 GGTTTACACT TCACCTGTGT CAGCACCATC TTCAGGTGCT TAGAATGGCC TGGGAGCCTG 2100
 25 TTCTGTCTTG CATCTCCAT GACATGAAAG GGAGGCTGGC ACTTGTGAGT CAGGTAGAGG 2160
 TTACAAACCG TTTGAGGCCG TGCTACCACA TTCAGTGTG GAATCTTTAA TTCCAAGAA 2220
 TAAGTTTACA TTTCAACAAT AATGACCTAC AACAGCTAAA TTTTCTGGGG CTGGGAGTAA 2280
 TACTGACAA CCAATTTACTG TAGCTCTGCT TAATGTACTA CTTAGGAAAA TGTCCTGCT 2340
 TAATAATGTA AGCCAGCTA AATGATGGTT AAGTTATCA GGCCTCCCAT GAAATTGGGT 2400
 30 TCTTCTGCA TTGAAATAAA AACATTATTG GGAACCTAGA GAACACCTCT ATTTTAAAA 2460
 GGACTTTAAC GAACTCAAAC AACTTCTAAG ACTAGTGATT CACTGGGGCA TTAATTTGTTA 2520
 GAGGACCTTA AAATTTGTTA TTTTAAAT GTGATTCCTT TATGGCATTG GGTAAAGAT 2580
 GAAGCAATAA TTTTAAAT GTGTATGTGC ATATGAAGCA CAGACATGCA TGTGTGTGTG 2640
 35 TGCTGTGTG TGTGTGCGG TGTATGTGTG TGTGGTCTT AATGGTAATT TGCCTCAGTC 2700
 ATTTTAAAT TATTGTGAGT ACTTGATTTA GGATCTGTGG TGCAGGGCAT GTTCAAAGT 2760
 TTAGTCACAG CTTAAAAACA TTCAGTGTGA CTTAATATT ATAAATGAT TTCCCATGCC 2820
 ATAAATTTTC TGTCTATTAA ATGGGACAAG TGTAAAGCAT GCAAAAGTTA GAGATCTGTT 2880
 ATATAACAT TGTTTTGTGA TTGAACCTC TAGGAAAAAT ATGATTTTCA AAATGTAAAA 2940
 40 TGCACAGAAA TGCATGCAAT ACTTATAAGA CTTAAAAATT GTGTTTACAG ATGTTTATT 3000
 TGTGCATATT TTTACTACTG CTTTCTCTAA ATGCATACCT TATATAATTC TGTGTATTGT 3060
 ATAAATATT CTTCTACAT TATATTTTGA GAATATTTCG GAAATATACA TTTATGCTCT 3120
 TATATTGTAA TAAATATGTA CATATCTAGG TATATGCTTT CTCTCTGCTG TGAAATATT 3180
 TTTAGAAATTA TAATTCAGCT CTTGTCATAT TTCATCTGTA TACCTTCAAA TTCTCTGAAA 3240
 45 GTAAAAATAA AAGTTTTTAA ATATT

Seq ID NO: 43 Protein Sequence
 Protein Accession #: NP_000773.1

50 1 11 21 31 41 51
 | | | | |
 MSSPISKSR LAAFLQQLRS PRQPPRLVTS TAYTSPQPRE VPVCPITAGG ETQNAALPG 60
 PISWPLLASL LQILNKGGLK KQHDTLVEYH KRYKIFRMK LGSFBSVHLG SPCLLEALYR 120
 TESVPQRL EIPWKAYRDYR KEGYGLLILE GEDWQVRSA PQKMLMPKPE VMKLDNKINE 180
 VLADFMGRID ELCDEHGHVE DLYSELNKS FESICLVLYE KRFGLLQKNA GDEAVNFIMA 240
 55 IKTMSTFGR MMVTPVELHK SLNTRVWQGH TLAWDTIFKS VKACIDNRL KYSQQPSADF 300
 LCDIYHNR LSKELYAAVT ELQLAAVET ANSLMWILYN LSRNPQVQK LLKBIQSVLP 360
 ENQRPREDL RNMPYLKACL KESMRLTPGV PFTTRTLDKA TVLGEYALPK GTVLMNTQV 420
 LGSSDNEFED SSQFRPERWL QEKEKINPFA HLPFGVGKRM CIGRRLEALQ LHLALCWIVR 480
 60 KYDIQATDNE PVEMLHSGTL VPSRELPIAF CQR

Seq ID NO: 44 DNA sequence
 Nucleic Acid Accession #: NM_007000.2
 Coding sequence: 1-777

65 1 11 21 31 41 51
 | | | | |
 ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA 60
 GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCCTGTCCC TGTGTGCTGA GACCATATGG 120
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180
 70 TCGCTGGTGG CCTGGATTGC CATCTTCTCG GCGTTCTCCT TCTTCATGGT AGCCAGTTT 240
 GGTGTGGGTG CCGCACTCTG CCGCCGCGGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
 CTCATGTCCT ACATCTTCTG GTGCGCCTCC TGCACTACGT CCTACACCCA CGTGACTAC 360
 ATGGTGTCCA ACCATCCCT GATCACAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
 GACCAGGGCC AGGAGCTGAC CCGCCTCTGG GACCGGTGCA TGATTGAGCA AGAATGCTGT 480
 75 GGCAATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG 540
 GAGGTGGTGT TCCCTGGCC CCCACTGTGC TGTGCGCGGA CGGGAACTT CATCCCCCTC 600
 AACGAGGAGG GCTGCCGCTC GGGGCACATG GACTACCTGT TCACCAAGG CTGCTTCGAA 660
 CACATCGGCC ACGGCATOGA CAGCTACAG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720

5 CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGAGGG 780
 ACAGAGAGGG AAGGCAACAT ACACACCCCG GACTCCTCCG CATCTCTCTC CTGCTTCTCTC 840
 CGCTGGGCGT GGATGGCTGC CTCACCTCTC ACCTCCCAAC GTCCCTAGCC CTACGCTCCT 900
 TCCACTTCCA AGATCTTTT CCAGGTTCTT GAGCCCTACT GTGTCTCAGG TGTGCCCTGA 960
 AACCCACGGG CTGTGTGCA CATATCCTTA GCCCATCTTT CAAGGGACCT CTCCATGATC 1020
 CCACCTCCA TTACAGATA CCTCTCTGT AGCTCTCTGA CCTCTCTCTT CATGGCAGGC 1080
 ATGCCCATTC TTGCTGAACC GTTTGTGATT GCCATTGAG CTCTGGAAGC CTCTATTGCC 1140
 ATGAGAGTTC TGTACGGTC ACTTTACTGT CCCCATCATC ACCCAGCAGC GGGCTAAGCA 1200
 TATACTAGAT AGTCAATAAA TAA

Seq ID NO: 45 Protein sequence:
 Protein Accession #: NP_008931.1

15 1 11 21 31 41 51
 MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMVSGVKDDV 60
 FAGAWIAIFC GFSFFMVASF VGGAALCRRR SMVLTYLVLM LIVIYIPECAS CITSYTHRDY 120
 MVSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGPMDWNV FTSAFRAATP 180
 EVVFPWPLLC CRRTGNFIPL NEEGCRLGHM DYLFTRKGCPE HIGHAIDSYT WGISWFGFAI 240
 LMWTLFVMLI AMYFYITML

Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_006760.1
 Coding sequence: 39..593

25 1 11 21 31 41 51
 GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCACGAT GGCACCCCTG CTGCCCATCC 60
 GGACCTTGCC CTGTGCTCTG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
 ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGTTGCTCT 180
 TGCCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGGA GCCAATGACA 240
 GCAAAAGTGT GAGTCCAGC TTTGTGGTGC CTCGCTGCCG TGGGCGCAGG GAACTGGTGA 300
 GTGTGGTGA CAGTGTGTCT GGCTTCACAG TCACCTCGCT CAGTGCATAC CAGGTGACAA 360
 ACCTCGTGCC AGGAACCAAA TTCTACATT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420
 AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGA TCCATTGGGC 480
 TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTCGCCATGT 540
 TCCTGCTGGT GCTGGGCTTC ATCATTGCC TGGCACTGGG CTCGCGCAAG TAAAGGAGTC 600
 TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGCGACCA TCCAGTCCC CAGCCACCT 660
 GCTCCAGGC CCCAGGCTCT TGGCTCCCTT GGTGCCCTCG CCTCCTCTCT CTGCCCTCT 720
 CTCGCCCTAGA GCCCTCTCCT CCTCTGTCC CTCTCCTTGC CCCAGTGCC TCACCTTCCA 780
 ACATCCATT ATTCTCTCA CCCCACTCCT GTCCAGATTG ACTTCTCTCC CATTTTACCA 840
 CTTTAAACAC CCCATAACA ATCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
 GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

Seq ID NO: 47 Protein Sequence
 Protein Accession #: NP_006751.1

50 1 11 21 31 41 51
 MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGNGATL 60
 MVRRANDSKV VTSFVVPVPP RGRRELVSUV DSGAGFTVTR LSAYQVTNLV PGTKFYISYL 120
 VKKGTATESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLL VLGPFIILAL 180
 GSRK

Seq ID NO: 48 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 200-2932

60 1 11 21 31 41 51
 ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGGC TCAGATACTG 60
 ATACTTTCTT TCCAAACAGC ATAAGAAGTG ATTGAGCCAC AAGTATACTG AAGGAAGGGC 120
 TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCGAGCTGCT 180
 GCTGTTCAGT CCAGGGAAGAA TGAAAGTTGG AGTGCTGTGG CTCAATTCTT TCTTCACCTT 240
 65 CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAAACAA AAAAAGAACT 300
 CATTGTGAAT AAGAAAAAAC ATCTAGGCC AGTCGAAGAA TATCAGTGC TGCTTCAGGT 360
 GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC 420
 TCCATTATTA TGGTCACATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG 480
 CAACAGCCTG AATGGAGTCC TGCAAGTGTAC CTGTGAAGAC AGCTACACCT GGTTCCTCC 540
 70 CTCATGCCCTT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA 600
 ATGTACATCT AACAACTCA GCCAGAGTGT CAATTTCTGT GAGAGAACAA AGATTGGGG 660
 CACTTTCAAA ATTAATGAAA GTTTTACAAA TGACCTTTTG AATTCTCTT CTGCTATATA 720
 CTCAAAATAT GCAAATGGA TTAATTTCA ACTTAAAAA GCATATGAAA GAATTCAGG 780
 TTTTGAAGTC GTTCAGGTCA CCCAATTTG AAAATGGAAGC ATCGTTGCTG GGTATGAAGT 840
 75 TGTGGCTCC AGCAGTGCAT CTGAACGTCT GTCAGCCATT GAACATGTTG CCGAGAAGGC 900
 TAAGACAGCC CTTCACAAGC TGTTCATTG AGAAGACGGC TCTTTCAGAG TGTTCGGAAG 960
 AGCCAGTGT AATGACATTG TCTTTGATT TGGGTCCAAG GATGATGAAT ATACCTGCC 1020
 CTGCAGCAGT GGCTACAGGG GAAACATCAC AGCCAAGTGT GATCCTCTG GGTGGCAGGT 1080

5 CATCAGGAG ACTTGTGTGCT TCTCTGTGCT TGAAGAACTG AACAAAGAATT TCAGTATGAT 1140
 TGTAGGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCTGT CAAAATCTTT CTGTCAATCAT 1200
 TCGGCAAAAC CCATCAACCA CAGTGGGGAA TCTGGCTTCG GTGGTGTGCA TTCTGAGCAA 1260
 TATTTTCATCT CTGTCACTGG CCAGCCATTT CAGGGTGTCC AATTCAACAA TGGAGGATGT 1320
 CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCCACTGGA CAGTCTTACT 1380
 GCGGGAAGAA AAGATGTCGA GCTCAGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT 1440
 GGTGCTCCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCAATTGACT GGAAGGGAT 1500
 TCCAGTGAAC AAAAGCCAA TCAAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCA 1560
 10 AAATACATCT ATTCCATCA GAGGCCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC 1620
 CCTTCCAGAA ACTATTATCA GCATGGCCTC GTTACTCTGT GGAACATTTC TACCCGTTTC 1680
 CAAAATGGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGTTTATTC AAAACTATTC 1740
 CATAAATGAA GTTTTCCTAT TTTTTCCTAA GATAGAGTCA AACCTGAGCC AGCCTCATTTG 1800
 TGTGTTTTGG GATTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA 1860
 AACTCAAGAC ATCGTGAGCT GCCAATGTAC TCACTTGACC TCCTTCTCCA TATTGATGTC 1920
 15 ACCTTTTGTG CCTCTACAA TCCTCCCGT TGTAAAATGG ATCACTATG TGGGACTGGG 1980
 TATCTCCATT GGAAGTCTCA TTTTATGCTT GATCATOGAG GCTTTGTTTT GGAAGCAGAT 2040
 TAAAAAAGC CAAACCTCTC ACACAGCTCG TATTGTCATG GTGAACATAG CCCTGTCCCT 2100
 CTGATTGCT GATGTCGTGT TTATTGTTGG TGCCACAGTG GACACCAAGG TGAACCCCTC 2160
 TGGAGTCTGC ACAGCTGTCT GTTCTTTTAC ACACCTCTTC TACCTCTCTT TGTCTCTCTG 2220
 20 GATGCTCATG CTGGGATCC TGCTGGCTTA CCGGATCATC CTCGTGTGTC ATCACATGGC 2280
 CCAGCATTTG ATGATGGCTG TTGGATTTTG CCTGGGTTAT GGGTGCCTC TCATTATATC 2340
 TGTCAATTAC ATTTGCTGTC CGCAACCTAG CAATACCTAC AAAAGGAAAG ATGTGTTG 2400
 GCTTAACTGG TCCAATGGAA GCAAACTACT CCTGGCTTTT GTTGTCCCTG CACTGGCTAT 2460
 TGTGGCTGTG AACTTGTGTT TGTGCTGTCT AGTCTCTACA AAGCTCTGGA GCGCCACTGT 2520
 25 TGGGGAAGAA CTGAGTCGGG ATGACAAAGC CACCATCATC CGCGTGGGGA AGAGCCTCCT 2580
 CATTCTGACC CCTCTGCTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640
 CCAGAATCTG GCTTGGCATC TTATTTTTCG TTACTCAAT GCATTCCAGG GATTTTAT 2700
 CTTATGCTTT GGAATACTCT TGGACAGTAA GCTGOGACAA CTTCTGTTC ACAAAGTTGTC 2760
 TGCCCTAAGT TCTTGGGAGC AAACAGAAAA GCAAACTCA TCAGATTAT CTGCCAAACC 2820
 30 CAAATTTCA AAGCCTTTCA ACCACTGCA AAACAAAGGC CATTATGCAT TTTCTCATC 2880
 TGGAGATTCC TCCGACAAAC TCATGCTAAC TCAGTTTGTG TCAATGAAT AAGGCAAGGA 2940
 ATCATAAAT CAGAAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000
 AGAAATTATG CTAGATATTC GATCGGGTTT TCTGATTAG GGGTCTGGGA ATAAACAAG 3060
 35 AATGTCTCAG TGGCTTCA

Seq ID NO: 49 Protein sequence:
 Protein Accession #: EOS sequence

40 1 11 21 31 41 51
 MKVGVWLWIS PFTPTDGHGG FLGKNDGIKT KEELIVNKKK HLGPEVEEYQL LLQVTYRDSK 60
 EKRLRLNFKL LLKPPLLWSH GLIRIIRAKA TDCNSLNGV LQCTCEDSYT WFFPSCLDPQ 120
 NCYLHTAGAL PSCECHLNLI SQSVNFCERT KIWGTFKINE RFTNDLNLSS SAIYSKYANG 180
 45 IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSEA SELLSAIBHV AEKAKTALHK 240
 LFPLEDGSPR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
 LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNLISSLSL 360
 ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPTAL 420
 50 PLNFSRKPID WKGIPIVKNKS LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRLSPETII 480
 SMASLTGLNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540
 HLOWNDAGCH LVNETQDIDV CQCTHLTSFS ILMSPFVPST IPFVVKWITY VGLGISIGSL 600
 ILCLIEBALF WKQIKKQSTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPBGVCTAA 660
 VFPTHFYLS LFFWMLMGI LLAYRIILVF HHMAQHLMMA VGFCLGYGCP LIISVITIAV 720
 TQPSNTYKRR DVCWLNWSNG SKPLAFVVP ALAIVAVNPF VVLLVLTCLW RPTVGERLSR 780
 55 DDKATIIRVG KSLILITPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFO GPFFILCFGL 840
 LDSKLRLQLF NKLSALSSWK QTEKGNSSDL SAKPKFSKPF NPLQNKGHYA FSHTGDSNDN 900
 IMLTQFVNSE

60 Seq ID NO: 50 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 63-3224

65 1 11 21 31 41 51
 CAGGAATTGG TGGCGGAGAG GGCAATAAAC TGCGGCTCTC CCGGCGCCCC GATGCTCGCA 60
 CCATGTCGAG GCGCAAGCAG GCGAAACCCC AGCACATCAA CTCGGAGGAG GACCAGGGGG 120
 AGCAGCAGCC GCAGCAGCAG ACCCCGAGT TTGCAGATGC GGCOCACAGG GCGCCCGGG 180
 CGGGGAGCTG GGGTGTCTCA GTGAACCAAC CAGGGAATGA CGAGGTGGCG AGTGAGGATG 240
 AAGCCACAGT AAAGCGGCTT CGTCGGGAGG AGACGCACGT CTGTGAGAAA TGCTGTGCGG 300
 70 AGTTCTTCAG CATCTCTGAG TTCTGTGAAC ATAAGAAAAA TTGCATAAAA AATCCACCTG 360
 TCCTCATCAT GAATGACAGC GAGGGGCTTG TGCTTTCAGA AGACTTCTCC GGAGCTGTAC 420
 TGAGCCACCA GCCCACCAGT CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG 480
 CAGAGGACAT GAAGGAGAAG CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG 540
 CCTTGCCACC CACCCCCAGC GACATAAGCT ATTTAGCCAA AGGCAGAGTG GCCAACACTA 600
 ATGTGACCTT GCAGGCACCTA CCGGACCAAC AGGTGGGGGT GAATCAGCGG AGCGCGGATG 660
 75 CACTCCCTGC CCGGTCCTCT GGTGCCAACA GCATCCCGTG GGTCTCTGAG CAGATCTTGT 720
 GTCTGCAGCA GCAGCAGCTA CAGCAGATCC AGCTCACCAG GCAGATCCCG ATCCAGGTGA 780
 ACATGTGGGC CTCGCCAGCC CTCCTACTCA GCGGGGAGG GGCAGACACT CTGAAGACCT 840
 TGGGCAGCCA CATGTCTCAG CAGGTTTCTG CAGCTGTGGC TTTGCTCAGC CAGAAAGCTG 900

GAAGCCAAGG TCTGTCCTG GATGCCCTGA AACAAAGCCAA GCTACCTCAC GCCAACATCC 960
 CTTCTGCCAC CAGCTCCCTG TCCCCAGGGC TGGCACCCCTT CACTCTGAAG CCGGATGGGA 1020
 CCGGGTGCT CCGGAACGTC ATGTCCCGCC TCCCGAGCGC TTTGCTTCTT CAGGCCCCCG 1080
 5 GTGGGTGCT CTTCCAGAGC CTTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA 1140
 AGGGGAAGCC ACCGAACATC TCCGCGGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT 1200
 ACAAGCAAA GTGTAAGTAC TGTAAGCAAG TTTTGGGAC TGATAGCTCC TTGCAGATCC 1260
 ACCTCCGCTC CCACACTGGA GAGAGACCCCT TCGTGTGCTC TGTCTGTGGT CATCGCTTCA 1320
 CCACCAAGGG CAACCTCAAG GTGCACCTTC ACCGACATCC CCAGGTGAAG GCAAAACCCC 1380
 10 AGCTGTTTGC CGAGTTCAG GACAAAGTGG CGGCCGCA TGGCATCCCC TATGCACTCT 1440
 CTGTACTTGA CCCCATAGAT GAACCGAGTC TTTCTTTAGA CAGCAAACCT GTCCTTGTA 1500
 CCACCTCTGT AGGCTACCT CAGAATCTTT CTTCGGGAC TAATCCCAAG GACCTCACGG 1560
 GTGGCTCCTT GCCCGTGAC CTGCAGCCTG GGCCTTCTCC AGAAAGTGAG GGTGGACCCA 1620
 CACTCCCTGG GGTGGGACCA AACTATAATT CCCCAGGGC TGGTGGCTTC CAAGGGAGTG 1680
 GGACCCCTGA GCCAGGCTCA GAGACCTTGA AATTGCAGCA GTTGGTGGAG AACATTGACA 1740
 15 AGGCCACAC TGATCCCAAC GAATGTCTCA TTTGCCACCG AGTCTTAAGC TGTGAGAGCT 1800
 CCCTCAAGAT GCATTATCGC ACCCAACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG 1860
 GCGGAGCCTT TTCTACCAA GGTAAACCTGA AGACACACCT TGGGGTTCAC CGAACCAACA 1920
 CATCCATTAA GAGCAGCAT TCGTGCCCA TCTGCCAGAA GAAGTTCAT AATGCCGTGA 1980
 20 TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTACAGT TCCCAACAG CCCCTGCCAG 2040
 AGAATCCCTG TGACTTTAGC GGTTCAGAG CAATGACCGT GGGTGAGAAC GGCAGCACCG 2100
 GCGCTACTG CCATGATGAT GTCATCGAAA GCATCGATGT AGAGGAAGTC AGCTCCACGG 2160
 AGGCTCCAG CAGCTCTCC AAGGTCCCA CCGCTTCTCC CAGCATCCAC TCGGCATCAC 2220
 CCACGCTAGG GTTGGCATG ATGGCTTCT TAGATGCCCC AGGGAAGTG GGTCTGCCCC 2280
 25 CTTTAACTT GCAGCGCCAG GGCAGCAGAG AAAACGTTT CGTGGAGAGC GATGGCTTGA 2340
 CCAACGACTC ATCTCGCTG ATGGGAGACC AGGAGTATCA GAGCCGAAGC CCAGATATCC 2400
 TGAAGACCA ATCTCTCCAG GCATCTCCCC CGGCCAATAG TCAAGCCGAA AGCATCAAGT 2460
 CAAAGTCTCC GATGCTGGG AGCAAAGCAG AGAGTCCGA GAACAGCCGC ACTGAGATGG 2520
 AAGTTCGAG CAGTCTCCCT TCCACGTTA TCCGAGCCCC GCGCACTAT GTCAAGGTTG 2580
 30 AAGTTCCTGG CACATTTGTG GGACCTCGA CATTTGCTCC AGGGATGACC CCTTTGTTAG 2640
 CAGCCAGCC ACGCCAGAC GCCAAGCAAC ATGGCTGCAC ACGGTGTGGG AAGAACTTCT 2700
 CGTCTGCTAG CGCTCTTCA ATCCACGAGC GGACTCACAC TGGAGAGAAG CCTTTTGTGT 2760
 GCAACATTTG TGGCGAGCT TTTACCAACA AAGGCAACTT AAAGGTTTAC TACATGACAC 2820
 ACGGGCGAA CAATAACTCA GCCCGCCGTG GAAGGAAGTT GGCCATCGAG AACACCATGG 2880
 35 CTCTGTTAGG TACGGACGGA AAAAGAGTCT CAGAAATCTT TCCCAAGGAA ATCCTGGCCC 2940
 CTTCAAGTAA TGTGGACCTT GTTGTGTGGA ACCAGTACAC CAGCATGCTC AATGGCGGTC 3000
 TGGCGGTAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGGTCTCT ACCCTCCCGG 3060
 TTTCTTGGG GGCACCTCC GTTGTGAATA ACGCACTGT CTCCAAGATG GATGGCTCCC 3120
 AGTCGGGTAT CAGTGCAGAT GTGAAAAAC CAAGTGCTAC TGACGGCGTT CCAAAACACC 3180
 40 AGTTTCTCTA CTCTCTGAA GAAAACAAGA TTGCGGTGAG CTAAGGAGAG ACTTGGCTGG 3240
 AAGGAGCAAT GAGACACAG TGAATCTCT AGAATCTGCT TTGTTTGTGA AGAACTCATC 3300
 TCTCTGTTT TCTTTTCT TACTGATATG CAAATGATGT TTACTACGTT GGTGTGAC 3360
 ACAACCTCAG GCAAGTGCTA CAATCAGAT GTTGTCTATG CTGCTTTGCA AAAAGTTG

Seq ID NO: 51 Protein sequence:
 Protein Accession #: NP_065169.1

1 11 21 31 41 51
 MSRRKQAKPQ HINSEEDQGE QFPQQQTPEF ADAAPAAPAA GELGAPVNPV GNDEVASEDE 60
 50 ATVKRLRREE THVCEKCAAE FFSISEFLEH KKNCTKNPPV LIMNDESEPV PSEDFSGAVL 120
 SHOPTSPGSK DCHRENGGSS EDMKEKPDAA SVVYLKTETA LPPTPDISY LAKGKVANT 180
 VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQLQQIQI LTEQIRIQVN 240
 MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP 300
 55 SATSSLSPLG APFTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK 360
 GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSLSLIH LRSHTGERPF VCSVCGHRFT 420
 TKGNLKVHFE RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSKPLVLT 480
 TSVGLPQNLN SGTNPKDLTG GSLPGDLQPG PSPSEGGPT LPGVGNPNYS PRAGGFQSGG 540
 60 TPEPGSETLK LQQLVENIDK ATTDPNELCI CHRVLSCQSS LQMHYRTHTG ERPFQCKICG 600
 RAFSTGNLTK THLGVHRTNT SIKTQHSCTP CQKKFTNAVY LQQHIRMHMG GQIPNTPLPE 660
 NPCTFTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP 720
 TLGFAMMASL DAPGKVGAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL 780
 65 ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPTPI RAPPTYVKVE 840
 VPGTFVGPST LSPGMTPLLA AQPRRQAKQH GCTRCGNFNS SASALQIHER THTGKPFVVC 900
 NICGRAFTTK GNLVKHYMTH GANNNSARRG RKLAIENYMA LLGTGDKRVS EIFFKEILAP 960
 SVNVDPVVWN QYTSMLNGLL AVKTNEISVI QSGGVPTLPV SLGATSVVNN ATVKMDGSGQ 1020
 SGISADVEKP SATDGVPKHQ FPHFLEENKI AVS

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCTAGCATTA AAGGAAGAAA CCCCCTCTTG CAACGAAGGC CTCAAAGAGG TCCAAATATC 60
 70 AACTTGCGA CATAACAAGC AGAGTGTTC TAACTGCTC TAAGAAAGA AAGTTAAAC 120
 TCTGTGAGTT GAAGGCACAC ATCACAAGT AGTTTCTGAG AATGATTCTG TCTAGTTTTT 180
 75 ATTTGAAGAT ATTTCTCTTT CTACTGTGAG CATCAATCG CTTGAAATCT CCACCTTGCAA 240
 ATTCCACAAA AAGAGTGTTT CAAATCTGCT CTGTGTAAAG GGACGTTCCA CTCTGTGAGT 300
 TGAATACACA CAACACAAGG AAGTTACTGA GAATCTCTCT GTCTAGCATG ATATGAAGAA 360

ATCCCGTTTC CAACGAAGGC CTCAATGAGG TCTATATATC CACTTGCAGA CTTTACAAAC 420
AGAGTGTTC CTAAGTCTCT TATGAAAAGA AAGGTTAAAC TCTGTGGAGT TGAACGCACA 480
CATCACAAAA GGAGTTTCTG AGAATCATTC TGCTAGTTT TTTTAGGAAG ATATTTCCTT 540
TTCTACCGTT GACTTCAAAG CGGCTGAAAT

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_001910.1
Coding sequence: 50..1240

1 11 21 31 41 51
GGAGAGAAGA AAGGAGGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACA TGAACACGCT 60
CCTTCTTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CAAGGATCCC TTCACAGGGT 120
GCCCCACAG AGGCATCCGT CCCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA 180
15 GTTCTGAAA TCCATAATT TGGACATGAT CCAGTTCACC GAGTCTGTCT CAATGGACCA 240
GAGTGCCAAAG GAACCCCTCA TCAACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT 300
TGGCTCCCCA CCACAGAACT TCACTGTCTT CTTGACACT GGCTCTCTCA ACCTCTGGGT 360
CCCTCTGTGT TACTGCACCT GCCAGCCTG CAAGACGCAC AGCAGGTTCC AGCCTTCCCA 420
GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGAGCTT 480
20 GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGCA CTACCGTGG TTGGCCAGCA 540
GTTTGAGAAA AGTGTACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600
TCTGGGCGCTG GGATACCCCT CTTGGCTGTG GGGAGGAGTG ACTCCAGTAT TTGACAACT 660
GATGGCTCAG AACCTGGTGG ACTTGGCGAT GTTTCTGTCT TACATGAGCA GTAAACCCAGA 720
AGGTGTGTGG GGGAGCGAGC TGATTTTGG AGGCTAOCAC CACTCCCAT TCTCTGGGAG 780
25 CCTGAATTGG GTCCAGTCA CCAAGCAAGC TTAAGTGCAG ATTGCACTGG ATACATCCA 840
GGTGGGAGGC ACTGTTATGT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC 900
TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAACGCCCA TTGGGGCAGC 960
CCCGTGGAT GAGAAATATG CTGTGGAGTG TGCCAACTT AACCTCATGC CGGATGTCTAC 1020
CTTCACATT AACGAGTCC CTTATACCT CAGCCCAACT GCCTACACCC TACTGGACTT 1080
30 CGTGGATGGA ATGCACTTCT GCAGCAGTGG CTTTCAAGGA CTTGACATCC ACCCTCCAGC 1140
TGGGCCCTCT TGGATCCTGG GGGATGTCTT CATTCGACAG TTTTACTCAG TCTTTGACCG 1200
TGGGAATAAC CGTGTGGGAC TGGCCCCAGC AGTCCCTTAA GGAGGGGCGT TGTGTCTGTG 1260
CCTGCTGTCT TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTACA CCTACAAAAA 1320
35 GTTATTTTCT AGAGAATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1380
ACATGAGAAT ACACACACAC ACACACATAT ACACACACAC ACACCTTACA CATACACACC 1440
ACTCCACCA CCGTCATGAT GGAGGAATTA CGTTATACAT TCAATTTTGT TATTGATTTT 1500
TGATTATGAA AATCAAAAAT TTTACATTG GATTATGAAA ATCTCCAAAC ATATGCACAA 1560
GCAGAGATCA TGGTATAATA AATCCCTTTG CAACTCCACT CAGCCCTGAC AACCCATCCA 1620
40 CACACCGCCA GCGCTGTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT 1680
GTACCTGGAT CATTCTGAAG CAAATTCGGA GCATTACATC ATTTGTGTTA TAAATATTTT 1740
TAACATCCTT AAATATACAA TCGGAATTCA AGCATCTCCC ATTTGCCAC AAATGTTTGG 1800
CTGTTTTTGT AGTTGGATTG TTTGTATTAG GATTCAAGCA AGGCCATAT ATTGCATTTA 1860
TTTGAATGT CTGTAGTCT CTTTCCATCT ACAGAGTTTA GCACATTGA ACGTTGTCTG 1920
45 TTGAATCCC GAGGTGTCT TGTACATGGT TCTCTGAACT TATCTTCTCT ATAAAAAGGT 1980
AGTTAGATCT GGAGGTCTGA TTTTGTGGCA AAAAATCTTC CTAGGTGGTG CTGGGTACTT 2040
CTTGTTCAT CCTGTACAGA GGCAGATAAT GCTGGTGCTT CTCTATTGTT AATGTTAAGA 2100
CTGCTGGGTG GGTTTGAGT TCTTGGCTTT AATCATTCAT TACAAAGTTC AGCATTTT

Seq ID NO: 54 Protein Sequence
Protein Accession #: NP_001901.1

1 11 21 31 41 51
MKTLILLLLV LLELGEAQGS LHRVPLRRHP SLKKKLRRAS QLSEFWKSHN LDMIQFTESC 60
55 SMDQSAKEPL INYLDMEYFG TISIGSPPQN PTVIFDTGSS NLWVPSVYCT SPACKTHSRF 120
QPSQSSTYSQ PQSPFSIQYG TGSLSGIIGA DQVSVEGLTV VQQPGESVT EPCQTFFVDAE 180
FDGILGLGYP SLAVGGVTPV FDNMMAQNLV DLPMPFSVYMS SNPEGGAGSE LIPGGYDHS 240
FSGSLNWVFP TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSITGP SDKIKQLQNA 300
60 IGAAFPVDGEY AVECANLNVN PDVTFPTINGV PYTLSPATY TLLDFVDGMQF CSSGFGQLDI 360
HPPAGPLNLL GDVPIRQFYS VFDRGNRRVG LAPAVP

Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

1 11 21 31 41 51
TACGCGCTGC GGGACCGGCA GGGGAACGCC ATCGGGGTCA CAGCCTGCGA CATCGACGGG 60
70 GACGGCCGGG AGGAGATCTA CTTCTCAAC ACCAATAATG CTTCTCGGG GGTGGCCACG 120
TACACGACA AGTTGTTCAA GTTCCGCAAT AACCGTGGG AAGACATCCT GAGCGATGAG 180
GTCAACGTGG CCGTGTGTGT GGGCAGCCTT TTTGCCGGAC GCTCTGTGCG CTGTGTGGAC 240
AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCCTACG TAATGTGGGC 300
CCTGATGCCCT TCAATGAAAT GGACCTGAG GCCAGTGACC TCTCCCGGG CATTTCTGGC 360
75 CTCAGAGATG TGGCTGCTGA GGCTGGGGTC AGCAATATA CAGGGGGCGG AGGCGTCAGC 420
GTGGGCCCA TCTCAGCAG CAGTGCTCG GATATCTTCT GCGACAATGA GAATGGGCCT 480
AACTTCTTTC TCACAAACCG GGGCGATGGC ACCTTTGTGG ACGCTGCGGC CAGTGTGGT 540
GTGGAGCACC CCACACAGCA TGGGCGAGGT GTCGCCCTG CTGACTTCAA CCGTATGGC 600
AAAGTGACA TCGTCTATGG CAACTGGAAT GGCCCCACC GCCTCTATCT GCAATGAGC 660

5
10
15
20
25

```

ACCCATGGGA AGGTCGGCT CCGGACATC GCCTACCCA AGTTCTCCAT GCCCTCCCCT 720
GTCCGACCGG TCATCACCAG CGACTTTGAC AATGACCAGG AGCTGGAGAT CTCTCTCAAC 780
AACATTGCGCT ACCGCGAGTC CTCAGCCAAC CGCCTCTTCC GCGTCATCCG TAGAGAGCAC 840
GGAGACCCCC TCATCGAGGA GCTCAATCCC GGCGACGCTT TGGAGCCTGA GGGCCGGGGC 900
ACAGGGGGTG TGGTGACCGA CTTCGACGGA GACGGGATGC TGGACCTCAT CTGTGCCCAT 960
GGAGAGTCCA TGGCTCAGCC GCTGTCCGTC TTCCGGGGCA ATCAGGGCTT CAACAACAAC 1020
TGGCTGCGAG TGGTGCCAGG CACCCGGGTT GGGGCCCTTT CCAGGGGAGC TAAGTCCGTG 1080
CTCTACACCA AGAAGAGTGG GGGCCACCTG AGGATCATCG ACGGGGGCTC AGGCTACCTG 1140
TGTGAGATGG AGCCCGTGGC ACACCTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG 1200
GTGACGTGGC CAGATGCGAA GATGCTGAGC CGGAACGTGG CCAGCGGGGA GATGAACTCA 1260
GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
ACACCTATGG AAGCTACAGG TGCCGAGCCA ACAAGAAGTG CAGTCGGGGC TAGGAGCCCA 1440
ACGAGGATGG AGCCCGTGGC TTGGGGACTC TCGGCCAGTC ACCGGGGCCC CGCCCCACCA 1500
CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
CACCGGTCCT CGTAGATGGA GATCTCAATC TGGGTCGCT GGTAAAGGAG AGCTGCGAGC 1620
CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCCCT 1740
CCCAAGCCCA TCCATGCACA TTACTTAGCT AACAAATAGG GAGACTCGTA AGGCCAGGCC 1800
CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCGAGGGA GGTGTGTGTA 1920
CTGCACAGGA AGTATGAGGA CTTTAGTGTG CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTAGC CATCCATTAT CGCATCTGCA 2040
AAATGGGGAT TAAGAAATGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
GACACTTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAACAAGT GCCTCTCACT 2160
GGGCTTTGTC AACACGTG

```

Seq ID NO: 56 Protein Sequence
Protein Accession #: NP_060528.1

30
35
40

```

1 11 21 31 41 51
MDPEASDLR GILALRDVAA EAGVSKYTG RGVSVGPILS SSASDIFCDN ENGNFLFHN 60
RDGTFVDAAS ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
FRDIASPKFS MPSPVRVIT ADFDNDQELE IFNNIAYRS SSANRLFRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQ FNNNWLVRVP 240
RTRVGAFARG AKVLYTKKS GAHLRIIDGG SGYLCEMEPV AHFGLKDEA SSVEVTWPDG 300
KWSRNVASG EMNSVLEILY PRDEDTLQDP APLETFMNAS SSHSCALET PVSSTPMET 360
GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPFPPLLL PLPLLLPLLE LPLLRHRS

```

Seq ID NO: 57 DNA sequence
Nucleic Acid Accession #: AJ279016.1
Coding sequence: 1..1962

45
50
55
60
65
70
75

```

1 11 21 31 41 51
ATGTCACAGGA TGTATACCGT CCTGCTGCTG CTCTGGTTTC TGCCCATCAC TGAGGGGTCC 60
CAGCGGGCTG AACCCATGTT CACTGCAGTC ACCAACTCAG TTCTGCCTCC TGACATATGAC 120
AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
CAGAAGCGGC TGGTGAACAT CGCGGTGATG GAGCGCAGCT CACCCTACTA CGCGCTCGCG 300
GACCGGCAGG GGAACGCCAT CGGGGTCAAC GCCTGCAGCA TCGACGGGGA CGGCCGGGAG 360
GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420
TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
CGTGGTGTGG CCAGCCTCTT TGCCGAGCGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
GGACGCTACT CTATCTACAT TGCCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600
ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
GCTGCTGAGG CTGGGTGAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
CTCAGCAGCA GTGCTCGGCA TATCTCTGCG GACAATGAGA ATGGGCTTAA CTTCCTTTTC 780
CACAAACGGG GCGATGGCAG CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGAACGACCC 840
CACCAGCATG GCGGAGGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
GTCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCTGT CCGCACGGTC 1020
ATCACCGCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCCTAC 1080
CGCAGCTCCT CAGCCAACCG CCTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140
ATCGAGGAGC TCAATCCCGG CGACGCTTG GAGCCTGAGG GCCGGGGCAC AGGGGTGTG 1200
GTGACCGCAT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
GCTCAGCGCG TGTCCGCTCT CGGGGCAAT CAGGGCTTCA ACAACAACCT GCTGCGAGTG 1320
GTGCCACGCA CCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTGCTGCT CTACACCAAG 1380
AAGAGTGGGG CCCACTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
CCCGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
GATGGCAAGA TGGTGAAGCG GAACGTGGCC AGCGGGGAGA TGAATCTCAG TCTGGAGATC 1560
CTCTACCCCC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620
TTCTCCGAGC AGGAAAATGG CCATTGCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGTACAG GTGCGGAGC 1740
AACAGAAGT GCAATCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800
CTCGGCCAGT CACCGGGGCC CCGCCCCACC ACCCCACCG CTGCTGCTGC CACTGCCGCT 1860
GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920

```

5 CTGGGGTGGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT 2040
 AGGGATGTAA AGGCGCTGGG GCTAGACCCCT CCCAAGCCC ATCCATGCAC ATTACTTAGC 2100
 TAACATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCAGTG GGTCTAATGA CCATATCTTA 2220
 GGACACAGAT GTGCCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACITTAGTGT 2280
 CCTGAGTTCA AATCCTGATT CAGGAACCTCA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
 AACTTGTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400
 10 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
 AAAGGCTCAA TAAAAACAAG TGCCTCTCAC TGGGCTTTGT CAACAGC

Seq ID NO: 58 Protein Sequence
 Protein Accession #: CAC08451.1

15 1 11 21 31 41 51
 MSRLPFLLL LWFLPITEGS QRAEPMFTAV TNSVLPPDYD SNPTQLNYGV AVTDVDHGD 60
 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 20 BIYPLANTNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180
 GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNPFLF HNRGDGTFVD AAASAGVDDP HQHGRGVVALA DFNRDGKVDI 300
 VYGNWNGPHR LYLQMSHKG VRFRDIASPK FSMPSPVRTV ITADFDNDQE LEIPFNNIAY 360
 RSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTFDGDGML DLILSHGESM 420
 25 AQPLSVFRGN QGFNNWLRV VPRTRFGAFA RGAKVLYTK KSGAHLRIID GSGGYLCME 480
 PVAHFLGKD EASSVEVTWP DGKMSVRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQGENGHRM DTNECIQFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
 LGQSPGPRPT TPTAAAAATA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

30 Seq ID NO: 59 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

35 1 11 21 31 41 51
 ATGGCGTGTG CGGGAGGACT CCCAGCCCCT TGCTCTGGTT GGATGGGACT GGGTGGGCCC 60
 AGCGGCTCCT CCCAGCATC CCTCCCAT TCCTCTCCA GGTACAATGG ACCCAACCTG 120
 GTTCTGAAGT ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGTGA TGAGCGCAGC 180
 TCACCTACT ACGCGCTCGG GGACCGGCG GGGAAACGCA TCGGGTGCAC AGCCTGCGAC 240
 40 ATGACCGGGG ACGGCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTTCTCGGGC 300
 CACAGCAGCT CAGCGCAGGT CCTCTCTGGG CTCCACAGAA ACAGGCTGT GCTGAAGCCT 360
 CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC 420
 TCTCCCTGG GTCCAGGCTTC TCCGACAGC AGGCAGGGAG AGAGGCTGCC GGTTCCTGTC 480
 TGTCCGGGTG GACTGAGACC TACCATGAA CCAGAACCAT TTCTCTGAG ACCCAATCA 540
 45 GGGGTGGCCA CGTACACGA CAAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAAGCT GGCCCGTGGT GTGGCCAGCC TCTTTGCGG AGCTCTGTG 660
 GCCTGTGTGG ACAGAAAGGG CTCTGAGCGC TACTCTATCT ACATTGCCAA TTACGCTTAC 720
 GGTAATGTGG GCCCTGATGC CCTCATTGAA ATGGACCTG AGGCCAGTGA CCTCTCCCG 780
 GGCATTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAATA TACAGAAAGC 840
 50 TTCTCCCACT CTGCCTCTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
 GGAGGAGACC CAGAGAGGCG AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACCTG 960
 TGCCCGCTGG GCTGGAAGGA CGGCGAGTTC AAGGAAGAAG CAGCAGCTT GGTGAGGAA 1020
 CAGAGGGAGG CTGGGGCAGC TGGCGTGCCC AGAGGACGTG TTGGAACAGC TCTGAGACT 1080
 TCCAAAGCC ATTTGGCTGA CAAGAACCTA TTTGGCCAC CATGTTACTA TTCTGTCTGC 1140
 55 GCGCTTCTC CAGCCACCC TTTCCCTGCC CGCCAAGCCC CCCAACACTA CCCTGTAGCC 1200
 CCCCCTGTCA CTCAGCTAAT GACACATGGA GGTCTGGCTG GAAACTAGC CCGGAGTGT 1260
 CCGCACCCCG GAGCCCCAGG AATGGACCCC AAATGTAAGG GCCGCCATGC TGAGCCCGGC 1320
 CTGATGGCTG AGGCTTTGGG CGCGTGGCCA GCGCTCAGCA CCACTGTGGT GCCAGGGGGC 1380
 CTGAGAAGCT GGGAGGAAG CAGGCAGAGG GGGCAGGCCA TGTCCAGATG TGCACTCAGG 1440
 60 GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCACCTGC CTGCTAGAGA GCTGTATGAC 1500
 CTGGGAGAAC CTCCATTITT ACAAGAACA GACGAGATC CAGGGAGGAG AAGGGACTCG 1560
 CCCAAGGTCA CACAGGAGTG CCATCTAGTG GCCACCATGC CAGCTCTCGG GGGACTCGAG 1620
 GGCCCCGGGA GGGTGGCCAA GCGAGAGATT GGGAGAGAGA CTGGGGCAGT AGGAAGACCA 1680
 65 CTCTCCATC CCCTGTGCCC CAACTTCCCC AGCTGCTTGA GGCCTCTTGA AGCCGGGACA 1740
 GTGCCGGGAG CTGCCCTGCC TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAGGCC 1800
 CTGGCGTGA ACCAGATGGA AAAAGAGGAG GGGAGATTG ATGGAGACCA TGAGCCGAGA 1860
 TTTAGGCTCA GGAAGACAG GGAAGCAGAA TTCCCCCAG GCTCCTCTGA GGAGCCTCTG 1920
 CTGCAGTTCC CTTCAAGCCT CAGAGGCAGC CCTGTCTTCC AGGTGGGCTT GGGGCTTGCT 1980
 TCTGCCATC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC 2040
 70 ATCTCAGCA GCAGTGCCCT GATATCTTTC TGCGACAATG AGAATGGGCC TAACTTCCTT 2100
 TTCCACAACC GGGGCGATGG CACTTTGTG GACGCTGCGG CCAGTGTCTGA ACGTGTGTTA 2160
 GCTTCATCG TTCACCTCAA ATATCACCTC TGCAGAGATT TTCTTCACTC CTTGTGCCAC 2220
 CTAGCAGAAA CTGGTCTCTC CTCTCTCTGC TGCCCGTGGC ATGCACGTCT TCTTCAGGCT 2280
 CCACATGGCC ATCATGTTT GTCTATGAGC TTTACAAGGA CCGGTCACG GTTCTATTCA 2340
 75 TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT 2400
 CAGGGGGCCC CACCTGCTCT TCTGGCAAGA GCTCCCTGTG TCTGGGGTCT TCTGATCCCC 2460
 ACTGCTATT ACATTGTCTT GTGGTCTGCC ATCCAGAGA GCCTGATGAC CCACAGCTAT 2520
 TTGTCTCTG AAAGAGTCAA CGTGGGTGTG GACGACCCC ACCAGCATGG GCGAGGTGTC 2580
 GCCCTGCTG ACTTCAACCG TGATGGCAAA GTGACATCG TCTATGGCAA CTGGAATGGC 2640

5
 10
 15
 20
 25
 30
 35

```

CCCCACCGCC TCTATCTGCA AATGAGCACC CATGGGAAGG TCCGCTTCCG GGACATCGCC 2700
TCACCCAAGT TCTCCATGCC CTCCTCTGTC CGCACGGTCA TCACCGCGGA CTTTGACAAT 2760
GACCAAGGAGC TGGAGATCTT CTTCACAAC ATTGCCTACC GCAGCTCCTC AGCCAAACGC 2820
CTCTTCCGAT GTCCATCCT GGCTCGTGGC TCTTCATCCT TGACAGCTGG TGGGAGGAAC 2880
GGTCAGGGAG AAGGTTTAAG AATCAGAAGG GGAGGGTTCC CAGGGCCAGG GGGTCAGGCC 2940
AAGGTCAACA CAGGTCCCTT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGACTGGGCA 3000
AGAGGCTGTG GGAATGACAG GCAAAGCCTG GCCAAGGAGC CGGCTCTGTC TATTGCAGGG 3060
AAAGGGGAAG GAAATGTGGC CCAAGTGTGT CCCAGAACCC AAGCGCCACA AGATACAAAG 3120
CCACACTACC ACAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG 3180
GTCCAATCAC TACCAAGAAA AGGGGCTACG GGGTCCAATC ACTACCAGGA AAAGGGGCTA 3240
CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC AATCACTACC AGGAAAAGGG 3300
GCTACGGGCT CCAATCACTA CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA 3360
AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA CAGGGTCCAA TCACTACCAC 3420
AGAAAGGGGC TACGGGCTCC AATCACTACC AGGAAAAGGG GCTACGGGGT CCAATCACTA 3480
CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC 3540
ACTACCAGGA AAAGGGGCTA CGGGTCCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC 3600
AATCACTACC AGGAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACAGG 3660
GTCCAATCAC TACCAGGAAA AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA 3720
CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGCTCC AATCACTACC AGGAAAAGGG 3780
GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA 3840
AGGGGCTATG GGGTCCAATC ACTACCAGAG AAAGGGGCTA CGGGGTCCAA CGTCATCCGT 3900
AGAGAGCACG AGGACCCCTT CATCGAGGAG CTCAATCCCG GCGACGCTTT GGAGCTGAG 3960
GGCCGGGCGA CAGGGGGTGT GGTGACCGAC TTCAGCGGAG ACGGGATGCT GGACCTCATC 4020
TTGTCCCATG GAGAGTCGAT GGCTCAGCCG CTGTCCGTCT TCCGGGGCAA TCAGGGCTTC 4080
AACACAACCT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT 4140
AAGGTCTGTC TCTACACCAA GAAGAGTGGG GCCCACCTGA GGATCATCGA CGGGGGCTCA 4200
GGCTACTGTT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGGAAGGA TGAAGCCAGG 4260
AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG 4320
ATGAACCTAG TGCTGGAGAT CCTCTACCCC CGGATGAGG ACACACTTCA GGACCCAGCC 4380
CCACTGGAGT GTGGCCAAAG ATTCTCCCAG CAGGAAAATG GCCATTGCAT GGACCCAAT 4440
GAATGCATCC AGTTCCCAAT CGTGTCCTCT CGAGACAAGC CCGTATGTGT CAACACCTAT 4500
GGAAGCTACA GTGGCCCGGAC CAACAAGAAG TGCAGTCCGG GCTACGAGCC CAACGAGGAT 4560
GGCAGAGCCT GGTGTGGTAC TGAGCTAGGC TTAGGCATA CAATGACGTG GAAACCAAGG 4620
CCCAAAAGG AGCTGCAACT TTCCAAGGC ATCTGCACCC CGCTCTGGTC CTTTTCTCTG 4680
CCGGGTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCAG CACCCTTCTC 4740
CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA
  
```

40
 Seq ID NO: 60 Protein Sequence
 Protein Accession #: FGENESH

45
 50
 55
 60
 65
 70

```

1      11      21      31      41      51
|      |      |      |      |      |
MACPGGLPAR CSGWMGLGPF SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
SPYYALRDRQ GNAIGVTACD IDGDGRBEEY FLNTNNAPSG HSSSAQVPSG LHRNRPVLKP 120
PPTTPAGLLG LPPLSGRDFP SSLGQASPDG RQGERVFPVC CRGGLRPTHE PEPFLLRPKS 180
GVATYTDKLF KFRNRRWEDI LSDEVNVARG VASLFAGRSV ACVDRKSGSR YSIYIANYAY 240
GNVGPDALIE MDPBASDLGR GILALRDVAA EAGVSKYTEG PSHTASPSIG BISGRTEERE 300
GGDPEADEEE HSGDGSTSQL CRLGWKDGQF KEAAAALVEE QREAGAAGVP RGRVRTALQT 360
SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV 420
PHPRAPGMDP KCKGRHAEPG LMAEALQAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR 480
ELGGPWQSAT QHLPARELYD LGEPPILQRT DGDPPRRRDS PKVTQECHLV ATMPALGGLL 540
GPGRVAKREI GRETAGVGRP LSHPLVFNFP SCLRPLEAGT VPGAALPGNP GNVWLDMAKA 600
LAWNQMEKEE KIHGDHEPR FRLRKAREAE FPPGSSEEP LQFPSGLRGS FVLQVGLGLA 660
SATHCGSMSP LGGRGVSVGP ILSSASDIP CDNENGPNFL FHNRGDGTFF DAAASAERRL 720
AFIVHLKYHL CRDPFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
FLTQGLASSA HRTLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
LSSERVNVGV DDPHQHGRGV ALADPNRDGK VDIVYGNWNG PHRLYLQMTS HGKVRFRDIA 900
SPKFSMPSPV RTVITADFDN DQELBIFPNV IAYRSSANR LFRCSILARG SSSLTAGGRN 960
QGQEGLRIRR GGFPGPGQA KVTGPLMKK QKGRKDEDAW RCGGNAGQSL AKEPASAIAG 1020
KKGKGNVAQSV PRTPAQDQTK PHYHKGLQGG PITTRKRGYV VQSLPGKGAT GSNHYQEKGL 1080
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140
RKGLRAPITT RRGVGVQSLP PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS 1200
NHYQEKGLQG PITTRKRGYR VQSLPQKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPQ KGATGSNVIR REHGDPLIEE LNPQDALEPE 1320
GRGTGGVVTG FDGDMGLDLI LSHGESMAQP LSVFRGNQGP NNNWLRVVPF TRFGAFARGA 1380
KVVLTYTKSG AHLRIIDGGS GYLCEMEFVA HFGLGKDEAS SVEVTWPDGK MVSRRNVASGE 1440
MNSVLEILYP RDEDTLQDPA PLECGQGFSG QENGHCMDTN ECIQFPFVCP RDKPVCVNTY 1500
GSYRCRTNKK CSRGVEPNED GTACVGTBLG SRHTMTWKPR PKKELQLSQG ICTPFWVSFFL 1560
PGCRLLLKRA QLQAAPSTLL QKAPGPEAQ VYEQDQE
  
```

75
 Seq ID NO: 61 DNA sequence
 Nucleic Acid Accession #: NM_000584.1
 Coding sequence: 75..374

```

1      11      21      31      41      51
|      |      |      |      |      |
AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GGAACCATCT 60
  
```

5 CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATTT 120
 CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAACTT AGATGTCACT 180
 GCATAAAGAC ATACTCCAAA CCTTCCACC CCAAAATTAT CAAAGAACTG AGAGTGATTG 240
 AGAGTGGACC ACACCTGCGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300
 TCTGTCTGGA CCCCAGGAA AACTGGGTGC AGAGGGTTGT GGAGAAAGTT TTGAAGAGGG 360
 CTGAGAAATC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420
 GAAACTTCAA GCAAACTCTAC TTCAACACT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480
 CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT 540
 CATTGTACCA TGAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600
 CAAAAAACAA CAAATAATTT TTAATATAA GGATTTCCT AGATATTGCA CGGGAGAATA 660
 TACAAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACCTTAAT TTCAGGAATT 720
 GAATGGGTTT GCTAGATGT GATATTTGAA GCATCACATA AAAATGATGG GACAATAAAT 780
 TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTAA ATCTGGCAAC 840
 CCTAGTCTGC TAGCCAAGAT CCACAAGTCC TTGTCCACT GTGCTTGGT TTTCTCTTA 900
 15 TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTACCTCAC AGTGATGTG TGAGGACATG 960
 TGGAAAGCACT TTAAGTTTTT TCATCATAAC ATAAATTATT TTCAAGTGA ACTTATTAAC 1020
 CTATTTATTA TTTATGTATT TATTTAAGCA TCAAAATATT GTGCAAGAAT TTGGAATAAT 1080
 AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTTA 1140
 GATATTAATAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTATGATT AAACAAAGAA 1200
 20 ACAATTGGGT ACCCAGTTAA ATTTTCATT CAGATAAACA ACAATAAATT TTTTAGTATA 1260
 AGTACATTAT TGTATTCTG AAGTTTTTAA TTGAACAAAC AATCCTAGTT TGATACTCCC 1320
 AGTCTTGTCA TTGCCAGCTG TGTGTGTAGT GCTGTGTGTA ATTACGGAAT AATGAGTTAG 1380
 AACTATTAAA ACAGCCAAAA CTCACAGTGC AATATTAGTA ATTTCTGTCT GGTGAAACT 1440
 TGTATTATAT GTACAAATAG ATTTCTTATA TATTATTAAA ATGACTGCAT TTTTAAATAC 1500
 25 AAGGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTACTGT 1560
 TTCTGATTGT ATGGAAATAT AAAAGTAAAT ATGAAACATT TAAATATAA TTTGTGTCA 1620
 AAGTAAAAAA AAAAAAAA

30 Seq ID NO: 62 Protein Sequence
 Protein Accession #: NP_000575.1

35 1 11 21 31 41 51
 MTSKLAVALL AAFLLISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKPIK ELRVIESGPH 60
 CANTEIIVKL SDGRELCIDP KENWVQRVVE KFLKRAENS

40 Seq ID NO: 63 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 52-1146

45 1 11 21 31 41 51
 GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60
 CAAGTGGTCA TCTTAAGCCT CATCCTACAT CTGGCAGATT CTGTAGCTGG TTCGTAAAG 120
 GTTGTGGGAG AGGCAGGTCC ATCTGTCACT CTACCTGCC ACTACAGTGG AGCTGTCACT 180
 TCCATGTGCT GGAATAGAGC CTCATGTTCT CTATTACATAT GCCAAATGAG CATTTGCTGG 240
 ACCAATGGAA CCCACGTGAC CTATCGGAAG GACACAGCT ATAGCTATT GGGGGACCTT 300
 TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT 360
 TGTGTCCGCT TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG 420
 50 ATTGTGCCAC CCAAGGTAC GACTACTCCA ATTGTCAACA CTGTTCCAAC CGTCACGACT 480
 GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTT CAATGACGAC TGTTCACAG 540
 ACAACTGTTT CAACAACAT GAGCAATCCA ACGACAAAGA CTGTTCTGAC GACAATGACT 600
 GTTTCAACGA CAACGAGCGT TCCAACGACA ACGAGCATTC CAACAACAC AAGTGTTCCT 660
 GTGACAACAA CTGTCTCTAC CTTTGTTTCT CCAATGCCTT TGCCCAAGCA GAACCATGAA 720
 55 CCAGTAGCCA CTTCAACATC TTCACCTCAG CCAGCAGAAA CCCACCTAC GACACTGCAG 780
 GGAGCAATAA GGAGGAAACC CACCAGCTCA CCATTGTACT CTTACACAA AGATGGGAAT 840
 GACACCGTGA CAGAGTCTTC AGATGGCCTT TGGAATAACA ATCAAACCTA ACTGTTCTTA 900
 GAACATAGTC TACTGACGCG CAATACCACT AAAGGAATCT ATGCTGGAGT CTGTATTCTT 960
 60 GTCCTGGTGC TTCTGTCTCT TTTGGGTGTC ATCATTGCCA AAAAGTATT CTTCAAAAG 1020
 GAGGTTCAAC AACTAAGTGT TTCATTTAGC AGCCTTCAAA TTAAGCTTT GCAAAATGCA 1080
 GTTGAAAAGG AAGTCCAAGC AGAAGACAAT ATCTACATTG AGAATAGTCT TTATGCCAGC 1140
 GACTAAGACC CAGTGGTGTCT CTTTGAGAGT TTACGCCCAT GAGTGCAGAA GACTGAACAG 1200
 ACATCAGCAC ATCAGACGCT TTTTAGACCC CAAGACAATT TTTCTGTTT AGTTTCACTT 1260
 GGCATTCCAA CATGTCACTG ATACTGGGTA GAGTAACCTT CTCACTCCAA ACTGTGTATA 1320
 65 GTCAACCTCA TCATTAATGT AGTCCTAATT TTTTATGCTA AAACCTGGCTC AATCCTTCTG 1380
 ATCATTTGAG TTTTCTCTCA AATATGAACA CTTTATAATT GTATGTTCTT TTTAGACCCC 1440
 ATAAATCCTG TATACATCAA AGAGAATAGT CCTGGGAAAC ATAGCAAAAT AACTTCTATC 1500
 TTGGCCATCA CAGCTGTCCA GAAGAGGGGA ATCTGTCTTA AAAACAGCA AATCCAACGT 1560
 70 GAGACTTCAT TTGGAAGCAT TGTATGATTA TCTCTGTGTT CTATGTGTTA CTTCCAAATG 1620
 TTGCAATTC TATGTTTTC AAAGGTTTCA AATCGTGGGT TTTTATTTC TCCGTGGGGA 1680
 AACAAAGTGA GTCTAATCA CAGGTTTAGC TGTCTTCTCA TAACTCTGGA AATGTGATGC 1740
 ATTAAGTACT GGATCTCTGA ATTGGGGTAG CTGTTTACC AGTTAAAGAG CCTACAATAG 1800
 TATGGAACAC ATAGACACCA GGGGAAGAAA ATCATTTGCC AGGTGATTTA ACATATTTAT 1860
 75 GCAATTTTTT TTTTTTTTTT TGAGATGGAG CTTTGTCTTT GTTGCCAGG CTCGAGTGG 1920
 ATGTTGAAAT TCCGGCTCAC GTTAACCTCC ACCTTCCGGG TTCAAGCAAT TCTCCGCTC 1980
 CAGCCTCAGC AGTAGCTGGG ATTACAGGTG TCCGCCACTA TGCTCAGCTA ATTTTTTGTA 2040
 TTTTCTTAGT AGAGACAGGG TTTCAATCAT TTGGCCAGAA TGATCTCGAA CTCTGAGCT 2100
 CAGAGGATCC AGCCTCCTTG GCCTTCCAAA GTGCTGGGAT TACAGGCATG AGCCACCGTG 2160

CCTGGTCCAT TTATGCAATT TTTATTACAC GTGTGTCATG GTGCTAAGCA TTTAAACAAC 2220
 CATCAGGCTT TCTGAACAAA TTTTGTAGAAC CAAGAAGATC AGCAATAAAA GAAAAAAGAA 2280
 AGGCGGGAGT AGGGAAGAGT CTGCCCTTTC TGCCCTTATA GTTACATTGC AGATATAAGT 2340
 5 GTTTGAAACT CACTAGTATT GACCCAAATT CTAAATCGCC TCCAAACCAC TTTCATGTTT 2400
 AAAATTGTTT AGGAGGCTAG CGCCGTGGCT CATGCCCTGA ATCCAGCAC TTTGTGAAGC 2460
 CAAGGTGGGC AGGTAGCTTG AGCCCAAGAG TTTGAGACCA GCCTGGGCAA CATGGCAATA 2520
 CCCCATTCTT ATTAAGAAAA AAATTTAAGG AAAAAAAGAA AAGATAAAT TGTTTTGAA 2580
 AGGCAAGGTG TCTTCTCAT ATCTAATCAA TTCCTGTATT TTTTTTTTTT TTTTTTTTAC 2640
 10 AATTCAATTA GGCTTATTGT AAGGATATCT TTAGTCAGTA TAAAAATATA TAAAAACAA 2700
 TTATACTAAA CCAGTATAAT TGTTTAGAAG TATATATTTG CCGGCCGGGC ATGGTGGCTC 2760
 ATGCCGTGAA TCCAGGGCTT TTGGAAGGCT GAGGTGAGTG GATCACTAGA GGTGGGGAGT 2820
 TTGAGACCAG CCGACCAAC ATGGAGAAAC ACTGTTCTCT ACTAAGTATA GATTGCAAG 2880
 GGCTAGATTT GTCAGAAAAG AACATTTCT ACATGAACAG TTAAGGCTGG GTATTAAATT 2940
 CAATTTCAGT TTGAGTAAAC TCTGAAATTA TTCATGGTTG AGGTTTCAGG CTACCCATAC 3000
 15 CATAGTTGTC TGGGGCAACA GGATGCTTGC TTTCAGAGGA AACTTTTTGT TTTTGTTTTT 3060
 GTTTTTTGA GATGGAGTTT TGCTCTTGTC ACCCAGGCTG AAATGCAATG GCACAACTCT 3120
 GGCTCACTGC AACCTCCAC TCCAGGTTT AAGTGATTCT CCTGCTCAG CCTCTGAGT 3180
 AGCTGGGATT ACAGATGCCG GCCACAACGC CCAGCTTATT TTTAGTAGAG ACAGGGTTTC 3240
 ACCATATTGG CCAGGCTGGC CTCCACTCC TGACCTCAGG TGAGCCACCC GCTTGGCCT 3300
 20 CCCCAGGTG TTGGGATTAC AGGCATAAGC CACCGCGCCC AGCCAGAGGC AACATTTTTT 3360
 AACGCACTTA TCATTCTAGG AAATTTATAG GTCCCTTGAA GAAAAATCT GTGGGCAAA 3420
 AAGATTGTGA TACATGGTAT TTCAGTTTTC CCAATGTGG CCAGCCGAT CTGGTCAAAA 3480
 ATTTTATTTT TAAAAAGCTA TAGTGTCTTT TTTCTTAAA TTTGAGGCAA CATGCACAAA 3540
 ATTTGAGATT TGAATTTAAA GCCAAGATT GTAGTTTCTC TGGAAAGACC TGGCAAGATT 3600
 25 GGACTGGATT GCTATGTGAC CAGGGTCCCA CTAGATGGGG CTGCATCCTC TAATCCCCAA 3660
 ATCCTTATGT TCCCTGCATG CTCACCTTTG TTACCTGCCT GACACCTGTG GGGCTTTTAA 3720
 CTTTATGGCA ACTGCCCTAT TCTCTGGATC CTCTCTGAGG ATTTATGATG CGTAATACTC 3780
 CAGGAATCTG GTTAGCTTTG CTTAACACAT TTCCAAAAC TGTTTGAATG CATGAGTACA 3840
 GTCACATGTA GCATTCTGTG CAGTACAATG TATGGGGGCT TAGGAGTTTA GGGTAGTATA 3900
 30 CAGGATTAGG GATAGGACTT GAGTCTAATC CTAACCTCTA GCAGTTACAC TGGATGACAT 3960
 TAGAGCAAT GGTCTTTTAC GTCTACATTT TCTTCACTG TAGATGTAAT AATTTCATA 4020
 TCAACTATGA TGTACAGTGC TAATCCAAAT GAAATGTAC ATGTGAGAAG TCTTTGAAAT 4080
 GTAAAAACA CTACAGATAC TGAAGCAGTT TGGAGAATTA AAAAACACTA CGAAAAACA 4140
 35 GCTTGGTAAA TAATTTTTTT TTCTTTTGA GACAGAGTCT GGCTCTGTCA TCCAGGCTAG 4200
 AGTGTAGTG

Seq ID NO: 64 Protein sequence:
 Protein Accession #: NP_036338.1

40 1 11 21 31 41 51
 MHPQVILSL ILHLADSVAG SVKVGGEAGP SVTLPCYHSG AVTSMCWNRG SCSLFTCQNG 60
 IWMNGTHVT YRKDTRYKLL GDLSRRDVSF TIENTAVSDS GYVCCRVEHR GWFNDMKITV 120
 45 SLEIVPKVT TPIVTVVPT VTTVRTSTV PTTTVPVPT VPTTMSIPT TTVPTMTVS 180
 TTSVPTTS IPTTISVPVT TTVSTFVPPM PLPRQNHBPV ATSPSSPQPA ETHPTTLQGA 240
 IRREPTSSPL YSYTTDGNVT VTESDGLWN NNQTLFLEH SLTANTTKG IYAGVCISVL 300
 VLLALLGVII AKKYFFKKEV QQLSVSPSSL QIKALQNAVE KEVQAEDNIY IENSLYATD

50 Seq ID NO: 65 DNA sequence
 Nucleic Acid Accession #: E05 sequence
 Coding sequence: 2932-4764

55 1 11 21 31 41 51
 AGAAGAAAGC TGGTAGGGGC TGGGAGAGGG TACCACAGGG GAGTATGATC TACTTGGGGG 60
 CCAGAGAAGG TTCCCTGAGG AAATAGTACC TGAACCTAGA CTTGAAGGAT AACAGATGTT 120
 AACTGGGAGG AGAGAATGTT CCAGGCAGAG GAAAAGGCAT ATGCAAAAGT CCAGCGCCTT 180
 GAAGGAGCAC AGCTGGGGTG CCTGGAGTGA GATGGAGCTG GAAAGATCCA GGTGGAGCTT 240
 60 GACCTGAAGT ACCAGCCCCC AGAGGGCGCT ACTGGAGCCT GGTGAGAGGA GACTTTGGG 300
 GCACCCATCC AGGACAGCTT CGAGTTAATC ATCCCCAATG TGGGCTTCCA GGAACCTGGAG 360
 CCTGGGGAGG CCCAGCTGGA GCGGCGGGCA GTGGCTCTAG GCCGCAAGCT AGCTCGAAGT 420
 CTAGGCCAGC AGGACGATGA AGAATATGAG CTGGAGCTTG AGCTGAGACA GGACCTGGAT 480
 GATGAGCCTG ACCTGGAAC TTTCTGGTGT ATGTTACAGC CCTCAAGAG CCGCGCCAGG 540
 65 GCCTGGGCC ATGGGGATCC CTTCCAGGTG TCCAGAGCTC AAGACTTCCA GGTGGGAGTC 600
 ACTGTGCTGG AAGCCAGAAA ACTGGTGGGA GTCAACATTA ACCCTATGT GGCCTGCAA 660
 GTGGGGGGGC AGCGCGGTGT GACCGCCACA CAGCGTGGGA CCAGTTGCCC CTTCTACAAT 720
 GAGTACTTCT TGTTCGAATT TCATGACAG CGGCTTCGTC TCCAAGACTT GCTGCTGGAG 780
 ATCAOGTGA GTGGGGTAGG GGTGACCACT GTCCCTCAGA GAAGGGGGGA TGAGAAAGCT 840
 70 GCAGGACTAA CACCACTTTC CCCCAGGCT TCCATTTCG AGACCTTCCC CTTTATGGCC 900
 ACCCGATAG GCACCTTCA GATGGACCTG GGCACTATCT TGGACCAAGC AGGTATGGAA 960
 TCGTCCCCCT ATTGAGACTC TGCAOAGACA AGGGCCCTAG AGATTGACCC TGCACTGACT 1020
 CGCATGGAC CCCTATACAC TCACTTCGGA GAGGGCCATC TCTGGCGGAG GCTGAACTCT 1080
 TGGCACTTCC GCGCTTCCCT GCTAGGCCAG AGAAGCCCTG GCCATTGTC GTCACCTCCA 1140
 75 TAGCTCAGG GCCACCTGT GGTTCGCGCC GGTGCGCCCT TACCCCTGGC TCGCCCTTCC 1200
 GGCCTTAGAT GGCAGTTCT ACCAAGATG GGTTCGCGCT CATGATCCCC GAGACACCCG 1260
 GCGCGGACC AAGGGTTTCA TTAAGGTAC CTTGTCCGTG AGGGCGCGCG GGGACCTGCC 1320
 CCTCCAATG CTACCCCCG CCCCAGGGCA CTGTTCCGAC ATCGAGAAGT GAGCCGGGT 1380
 GAGGTGGGA GGAGGACATG GATCGGGGG TGGCGTGGG GCGCGGATAA GGGGAGGGGC 1440

	CGAGATCCCA	GTTCCTCCCC	CCCCGCTCGG	TGCCCCCTCC	CCTAGGAACC	TGCTCCTGCC	1500
	GGCGGGGGTG	CCGCGCGAGA	GGCCATGGGC	GGGCTCCGC	GTGCGCTGT	ACCGCGCCGA	1560
	GGGGCTTCCC	GGGCTGGCC	TGGGGCTGCT	GGGCAGCCTG	GTCCGCGCCC	TGCACGACCA	1620
	GGCGGTCTCT	GTGGAGCCCT	ATGTGCGGGT	GTCTTTCCTG	GGGCAGGAGG	GGGAGACGTC	1680
5	GGTGAGCGCC	GAGGCGGGCG	CGCCCGAATG	GAACGAGCAG	CTGAGCTTCG	TGGAGCTCTT	1740
	CCCGCGCTG	ACGCGCAGCC	TCCGCTTGCA	GCTGCGGGAC	GACGCGCCCC	TGGTCGACGC	1800
	GGCACTCGCT	ACCGCAGTGC	CGGAACCTGAG	GCGGATCTCC	CATCCGSGCC	GGCGCGGGG	1860
	GTTTAAACCT	ACCTTCGGCC	CGGCTGGGT	GCCCTCTAT	GGCTCGCCCC	CCGCGCGGG	1920
10	GCTCCGGGAT	AGTCTTCAAG	GTCTCAACGA	AGGCGTTGGC	CAAGGCATT	GGTTCGCGG	1980
	CGGCTTCTG	CTGGCTGTGT	CCATGCAAGT	GTGGAAGGG	AGAGCTGAAC	CTGAGCCTCC	2040
	CCAGGCCCAG	CAGGGTCCA	CGTTGTCCCG	GCTCACCCGA	AAGAAGAAAA	AGAAAGCCAG	2100
	AAGGGATCAG	ACCCCAAGG	CGGTTCGCA	GCACTTGGAC	GCCAGCCCCG	GTGCCGAGGG	2160
	GCCTGAGATC	CCCGTGCCCA	TGGAGGTGGA	GGTGGAGGAG	CTGCTGCGCC	TGCCAGAGAA	2220
	TGTCTGGGG	CCCTGTGAAG	ATTTCTGTCT	TTTCGGTGTG	CTCTCGAGG	CCACCATGAT	2280
15	CGACCCACCC	GTGGCTTCCC	AGCCCATCAG	CTTCGAGATC	TCCATTGGTG	TGTGGCCTAG	2340
	CGGAACCCCT	GAGTGCCATT	TGAGACCTTA	GAACCTTGGA	AGGGGTGTGT	ACTTTCAGTC	2400
	GGCAGGGCG	TCTGGAGGAG	CAATTGGGCC	GAGGGTCCAG	GGCTGGGGAG	GGAACTGAGG	2460
	GTGCAGCCGT	GGAGGCTCAG	CCTCTGCTGG	GAGCCAGGCC	AGAGGAGGAG	AAAGAGGAGG	2520
20	AAGAACTGGG	GACCCATGCT	CAGCGGCTG	AGCCCATGGA	CGCAGTGGG	CCATACTTCT	2580
	GCTTGCCCT	CTGTCACTGC	AAGCCATGCA	TGCATGTGTG	GAGTGTCTGG	GAGGACCACA	2640
	CCTGGCGCT	CGAGAGCAGC	AACCTGCTGC	GCAAGTGGC	CGAGAGGCTG	GACCAGGGGC	2700
	TGCAGGAGGT	TGAGGACTG	CAGCGCAAGC	CGGGGCTGG	CGCCTGTGCA	CAGCTCAAGC	2760
	AGGCACTGGA	AGTACTGGTG	GCTGGGAGCA	GACAGTTTGT	CCACGCTGCC	GAGCGCAGGA	2820
25	CGATGACCCG	GCCCAATGCC	CTGGATCGAT	GCCGAGGGAA	ACTCCTGGTG	CACAGCCTGA	2880
	ACCTTTTGGC	TAAGCAAGGA	CTGCGACTTC	TACCGGCGCT	GAGACGCGCG	AATGTGCAAA	2940
	AGAAGGTGGC	ACTGGCCAA	AAGCTCTGG	CAAAACTGGC	CTTTCCTGGT	GAGGAGGCAC	3000
	CCGCGGCGC	CCCTGGTGG	GTCTGTGCCA	AGCTGGAGCT	CTTCTGCGG	CTGGGCGTGG	3060
	GCAAGCAAGC	CAAGGCTGCG	ACCTCTGAGC	TGCCCCCGGA	TTTGCTGCC	GAGCCCTCAG	3120
30	CCGCGCTGCC	CTCCAGCCTA	CACCGGGACG	GTCTGTGAGC	AGAAGCTGAG	CCCTCTGTGG	3180
	GATGAATCC	TGGTATTGGA	GCAGTGTATC	GTGGATGGGA	GGAGGGAGCA	CCTGCAGGAG	3240
	GAGCCTCCAT	TAGTGATCAT	CAATGTATTT	GACCACAATA	AGTTTGGCCC	CCCCGTGTTT	3300
	CTGGCAGGG	CAGTGGCGC	CCCAAGGGTA	AAGCTGATGG	AGGACCCATA	CCAAAGCCCA	3360
	GAGTTGCAGT	TCTTCCCTCT	GAGGAAGGGA	CCCTGGGCG	CCGAGAGGCT	CATTGCGGCC	3420
35	TTTCAACTCA	TTGAAC TAGA	CTACAGTGGC	CGACTTGAGC	CCTCAGTGCC	CAGTGAGGTG	3480
	GAGCCCCAGG	ATCTGGCACC	CCTGGTTGAG	CCCCACTCTG	GACGCGCTGC	CCTTCCACCC	3540
	AACGTGTGGT	CAGTCTCAG	GGAGTTCCGT	GTGAGGTGCG	TGTTCTGGGG	TCTTAGGGGA	3600
	CTTGGTGGTG	CCCTCTCTGA	CGAGTGGAG	CAGCCCCAGG	TTGTAAGTGA	GGTGGCTGGG	3660
	CAAGGTGTGG	AGTCTGAGGT	CCTGGCCAGC	TACCGTGAGA	GCCCAATTT	CACTGAGCTT	3720
40	GTACAGCATC	TGACAGTGGT	CTTCAAGAGC	ACAGCTCCCT	TCTTCCACCC	CCAGGACTTG	3780
	CGGAGCAGC	CTTACTTGCA	GCCTCCACTC	AGCATCTTGG	TGATTGAGCG	CCGGGCTTTT	3840
	GGCCACACAG	TCTTGTGGG	TTCCCACTT	GTCCCCACCA	TGCTGCGATT	CACATTTCGG	3900
	GGTCATGAGG	ATCTCTCTGA	GGAGGAAGGA	GAGATGGAGG	AGACAGGGGA	TATGATGCC	3960
	AAGGGACCTC	AAGGACAGAA	GTCCCTGGAT	CCCTTCTTGG	CTGAAGCGGG	TATATCCAGA	4020
45	CAGCTCTCTGA	AGCACAACCT	TGATGAAGAT	GAATGGATG	ATCCTGGAGA	TTCAGATGGG	4080
	GTCAACCTCA	TTTCTATGGT	TGGGAGATC	CAAGACCGAG	GTGAGGCTGA	AGTCAAAGGC	4140
	ACTGTGTCCC	CAAAAAAAGC	AGTTGCCACC	CTGAAGATCT	ACAACAGGTC	CCTGAAGGAA	4200
	GAATTTAAAC	ACTTTGAAGA	CTGGCTGAAT	GTGTTTCTCT	TGTAACGAGG	GCAAGGGGGC	4260
	CAGGATGGAG	CTGGAGAAGA	GGAAGGATCT	GGACACCTTG	TGGGCAAGTT	CAAGGGCTCC	4320
50	TTCTCTATT	ACCCTGAATC	AGAGGCAGTG	TTGTTCTCTG	AGCCCCAGAT	CTCCGGGGG	4380
	ATCCACAGAG	ACCGGCCCAT	CAAGCTCCTG	GTCAAGATGT	ATGTTGTAAA	GGCTACCAAC	4440
	CTGGCTCCTG	CAGACCCCAA	TGGCAAAGCA	GACCCCTACG	TGGTGGTGAG	CGCTGGCCGG	4500
	GAGCGGCAGG	ACACCAAGGA	ACGCTACATC	CCCAAGCAGC	TCAACCCCAT	CTTGGAGAG	4560
	ATCCTGGAGC	TAAGCATCTC	TCTCCACGCT	GAGACGGAGC	TGACGGTGGC	CGTATTGTAT	4620
55	CATGACCTCG	TGGGTTCTGA	CGACCTCATC	GGGGAGACCC	ACATTGATCT	GGAAAAACCA	4680
	TTCTATAGCC	ACCACAGAGC	AAACTGTGGG	CTGGCCTCCC	AGTATGAAGT	GTGGGTCCAG	4740
	CAGGGCCACG	AGGAGCCATT	CTGAGTTTCT	GGCCAAACAC	ATTCAAGCTC	ACATTCCCTT	4800
	TTGTGTCTCC	AGATCCTATG	ATTTCAAGGA	AGGGGACCTT	CCCAACCCACC	GCCACTGCCA	4860
	ACCAAGACAT	AGCTCAGTGG	TCAAGACTTG	GGCTTGGGAG	TGGGATCCT	GTAACGAATG	4920
60	TCACCTGACC	GCTTCTCTTT	TTTATGAAC	AGTCTCGCTC	TGTCCTCCAG	GTTGGAGTGC	4980
	AGTGGCAOGA	TCTCGGCTGA	CTGCAACCTC	CACCTCCTGG	GTTCAAGCGA	TTCTCTGCC	5040
	TCAGCCTCCC	CAGTAGCTGG	GATTACAGGC	GTGGGCCCCC	ATGTCCAGCT	AATTTTATA	5100
	TTTTCGCTCT	GTCTCCACGG	TGGAGTGCA	GTGGCAOGAT	CTCGGCTGAC	TGCAACCTCC	5160
	ACCTCCTGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	AGTAGCTGGG	ATTACAGCGG	5220
65	TGGGCCCCCA	TGTCAGACTA	ATTTTATAT	TTTATAGTAG	GACAGGGTTT	CACCATGTTG	5280
	TCCAGGCTGG	TCTTGAACCC	CTGACCTCAA	GTGATCCACC	CACCTCTGCC	TCCCAAGTGG	5340
	CTGGGATTAC	AGGTGTGAGC	CACCATGCCA	GGCCCTCTTA	ACCTCTTCAA	GTCTGTTCCT	5400
	TCATCTGCAA	AACAGAGSTA	ATAAGATCAG	TATCTTCTTA	ATGGAAGCAC	CTGGAATACA	5460
	TTTTTTTCAT	TCATTGTTAT	CATAAATGAG	GACTAACCTG	TCTCCCGTTG	GGAGTTTGA	5520
70	ACCTAGACCT	CATGTCTTCA	TGACGTCATC	ACTGCCCCAG	GCCCCAGCTG	GTCCCTACAC	5580
	CAGCCCCAGC	TGAGCATCT	TCTTTTCTG	CCTGTAGAGA	TGGTTACAAT	GCCTGGCGTG	5640
	ATGCATTCTG	GCCTTCGAG	ATCCTGGCGG	GGCTGTGCCA	ACGCTGTGGC	CTCCCTGCC	5700
	CTGAATACCG	AGCCGGTCTCT	TCACATGTGG	ATTGACATCT	TTCTCAAGA	TGTGCTGCT	5760
75	CCCTGCCCCC	AGGGATCTGT	TCACATGTGG	ATTGACATCT	ATGAGCTCAG	AGTTGTCTATC	5820
	CCACCCCCAG	TTGACATCAA	GCCTCGGCAG	CCAATCAGCT	TCACCGGAGA	GATGTGAGT	5880
	TGGAACACGG	AGGATGTGGT	TCTGGATGAC	GAGAATCCAC	TCACCGGAGA	GATGTGAGT	5940
	GACATCTATG	TGAAGAGCTG	GGTGAAGGGG	TTGGAGCATG	ACAAGCAGGA	GACAGACGTT	6000
	CACCTCAACT	CCCTGACTGT	GGAGGGGAAC	TTCAATTGGC	GCTTTGTGTT	CCGCTTTGAC	6060
	TACCTGCCCA	CGGAGCGGGA	GGTGAGCGTC	TGGCGCAGGT	CTGGACCTTT	TGCCCTGGAG	6120

Seq ID NO: 67 DNA sequence
Nucleic Acid Accession #: NM_002449.2
Coding sequence: 223..1026

	1	11	21	31	41	51	
35	GGGGGGGGGG	GGCAGGCTCT	CGGGAAGAGC	CAATCAG3GG	CGAGCGTCTT	CTGTGCGCAC	60
	GAGGCGCGCG	GGCGATTGGC	GGCGCGCGTC	TCCACTTTC	CCTCGGAGGA	AAGGCTCAGC	120
40	TCCACAGCGC	CCCTCCCGCT	CTCCGCGAGC	AAAAAGTTTG	AGTCCGCGCT	CGCGGGTTGC	180
	CAGCGGAGTC	GGCGGTCCGG	AGCTACGTAG	GGCAGAGAAG	TCATGGCTTC	TCCGTGCAAA	240
	GGCAATGACT	TGTTTTCCGC	CGACAGGAGG	GGCCACAGCA	TGGTGGCCCG	ACACGGCCCG	300
	GGGCTGGGGG	GGCGCTCGGG	GGCGCGCGAG	GAGCGCGCGG	TCAAGGTCCT	CAGCGTCGCC	360
	TTCCAGCTGG	AGGCGCTCAT	GTCGCGACAAG	AAGCCGCCCA	AGGAGTGC	CGCTGTGCC	420
45	CCCGAAGCGC	CCTCGGCGCG	GGCCCACTGC	GGCCCACTGC	TGCTGTCCGG	GGCAGCGCGT	480
	CGGGAAGCGC	ACAGCCCCGG	GGCGCTGGTG	AGCGCTTCG	AGACCGCTC	GCTCAAGTCG	540
	GGAAATTGAG	AAGATTGGAG	GGGCTGGATG	CAGGAACCCG	GCCGATATTC	CGCCCGCGCA	600
	AGACATATGA	GCCTTACCAC	CTGCACCTCT	AGGAACAACA	AGACCAATCG	GAGACCGTCA	660
	AGCGCTTTTA	CCACATCCCA	GCTCTCGCC	CTGGAGCGCA	AGTTCCGTCG	GAACCGCGCG	720
	CTCTCCATTG	CAGAGCGTGC	AGAGTTCTCC	AGCTCTCTGA	ACCTCACAGA	GACCCAGGAT	780
50	AAATCTGGT	TCCAGAACCG	AAGCGCCAA	GGGAAAAGAC	TGCAGGAGCG	GGAACTGGAA	840
	AAGCTGAAAA	TGGCTGCAAA	ACCTATGCTA	CCCTCCAGCT	TCAGTCTCCC	CTTCCCCATC	900
	AGCTCGCCCC	TGCAGGCGAC	GCTCATATAC	CGCAGCATCT	ACCCGTTCCA	TAGACTGTGT	960
	CTTCCCATCT	CGCCCGTGGG	ATCTATTGCC	ACGCCAGTGG	GATATGGCAT	GTACCACTGT	1020
55	TCCTAAGGAA	GACCCAGTCA	ATAGACTCCA	TGATGGATGC	TGTTTCAAA	GGGTTCTCTC	1080
	TCCCTCTCCA	CAAAAGGCATA	GGCAGCAGGT	ACTCTCGGTC	TGCTAAGCCC	TGCAGTGTGC	1140
	ACCCCAACCC	CTCTAACGCG	TAGCTGACAG	GGCCACACCA	CATAGCTGAA	ATTGTGTTCT	1200
	GTAGGCGGAG	GCACCAAGCC	CTGCTTTTCT	TGTTGTAAC	TCCAGAGTCC	CCCTTTTTTT	1260
	CCTTGCACCA	AAAGCTTGCG	TCATGTGGTT	TTTGTGGCAT	GATGTATATA	TATATATACG	1320
60	AAAAATACTA	CAGACCTTTT	TTTTCAGCAG	ACGTAAAAAT	TCAAATTATT	TTAAAAGGCA	1380
	AAATTTATAT	ACATATGTGC	TTTTTTTTCTA	TATCTCACT	TCCCAAAAAG	ACACATGTGT	1440
	AAGTGCATTT	GTGTATTTTT	CTTAAAGAGG	GAGACAAATT	CGGAGGAGCG	CCGCGCTCAAG	1500
	GTCCTCAGCC	TGCCCTTCAG	CGTGGAGGCG	CTCATGTCCG	ATTGTGCAAA	ATGTGCTAAA	1560
	GTCATATGAT	TTATCCGGGA	TTATTGACTT	TCGTTATATC	AAGAAGCCGC	CCAAGGAGTC	1620
65	GCCCGCTGTG	CTCTCCGAAG	GGCGCTCGGC	CGGCTCGCG	AAAAACAAAA	GAAACACAGC	1680
	ACATGCGAGC	AGCCACAGAA	TATTAGATAT	GGAGAGATTA	TGGCCACTGC	TGTGACCGAG	1740
	CACGCGCGTC	CGGGAAGCGC	ACAGCCCCGG	GGCGCTGGTG	ACAAGGTGA	ACCCACATCA	1800
	TATTTCTGCA	TTTACTTCTG	ATTTAAAGAA	ACCTCTTTAT	AAGCCCTTGG	AGACGCGCTC	1860
	GGTCAAGTCG	GGAAATTCAG	AAGATGGAGC	GGGCTGGATG	CTACATACGT	TGTTCCCTAT	1920
70	TCCGCGCCAC	GGCCACATAT	ATTTTAAAG	TTTATGGAA	CCCGGCCGAT	ATTCCGCGCC	1980
	GCCAAGACAT	ATGAGCCCTA	CCACTCGCAC	CTGACCTTT	TAAAGATAT	TTTGTAAAGA	2040
	CCAATACCTG	GGATGAGAAG	AATCCGTAGA	CTGCGGGA	CACAAGATCA	ATCGGAAGCC	2100
	CGCGACGCCC	TTTACCACAT	CCGAGCTTCT	CGCCCTGGAG	GTGAGGTAGA	AAAATTAGAA	2160
	ATACTTCTTA	ATTCTTCTCA	AGGCTGTGGT	TAACTTTGGA	GCGCAAGTTC	CGTCAGAAAC	2220
	AGTACCTTCT	CATTCGAGAG	GTGCGACAGT	TCTCTATTTC	AGATAATTGT	AGAGTAAAA	2280
75	GTTAAAAACC	GTGAGAGGAT	TGTACAGCTC	TCTGAACCTC	ACAGACCCCG	GTCAAAAGGT	2340
	TCTGAGAAAT	ACTAGGTACA	TTCTATCTCA	CAGATTGCGA	AGGTGCTTTT	GGTGGGGGTT	2400
	TAGTAATTTT	TGCTTAAAAA	AATGAGTATC	TTGTAAACAT	TACCTATATC	TAAATATTCT	2460
	TGAACAAATTA	GTAGATCCAG	AAAGAAAAAA	AAAATATGCT	TCTCTGTGTG	TGTACCTGTT	2520

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75

Seq ID NO: 68 Protein Sequence
 Protein Accession #: NP_002440.1

1 11 21 31 41 51
 MASPSKGNL FSPDEEGPAV VAGPGPGLGG AAGAAEERRV KVSSLPFSVE ALMSDKKPPK 60
 ESPAVPPEGA SAGAHRLPLL LSGHRAREAH SPGFLVKPFE TASVKSGNSE DGAAMWQEPG 120
 RYSPPPRHMS TCTTLRLKHK TNKRPRTPTF TSQLLALERK FRQKQYLSIA ERAEPSSSLN 180
 LTETQVKIWF QNRSKAKAKL QEAELEKLM AAKPMLPSSF SLPPFISSPL QAASIYAASY 240
 PFHRPVLPIP FVGLYATPVG YGMYHLS

Seq ID NO: 69 DNA sequence
 Nucleic Acid Accession #: NM_005603.1
 Coding sequence: 1..3756

1 11 21 31 41 51
 25 ATGAGTACAG AAAGAGACTC AGAAACGACA TTTGACGAGG ATTCTCAGCC TAATGACGAA 60
 GTGGTTCCCT ACAGTGATGA TGAACAGAAA GATGAACCTG ATGACCAGGG GTCTGCTGTT 120
 GAACCAAGAC AAAACCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA 180
 GAATGTACAT GGCAAGTCAA AGCAAAACGAT CGCAAGTACC ACGAACCAAC TCACTTTATG 240
 AACACAAAAT TCTTGTGTAT TAAGGAGAGT AAAATATGCGA ATAATGCAAT TAAAAATAC 300
 AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC 360
 AATTATATTT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT 420
 TGGTACACCA CACTAGTGCC CCTGCTTGTG GTGCTGGGCG TCACTGCAAT CAAAGACCTG 480
 GTGGACGATG TGGCTCGCCA TAAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC 540
 ATTAAGGATG GCAGGTTCAA AGTTGCTAAG TGGAAAGAAA TTCAAGTTGG AGACGTCATT 600
 CGTCTGAAAA AAAATGATTT TGTTCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT 660
 AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGGACGGAG AAACCAATTT AAAATTTAAG 720
 ATGTCACCTG AAATCACAGA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTTGAT 780
 GGTTTTATTG AATGTGAAGA ACCCAATAAC CGACTAGATA AGTTTACAGG AACACTATTT 840
 TGGAGAAACA CAAGTTTTC TTTGGATGCT GATAAAATTT TGTTACGTGG CTGTGTAATT 900
 AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTCAG GTGCTGACAC TAAATAATG 960
 AAGAATAGTG GGAAGACAG ATTTAAAGA ACTAAATTTG ATTACTTGAT GAACATACATG 1020
 GTTTACACGA TCTTTGTGT TCTTATCTG CTTTCTGCTG GTCTTGCCAT CGGCCATGCT 1080
 TATTGGGAAG CACAGGTGGG CAATTCCTCT TGGTACCTCT ATGATGGAGA AGACGATACA 1140
 CCCTCCTACC GTGGATTCCT CATTTCTGCG GGCTATATCA TTGTCTCAA CACCATGGTA 1200
 CCCATCTCTC TCTATGTCAG CGTGGAAAGT ATTCGTCTTG GACAGAGTCA CTTCATCAAC 1260
 TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCGG CAAAGCTAG AACCAACACA 1320
 CTCAATGAAC AGCTCGGGCA GATCCATTAT ATCTTCTCTG ATAAGACGGG GACACTCACA 1380
 CAAAATATCA TGACCTTTAA AAGTGTCTGT ATCAACGGGC AGATATATGG GGACCATCGG 1440
 GATGCCTCTC AACACAACCA CAACAAAATA GAGCAAGTTG ATTTTAGCTG GAATACATAT 1500
 GCTGATGGGA AGCTTGCAAT TTATGACCAC TATCTTATTG AGCAATCCCA GTCAGGAAAA 1560
 GAGCCAGAAG TACGACAGTT CTTCTTCTTG CTGCGAGTTT GCCACACAGT CATGGTGGAT 1620
 AGGACTGATG GTCAGCTCAA CTACCAGGCA GCCTCTCCCG ATGAAGTGC CCTGGTAAAC 1680
 GCTGCCAGGA ACTTTGGCTT TGCTTCTCTC GCCAGGACCC AGAACACCAT CACCATCATG 1740
 GAACCTGGCA CTGAAAGGAC TTACAATGTT CTTGCCATTT TGGACTTCAA CAGTGACCGG 1800
 AAGCGAATGT CTATCATTTG AAGAACCCCA GAAGGCAATA TCAAGCTTTA CTGTAAAGGT 1860
 GCTGACACTG TTATTATGA ACGGTTACAT CGAATGAATC CTACTAAGCA AGAAACACAG 1920
 GATGCCCTGG ATATCTTTGC AAATGAAACT CTTAGAACCC TATGCTTTG CTACAAGGAA 1980
 ATTGAAGAAA AAGAATTTAC AGAATGGAAT AAAAAGTTTA TGGCTGCCAG TGTGGCCTCC 2040
 ACCAACCGGG ACGAAGCTCT GGATAAAGTA TATGAGGAGA TTGAAAAAGA CTTAATTCTC 2100
 CTGGGAGCTA CAGCTATTGA AGACAAGCTA CAGGATGGAG TTCCAGAAAC CATTTCAAAA 2160
 CTTGCAAAA CTGACATTAA GATCTGGGTG CTTACTGGAG ACAAAGGAA AACTGCTGAA 2220
 AATATAGGAT TTGCTTGTA ACTTCTGACT GAAGACACCA CCATCTGCTA TGGGGAGGAT 2280
 ATTAATTCTC TTCTTCATCG AAGGATGGAA AACCAGAGGA ATAGAGGTGG CGTCTACGCA 2340
 AAGTTTGAC CTTCTGTGCA GGAATCTTTT TTTCCACCGG GTGGAAACCG TGCCCTTAATC 2400
 ATCACTGGTT CTTGGTTGAA TGAATTTCTT CTCGAGAAAA AGACCAAGAG AAATAAGATT 2460
 CTGAAGCTGA AGTTCCCAAG AACAGAAGAA GAAAGACGGA TGGGACCCA AAGTAAAGG 2520
 AGGCTAGAAG CTAAAGAAAG CAGCGGCAG AAAAATTTTG TGGACCTGGC CTGCGAGTGC 2580
 AGCGCAGTCA TCTGCTGCG CGTCACCCCC AAGCAGAAGG CCATGGTGGT GGACCTGGTG 2640
 AAGAGGTACA AGAAAGCCAT CACGCTGGCC ATCGGAGATG GGGCCAATGA CGTGAACATG 2700
 ATCAAACTCG CCCACATTGG CGTTGGAATA AGTGACAAAG AAGGAATGCA AGCTGTCATG 2760
 TCGAGTGACT ATTCTTTGCG TCAGTTCCGA TATCTGCGA GGCTACTGCT GGTGCATGGC 2820
 CGATGGTCTT ACATAAGGAT GTACTCTTTC TTCAATGGCT ACTCTGCGCA GACTGCATAC 2880
 TTTACTTTGG TTCAATTTCT GTACTCTTTC TTCAATGGCT ACTCTGCGCA GACTGCATAC 2940
 GAGGATTGGT TCATCAACCT CTACAAGTG CTGTACACCA GCCTGCCCCG GCTCCTCATG 3000
 GGGCTGCTCG ACCAGGATGT GAGTGACAAA CTGAGCCTCC GATTCCCTGG GTTATACATA 3060
 GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGTAAGCTT GTTGCATGGG 3120
 GTCTTAACAT CGATGATCTT CTCTTTCATA CCTCTTGGAG CTTATCTGCA AACCGTAGGG 3180
 CAGGATGGAG AGGCACCTTC CGACTACCAG TCTTTTGGCC TCACCATTGC CTCTGCTCTT 3240

5
10

```

GTAATAACAG TCAATTTCAC GATTGGCTTG GATACTTCTT ATTGGACTTT TGTGAATGCT 3300
TTTTCAATTT TTGGAAGCAT TGCACTTTAT TTTGGCATCA TGTITGACTT TCATAGTGCT 3360
GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG 3420
AGACAGCCAT ACATTGGTGT AACTATCATC CTGACTGTTG CTGTGTGCTT ACTACCCGTC 3480
GTTGCCATTC GATTCTCTGC AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG 3540
CATCGCAAGC GGTGTAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCCG 3600
GGCGTGTCAA CGCGGGCGCT GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC 3660
ATCTCTCCGG GGCAGAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT 3720
GGCACCGCGG AGTACAGGCG CACCGGGGAC AGCTGA

```

Seq ID NO: 70 Protein Sequence
Protein Accession #: NP_005594.1

15
20
25
30
35
40

```

1 11 21 31 41 51
MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGSAAV EPEQNRVNRE AEENREPPFRK 60
ECTWQVKAND RKVHEQPHFM NTKFLCIKBS KYANNAIKTY KYNAPTIFPM NLFEQPKRAA 120
NLYFLALLIL QAVPQISTLA WYTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV 180
IKDGRFKVAK WKEIQVGDVI RLKKNDFVPA DILLSSSEF NSLCYVETAE LDGETNLKFK 240
MSLEITDQVL QREDTLATFD GFIECEEPNN RLDKPTGTLF WRNTSFPLDA DKILLRGCVI 300
RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLMNYM VYTIFVVLIL LSAGLAIGHA 360
YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
WDLQMYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKKCC INGQIYGDHR 480
DASQHNHNKI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFPFL LAVCHTMVD 540
RTDQQLNQYA ASPDEGALVN AARNFGFAPL ARTQNTITIS ELGTERTYNV LAILDPNSDR 600
KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTLCLCYKE 660
IEEKEPTEWN KKFMAASVAS TNRDEALDKV YBSIEKDLIL LGATAIEDKL QDGVFPETISK 720
LAKADIKIWV LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFPAPPVQESF PPGGNRALI ITGSWLNBLI LEKKTKRNI LKLFKPRTEB ERRMRQSKR 840
RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM 900
IKTAHIGVGI SGQEGMQAVM SSDYSFAQPR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA 960
PTLVHVPYSE FNGYSAQTAY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI 1020
VGQRDLLEFN KRPFVSLHNG VLTSMILFPI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
VITVNFQIGL DTSYMTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSPAF QFTGTASNAL 1140
RQPYINLTII LTVAVCLLPV VAIRFLSMTI WSESDEKIQ HRRRLKAEQ WQRQVQVFR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPDLDAIVAD GTAERYRTGD S

```

Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_138784.1
Coding sequence: 334-816

45
50
55
60
65
70

```

1 11 21 31 41 51
GGGGATACGG AAAACAGAAT AGAAGCACAG AACAAGGACT ATTGTATATA AGAGAAGCAG 60
GTGTTAATGT AAGTTGCTGT GGAATGACTG TTTTCAAGAA GAGAGAAGGA GCCAATATAT 120
CTACTTTTAT TAAGAAGCTG AAATTAATTT TGGATTTCCT TCTTTCCAAA GCTGAGACAC 180
GATGGCCAAA AAGCGATTGC TGTGATTGGA GCTGGAATTA GCGGACTGGG GGCATCAAG 240
TGCTGCCTGG ATGAAGATCT GGAGCCCACC TGCTTTGAAA GAAATGATGA TATTGGACAT 300
CTCTGGAAAT TTCAAAAAAA TACTTCAGAG AAAATGCCTA GTATCTACAA ATCTGTGACC 360
ATCAATACCT CCAAGGAGAT GATGTGCTTC AGTGACTTCC CTGTCCCTGA TCATTTTCCC 420
AACTACATGC ACAACTCCAA ACTCATGGAC TACTTCGGGA TGATGCCAC ACACTTTGGC 480
CTCCTGAATT ACATTCGTTT TAAGACTGAA GTGCAAAAGT TGAGGAAGCA CCCAGATTTT 540
TCTATCAATG GACAAATGGA TGTTGTTGTG GAGACTGAAG AGAAACAAGA GACTTTGGTC 600
TTTGATGGGG TCTTAGTTTG CAGTGGACAC CACACAGATC CCTACTTACC ACTTCAGTCC 660
TTCCAGGCA TTAGAAATTT TGAAGGCTGT TATTTCCATA GTGCGGAATA CAAAAGTCCC 720
GAGGACTTTT CAGGGAAGAG AATCATAGTG ATCGGCATTG GAAATTCCTG AGTGGATATT 780
GCGGTGGAGC TCAGTCGTGT AGCAAAACAG ATTTGACCAG TAGGAACTGA GATTCAACGT 840
CCCCAAGACT GCAAAAGTAC CTACAATCAA ACAAAATTAAT ATATTTCCCTA ATTGGATCAG 900
CATGCAGACA AGTTTACAAA TATATTACAG AAAGATTGGA AGAGGGATTG TGGTTACGTT 960
CAGTTAAGCA GGACACTAAT CCTGAACAA CTGATGTATT AAAGTTTCTA ATGTTTGTAT 1020
CTTTGGTTTG ATGCATACAA TAGAGTGAA GTCTGTAGTA GTTAATATGA TGATAATTCTG 1080
CTTCTAAAT TAAATCTTTA TTTATATATG AAGCATAGCT ATGTCAATGT CCAGGGAAGC 1140
ATTTTTAAAT AGTAAATCAG AAACATGTAA ACTAGTGAAT ACAATTTTCT ATTTTTCATT 1200
CAGAAATTTG TTGTCATAGA TGCAGCCTTT ATCTGGAAT CAGTGGGCA CTCTGGTCAA 1260
GCACAGCATG GCGACCACTG TGTAGTATT TACCACCTAA TCCTTAGTAG CCAACACTGT 1320
TAAATCTGCA TAATGGGTAG CATATGAATA AAATAATATC TTGTAAAAA AAAAAAATAA 1380
AAAAAATAA AAAA

```

Seq ID NO: 72 Protein sequence:
Protein Accession #: NP_620139.1

75

```

1 11 21 31 41 51
MPSIYKSVTI NTSKEMMCFD DFPVPDHPFN YMHNSKLMYD FQMYATHFGL LNYIRFKTEV 60
QSVRKHPDFS INGQWVUVE TEEKQETLVF DGVLVCSGHH TDPYLPQLSF PGIEKPEGCY 120
FHSREYKSPD DFGSKRIIVI GIGNSGV DIA VELSRVAKQI

```

Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

```
5 1 11 21 31 41 51
| | | | |
ATGAGTGCAC TTTTCCTTGG TGTGGGAGTG AGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60
CAAAAGCTTC CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCCT CGGTGACTGG 120
GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180
AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240
GGATTCTGGG CTGCTGCTGA ACTGCCCCAG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
GACACCTTGG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG 360
TACAGAAACT GGTTCCTGAA AGAGTTCTCT CGGTGAAAA GTGAGCTTGA GGATAACATA 420
AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAAGGCAC CACCATGCC 480
AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCTCTGT CGGCATGGGT 540
CTGGCACCCT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
ATCACAGCCG CTTTGACCCG GATTACCAGC AGTACCATGG ACTACGAAA GAAAGTGGTG 660
ACACAAGCCC AAGCCCACGA CCTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGGTGAGG 720
GAGTTTTTGG GTGAGAACAT ATCCAACTTT CTTTCCTTAG CTGGCAATAC TTACCAATC 780
ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACCTGAG CAATCTCAGC TGAAGCGGT 900
GACACAGTGG AGAGGGTTAA TGAACCCAGC ATCCTGAAAA TGAGCAGAGG AGTCAAGCTC 960
ACGAGTGTGG CCCCTGTAAG CTTCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
TCAAAGCACT TACATGAGGG GGCAAAAGTC GAGACAGCTG AGGAGCTGAA GAAAGTGGCT 1080
25 CAGGAGCTGG AGGAGAAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140
CAAGAACTGT GA
```

Seq ID NO: 74 Protein Sequence
Protein Accession #: NP_003652.1

```
30 1 11 21 31 41 51
| | | | |
MSALFLGVGV RAEEAGARVQ QNVPSGTDTG DPOSKPLGDW AAGTMDPES IFIEDAIKYF 60
KEKYSTQNLL LLLTDNEAWN GFVAAAELEPR NEADELRKAL DNLARQMIMK DNMWHDKQQ 120
YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTLVGMG 180
LAPFTEGGSL VLLFPGMELG ITAALTGITS STMDYGGKMW TQAQADLVI KSLDKLKEVR 240
EPLGENISNF LSLAGNTYQL TRIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVE SKHLHEGAKS ETAELKKVA 360
QLEEKILNIL NNNYKILQAD QEL
```

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

```
45 1 11 21 31 41 51
| | | | |
ATGGGGACCT CTCGAGCAG CAGCACCGCC CTGCCTCCT GCAGCCGCAT CGCCCGCCGA 60
GCCACAGCCA CGATGATGCG GGGCTCCCTT CTCTGCTTGG GATTCTCTAG CACCACCACA 120
GCTCAGCCAG AACAGAAGGC CTGGAATCTC ATTGGCAGAT ACGCCATGTG TGACCGTGCC 180
ACCGGCCAGG TGCTAACCTG TGACAAAGTG CCAGCAGGAA CCTATGCTCT TGAGCATTGT 240
ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG 300
AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA 360
TTACCTTGTG TGCCTTTGAC TGACCGAGAA TGCACTTGCC CACCTGGCAT GTTCCAGTCT 420
AACGCTACCT GTGCCCCCA TACGGTGTGT CCTGTGGGT GGGGTGTGCG GAAGAAAGGG 480
ACAGAGACTG AGGATGTGGG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCTC 540
TCTAGTGTGA TGAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGTGTATC 600
AAGCCGGGGA CCAAGGAGAC AGACACGTC TGTGGCACAC TCCGTCCTT CTCCAGCTCC 660
ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCAGCCCTG AGCAGATGGA AACCCATGAA 720
GTCCCTTCTT CCACTTATGT TCCCAAAGGC ATGAACCTCA CAGAATCCAA CTCTTCTGCG 780
TCTGTTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC 840
TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC 900
CAGCAAGGCC CCCACCAACG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG 960
GGCGAGAAGT CCAGCAGGCC CATCAAGGGC CCCAAGAGGG GACATCCTAG ACAGAACCTA 1020
CACAAGCATT TTGACATCAA TGAGCATTTG CCCTGGATGA TTGTGCTTTT CCTGTGCTG 1080
GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAAGGG 1140
CCCCGGCAGG ATCCAGTGC CATTGTGGA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200
ACCCAGAACG GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG 1260
CTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320
AGTGAGAGGG AGGTGTGCTG TTTCTCCAAT GGGTACACAG CCGACCAAGA CGGGGCTAC 1380
CGAGCTCTGC AGCACTGGAC CATCCGGGGC CCGGAGGCCA GCCTCGCCCA GCTAATTAGC 1440
GCCCTGCGCC AGCACCAGG AACTAGTGT GTGGAAGAAG TTGCTGGGCT GATGGAAGAC 1500
ACCAACCAGC TGGAACTGA CAAACTAGCT CTCCGATGA GCCCAGCCC GCTTAGCCCG 1560
AGCCCATATC CCAGCCCAA CGCGAAACTT GAGAATTCGG CTCTCCTGAC GGTGGAGCCT 1620
TCCCAACAGG ACAAGACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCTT TCTCCGCTGT 1680
GACTCTACAT CAGTCGTGCG GCAGGTAGGC CTGACCCCTT GTGACTTGCA GCCTATCTTT 1740
AAGAAGGACA CAGTGTGTGG GCAGGTAGGC CTGACCCCTT GTGACTTGCA GCCTATCTTT 1800
GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAGA GATTCGCCAG 1860
GCTGAGGACA AACTAGACCG GCTATTTCGAA ATTATTGGAG TCAAGAGCCA GGAAGCCAGC 1920
```


CAGACCCTCC TGGACTCTGT TTATAGCCAT CTCCTGACC TGCTGTAG

Seq ID NO: 76 Protein Sequence
 Protein Accession #: NP_055267.1

5
 10
 15
 20

1	11	21	31	41	51	
MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLLGLFLSTTT	AQPEQKASNL	IGTYRHVDRA	60
TGQVLTCDDK	PAGTYVSEHC	TNTSLRVCS	CPVGTFTTRHE	NGIEKCHDCS	QPCPNPMIEK	120
LPCAALTDRE	CTCPPGMFOS	NATCAPHTVC	FVGMGVRKKG	TETEDVRCKQ	CARGTFSDVP	180
SSVMKCKAYT	DCLSQLNVI	KPGTKETDNV	CGTLPSPFSS	TSPSPGTALF	PRPEHMETHE	240
VPSSTVVPKG	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVNVH	300
QQGFHRRHIL	KLLPSMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNRKWIYY	CNGHGIDILK	420
LVAAQVGSQW	KDIYQPLCNA	SEREVAASFN	GYTADHERAY	AALQHEWTIRG	PEASLAQLIS	480
ALRHRRNDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPISP	SPISPSPNAKL	ENSALLTVEP	540
SPQDKNKGFP	VDESEPLLR	DSTSSGSSAL	SRNGSFITKE	KKDTVLRQVR	LDPCLQPIF	600
DDMLHPLNPE	ELRVIEEIPQ	AEDKLDRLFE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 77 DNA sequence
 Nucleic Acid Accession #: NM_003105.3
 Coding sequence: 123..6767

25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75

1	11	21	31	41	51	
GGCGCGGGCG	GCCTGGAGCC	CGGGAGCGG	CGCGCGCGGT	CCCGGCCAG	CCGGCTCTCC	60
TGGCCTCGCG	CTGCACATTC	TCTCCTGGCG	CGGGCGCCAC	CTGCAGTAGC	GTTCCGCCGA	120
ACATGGCGAC	ACGAGCAGC	AGGAGGGAGT	CGCGACTCCC	GTTCTCTATC	ACCCTGGTCG	180
CACTGCTGCC	GCCCGAGCT	CTCTGCGAAG	TCTGACGCA	GAGGCTGCAC	GGCGGCAGCG	240
CGCCCTTGCC	CCAGGACCGG	GGCTTCTCTG	TGGTGCAGGG	CGACCCGCGC	GAGCTGCQGC	300
TGTGGGCGCG	CGGGGATGCC	AGGGGGCGGA	GCCGCGCGGA	CGAGAAGCCG	CTCCGGAGGA	360
AACGGAGCGC	TGCCCTGCAG	CCCGAGCCCA	TCAAGGTGTA	CGGACAGGTT	AGTCTGAATG	420
ATTCCCAACA	TCAGATGGTG	GTGCACTGGG	CTGGAGAGAA	AAGCAACGTG	ATCGTGGCCT	480
TGGCCCGAGA	TAGCCTGGCA	TTGGCGAGGC	CCAAGAGCAG	TGATGTGTAC	GTGTCTTACG	540
ACTATGGAAA	ATCATTCAAG	AAAATTTTCA	ACAAGTTAAA	CTTTGGCTTG	GGAAATAGGA	600
GTGAAGCTGT	TATGCCCCAG	TTCTACCACA	GCCCTGCGGA	CAACAAGCGG	TACATCTTTG	660
CAGACGCTTA	TGCCCAGTAC	CTCTGGATCA	CGTTTGACTT	CTGCAACACT	CTTCAAGGCT	720
TTTCCATCCC	ATTTGGGSCA	GCTGATCTCC	TCCTACACAG	TAAGGCCTCC	AACCTTCTCT	780
TGGGCTTTGA	CAGGTCCAC	CCCAACAAGC	AGCTGTGGAA	GTCAAGTAGC	TTTGGCCAGA	840
CCTGGATCAT	GATTGAGGAA	CATGTCAAGT	CCTTTTCTTG	GGGAATTGAT	CCCTATGACA	900
AACCAAAATC	CATCTACATT	GAACGACACG	AACCTCTCTG	CTACTCCACT	GTCTTCCGAA	960
GTACAGATTT	CTTCCAGTCC	CGGAAAACC	AGGAAGTGAT	CCTTGAGGAA	GTGAGAGATT	1020
TTACAGTTCT	GGACAAGTAC	ATGTTTGCTA	CAAAGGTGGT	GCATCTCTTG	GGCAGTGAAC	1080
AGCAGTCTTC	TGTCAGCTC	TGGGTCTCCT	TTGGCCGGAA	GCCCATGAGA	GCAGCCAGT	1140
TTGTACAAAG	ACATCCTATT	AATGAATATT	ACATCGCAGA	TGCTCCGAG	GACCAAGTGT	1200
TTGTGTGTGT	CAGGCACAGT	AACAACCGCA	CCAAATTATA	CATCTCAGAG	GCAGAGGGGC	1260
TGAAGTTCTC	CTGTGCTTGT	GAGAACGTGC	TCTATTACAG	CCCAGGAGGG	GCGGCAGTGT	1320
ACACCTTGGT	GAGGTATTTT	GCAAAATGAC	CATTGTCTGA	CTTCCACCGA	GTGGAAGGAT	1380
TGCAAGGAGT	CTACATTGCT	ACTCTGATTA	ATGGTTCTAT	GAATGAGSAG	AACATGAGAT	1440
CGGTCAACAC	CTTTGACAAA	GGGGGAACCT	GGGAGTTTCT	TCAGGCTCCA	GCCTTCAOAG	1500
GATATGGAGA	GAAATCAAT	TGTGAGCTTT	CCCAGGCGTG	TTCCCTTCAT	CTGGCTCAGC	1560
GCCTCAGTCA	GCTCCTCAAC	CTCCAGTCC	GGAGAATGCC	CATCCTGTCC	AAGGAGTCGG	1620
CTCCAGGCCT	CATCATCGCC	ACTGGCTCAG	TGGGAAAGAA	CTTGGCTAGC	AAGACAAACG	1680
TGTACATCTC	TAGCAGTGT	GGAGCCAGGT	GGCGAGAGGC	ACTTCTTGGA	CCTCACTACT	1740
ACACATGGGG	AGACCAOCCG	GGAATCATCA	CGGCCATTGC	CCAGGGCATG	GAAACCAACG	1800
AGCTAAATAA	CAGTACCAAT	GAAGGGGAGA	CCTGGAAAAC	ATTCACTCTC	TCTGAGAACG	1860
CAGTGTTTGT	GTATGCTCTC	CTCAGAGAAC	CTGGGGAGAA	GAGCACTGTC	TTCAACCATCT	1920
TTGGCTCGAA	CAAGAGAGAT	GTCCACAGCT	GGCTGATCCT	CCAGGTCAAT	GCCACGGATG	1980
CCTTGGGAGT	TCCCTGCACA	GAGAATGACT	ACAAGCTGTG	GTCAACCATCT	GATGAGOGGG	2040
GGAAATGAGT	TTTGTGGGA	CACAAGACTG	TTTTCAAACG	GCGGACCCCC	CATGCCACAT	2100
GCTTCAATGG	AGAGGACTTT	GACAGGCCGG	TGGTCTGTGC	CAACTGCTCC	TGCACCCGGG	2160
AGGACTATGA	GTGTGACTTC	GGTTTCAAGA	TGAGTGAAGA	TTTGTCAATTA	GAGGTTTGTG	2220
TTCCAGATCC	GGAAATTTCT	GGAAAGTCAT	ACTCCCTTCC	TGTGCTTGTG	CCTGTGGGTT	2280
CTACTTACAG	GAGAACGAGA	GGCTACCGGA	AGATTTCTGG	GGACACTTGT	AGCGGAGGAG	2340
ATGTTGAAGC	GCGACTGGAA	GGAGAGCTGG	TCCCTGTGCC	CCTGGCAGAA	GAGAACGAGT	2400
TCATTCTGTA	TGCTGTGAGG	AAATCCATCT	ACCGCTATGA	CCTGGCCTCG	GGAGCCACCG	2460
AGCAGTTGCC	TCTCACCGGG	CTACGGGCAG	CAGTGGCCCT	GGACTTTGAC	TATGAGCACA	2520
ACTGTTTGTA	TTGGTCCGAC	CTGGCCTTGG	ACGTCAATCA	GCGCCTCTGT	TTGAATGGAA	2580
GCACAGGGCA	AGAGGTGATC	ATCAATTCTG	GCCTGGAGAC	AGTAGAAGCT	TTGGCTTTTG	2640
AACCCCTCAG	CCAGCTGCTT	TACTGGGTAG	ATGCAGGCTT	CAAAAAGATT	GAGGTAGCTA	2700
ATCCAGATGG	CGACTTCCGA	CTCACAATCG	TCAATTCTCT	TGTGCTTGAT	CGTCCCGAGG	2760
CTCTGGTCTCT	CGTGCCCAAC	GAGGGGGTGA	TGTTCTGGAC	AGACTGGGGA	GACCTGAAGC	2820
CTGGGATTTA	CTGGAGCAAT	ATGGATGGTT	CTGCTGCCTA	TCACTGGGTG	CTGAGGATG	2880
TGAAGTGGCC	CAATGGCATC	TCTGTGGACG	ACCAGTGGAT	TTACTGGAGC	GATGCCATACC	2940
TGGAGTGCAT	AGAGCGGATC	ACGTTTCAAGT	GCCAGCAGCG	CTCTGTTCAT	CTGGACAACC	3000
TCCCGCACCC	CTATGCCATT	GCTGTCTTTA	AGAAATGAAAT	CTACTGGGAT	GACTGGTCAC	3060
AGCTCAGCAT	ATTCCGAGCT	TCCAAATACA	GTGGGTCCCA	GATGGAGATT	CTGGCAAACC	3120
AGCTCAGCGG	GCTCATGGAC	ATGAAGATTT	TCTACAAGGG	GAAGAACACT	GGAAGCAATG	3180

5
10
15
20
25
30
35
40
45
50
55
60
65

CCTGTGTGCC CAGGCCATGC AGCCTGCTGT GCCTGCCCAA GGCCAACAAC AGTAGAAGCT 3240
GCAGGTGTCC AGAGGATGTG TCCAGCAGTG TGCTTCCATC AGGGGACCTG ATGTGTGACT 3300
GCCCTCAGGG CTATCAGCTC AAGAACAATA CCTGTGTCAA AGAAGAGAAC ACCTGTCTTC 3360
GCAACCACTA TCGCTGCAGC AACGGGAAC GTATCAACAG CATTGTGGTG TGTGACTTTG 3420
ACAAACGACTG TGGAGACATG AGCGATGAGA GAAACTGCCC TACCACCATC TGTGACCTGG 3480
ACACCCAGTT TCGTGTCCAG GAGTCTGGGA CTGTATATCC ACTGTCTCAT AAATGTGACC 3540
TTGAGGATGA CTGTGGAGAC AACAGTGATG AAAGTCATTG TGAATGCAC CAGTGCCGGA 3600
GTGACGAGTA CAATCTGCAGT TCCGGCATGT GCATCCGCTC CTCTGGGTA TGTGACGGGG 3660
ACAACGACTG CAGGGACTGG TCTGATGAAG CCAACTGTAC CGCATCTAT CACACCTGTG 3720
AGGCCTCCAA CTTCCAGTGC CGAAACGGGC ACTGCATCCC CCAGCGGTGG GCGTGTGACG 3780
GGGATACGGA CTGCCAGGAT GGTTCGGATG AGGATCCAGT CAACTGTGAG AAGAAGTGCA 3840
ATGGATTCCG CTGCCCAAAC GGCACCTGCA TCCCATCCAG CAAACATTGT GATGGTCTGC 3900
GTGATTGTCT TGATGGCTCC GATGAACAGC ACTGCGAGCC CCTCTGTACG CACTTCATGG 3960
ACTTTGTGTG TAAGAACCOC CAGCAGTGCC TGTTCACCT CATGGTCTGT GACGGAATCA 4020
TCCAGTGCOC GCAGCGGTCC GATGAGGATG CGGCGTTTGC AGGATGTCTC CAAGATCCCTG 4080
AGTTCCACAA GGTATGTGAT GAGTTCGGTT TCCAGTGTCA GAATGGAGTG TGCATCAGTT 4140
TGATTGTGAA CTGCGAGCGG ATGGATGATT GCGGCGATTA TTCTGATGAA GCCAACTGCG 4200
AAAACCCAC AGAAGCCCCA AACTGCTCCC GCTACTTCCA GTTTCGGTGT GAGAAATGGCC 4260
ACTGCATCCC CAACAGATGG AAATGTGACA GGGAGAACGA CTGTGGGGAC TGGTCTGATG 4320
AGAAGGATTG TGGAGATTCA CATATTCTTC CCTTCTCGAC TCCTGGGGCC TCCACGTGTC 4380
TGCCCAATTA CTACCGCTGC AGCAGTGGGA CCTGCGTGAT GGACACCTGG GTGTGCGACG 4440
GGTACCGGAA TTGTGAGATG GGCCTGACG AGGAAGCCTG CCCCTTGCTT GCAAACTGCA 4500
CTGCTGCCTC CACTCCACCC CAACTTGGGC GATGTGACCG ATTTGAGTTC GAATGCCACC 4560
AACCAGAGAC GTGTATTCCC AACTGGAAGC GCTGTGACGG CCAACAAGAT TGCAGGATG 4620
GCCGGGACGA GGCCAAATTGC CCCACACACA GCACCTTGAC TTGCATGAGC AGGGAGTTCC 4680
AGTGCAGGGA CGGGGAGGCC TGCAATTGTGC TCTCGGAGCG CTGCGACGGC TTCTTGGACT 4740
GCTCGGACGA GAGCGATGAA AAGGCGTGA GTGATGAGTT GACTGTGTAC AAAGTACAGA 4800
ATCTTCAGTG GACAGCTGAC TTCTCTGGGG ATGTGACTTT GACCTGGATG AGGCCCAAAA 4860
AAATGCCCTC TGCTTCTTGT GTATATAATG TCTACTACAG GGTGGTTTGA GAGAGCATAT 4920
GGAAGACTCT GGAGACCCAC AGCAATAAGA CAAACACTGT ATTAAAAGTC TTGAAACCAAG 4980
ATACCACTGA TCAGGTATAA GTACAGGTTT AGTGTCTCAG CAAGGCACAC AACACCAATG 5040
ACTTTGTGAC CTTGAGGACC CCAGAGGGAT TGCCAGATGC CCCTCGAAAT CTCACGCTGT 5100
CACTCCCCAG GGAAGCAGAA GGTGTGATG TAGGCCACTG GGCTCTCCC ATCCACACCC 5160
ATGGCCTCAT CCGTGAGTAC ATTGTAGAAT ACAGCAGGAG TGGTTTCAAG ATGTGGGCTC 5220
CCGAGAGGGC TGCTAGTAAC TTTACAGAAA TCAAGAACTT ATTGGTCAAC ACTCTATACA 5280
CCGTGAGAGT GGTCTGCGTG ACTAGTCCGT GAATAGGAAA CTGGAGCGAT TCTAAATCCA 5340
TTACCAACAT AAAAGGAAA GTGATCCAC CACCAGATAT CCACATTGAC AGCTATGGTG 5400
AAAATTATCT AAGCTTCACC CTGACCATG AGAGTGATAT CAAGGTGAAT GGCTATGTGG 5460
TGAACTTTT CTGGGCATT GACACCACA AGCAAGAGAG GAGAACCTTG AACTTCCGAG 5520
GAAGCATATT GTACACAAA GTTGGCAATC TGACAGCTCA TACATCCTAT GAGATTTCTG 5580
CCTGGGCCAA GACTGACTTG GGGGATAGCC CTCTGGCATT TGAGCATGTT ATGACCAGAG 5640
GGGTTCGCCC ACCTGCACCT AGCCTCAAG CCAAGGCCAT CAACCGACT GCAGTGGAAAT 5700
GTACCTGGAC CGGCCCCCGG AATGTGGTTT ATGTGATTTT CTATGCCACG TCCTTTCTTG 5760
ACCTCTATCG CAACCCGAAG AGCTTGACTA CTCTACTCCA CAACAAGAGC GTCATTGTCA 5820
GTAAGGATGA GCAATATTG TTTCTGGTCC GTGTAGTGGT ACCCTACCAG GGGCCATCCT 5880
CTGACTACGT TGTAGTGAAG ATGATCCCGC ACAGCAGGCT TCCACCCCGT CACCTGCATG 5940
TGGTTTCATC GGGCAAAACC ATTGCAGTCA AAGATCTCAT AAGAAGACT GACAGGAGCT 6000
ACCAGGACTT GTTGTATGCA ATTCAGTCA AAGATCTCAT AAGAAGACT GACAGGAGCT 6060
ACAAATATAA ATCCCGTAAC AGCACTGTGG AATACACCTT TAACAAGTGT GAGCCTGGCG 6120
GGAAATACCA CATCATTTGT CAACTGGGGA ACATGAGCAA AGATTCCAGC ATAAAAATTA 6180
CCACAGTTTC ATATCAGCA CCTGATGCCT TAAAAATCAT AACAGAAAAT GATCATGTTT 6240
TTCTGTTTTG GAAAAGCTGT GCTTTAAAG AAAAGCATTT TAATGAAAAG AGGGGCTATG 6300
AGATACACAT GTTTGATAGT GCCATGAATA TCACAGCTTA CCTTGGGAAT ACTACTGACA 6360
ATTTCTTTAA AATTTCCAAC CTGAAGATGG GTCAATAATTA CACGTTTACC GTTCAAGCAA 6420
GATGCCTTTT TGGCAACCAG ATCTGTGGGG AGCCTGCCAT CCTGCTGTAC GATGAGCTGG 6480
GGTCTGGTGC AGATGCATCT GCAACGCAAG CTGCCAGATC TACGGATGTT GCTGCTGTGG 6540
TGGTGCCCAT CTTATTCCCTG ATACTGCTGA GCCTGGGGGT GGGGTTTGCC ATCCCTGTACA 6600
CGAAGCACCG GAGGCTGCAG AGCAGCTTCA CCGCCTTCGC CAACAGCCAC TACAGCTTCA 6660
GGCTGGGGTG CGCAATCTTC TCCTCTGGGG ATGACCTGGG GGAAGATGAT GAAGATGCCC 6720
CTATGATAAC TGGATTTTCA GATGACGTCC CCATGGTGAT AGCCTGAAAG AGCTTTCTCTC 6780
ACTAGAAACC AAATGGTGTA AATATTTTAT TTGATAAAGA TAGTTGATGG TTTATTTTAA 6840
AAGATGCACCT TTGAGTTGCA ATATGTTATT TTTATATGGG CCAAAACCAA AAAACAAAAA 6900
AAAAAA

70
75

Seq ID NO: 78 Protein Sequence
Protein Accession #: NP_003096.1

1 11 21 31 41 51
MATRSSRRES RLPLFLTLVA LLPPGALCEV WTQRLHGSSA PLPQDRGFLV VQGDPRELRL 60
WARGDARGAS RADEKPLRRK RSAALQPEPI KVGQVSLND SHNQMVVHWA GEKSNVIVAL 120
ARDSLALARP KSSDVVYSYD YGKSFKKISD KLNFGILGNRS EAVIAQFYHS PADNKRYIFA 180
DAYAQYLWIT FDPCTNLQGF SIPFRAADLL LHSKASNLLL GFDRSHPNKQ LKWSDDFGQT 240
WIMIQEHVKS FSWGIDPYDK PNTIYIERHE PSGYSTVFRS TDFPQSRENY EVILEEVRF 300
QLRDKYMFAT KVVHLLGSEQ QSSVQLWVSF GRKPMRAAQF VTRHPINEY IADASEQVVF 360
VCVSHSNRRT NLYISEAEGL KFSLSLENVL YYSPPGAGSD TLVRYFANEP FADPHRVEGL 420
QGVYIATLIN GSMNEENMRS VITFDKGGTW EFLQAPAFITG YGEKINCELS QGCSLHLAQR 480
LSQLNLQLR RMPILSKESA PGLIATGVSF GKNLASKTNV YISSAGARW REALPGPHY 540

TWGDHGGIIT AIAQGMETNE LKYSTNEGET WKTFFIFSEKP VFVYGLLTPG GEKSTVFTTIF 600
 GSKNENHSHW LILQVNA7DA LGVPTCTENDY KLVSPSDERG NECLLGHKTV FKRRTPHATC 660
 FNGEDFDRPV VVNSCSTRE DYECDFGFKM SEDLSLEVCV PDPEFSGKSY SPVPVPCFVGS 720
 TYRRTRGYRK ISGDTCSGSD VEARELEGLV PCPLAENEF ILYAVRKSII RYDLASGATE 780
 QLPLTGLRAA VALDFDYEHN CLYWSDLALD VIQRLCLNGS TGQEVIIINS LETVEALAFE 840
 FLSQLLYWVD AGFKKIEVAN PDGDPRLTIV NSSVLDRPRA LVLVPQEGVM FWTDMGDLKP 900
 GIYRSNMDGS AAYHLVSESDV KWPNGISVDD QWIYWDAYL ECIERTIFSG QQRSVILDNL 960
 PHPYAIAVFK NEIYWDWDSQ LSIFRASKYS GSQMEILANQ LTGLMDMKIF YKGKNTGSNA 1020
 CVPRPCSLLC LFKANNRSRC RCPEDVSSSV LPSGDLMDCC PQGYQLKNNT CVKEENTCLR 1080
 NQYRCNGNRC INSIWNCDFD NDCGDMSDER NCPTTICDLG TQFRQESGT CIPLSYKCDL 1140
 EDDCGNDSDE SHCEMHQCRS DEYNCSGSMC IRSSWVCDGD NDCRDWSDA NCTAIYHTCE 1200
 ASNFQCRNGH CIPQWACDG DTDCCQDGSDE DPNVCEKKN GFRCPNGTCI PSSKHCDGLR 1260
 DCSGDSDEQH CEPLCTHFMF FVCKNRQCL FHSVMDGII QCRDGSDEDA AFAGCSQDPE 1320
 FHKVCEFGF QCGNGVCISL IWKCDGMDCC GDYSDEANCE NPTAEPNCSR YQFRCENGH 1380
 CIPNRNKKDR ENDCGDSDE KDCGDSHILP FSTPGPSTCL PNYRCSSGT CVMdTWVCDG 1440
 YRDCAGDSDE EACPLLANVT AASTPTQLGR CDRFEFECHQ PKTCIPNWKR CDGHQDCQDG 1500
 RDEANCPHSL TLTCMSREFO CEDGEACIVL SERCDGFLDC SDESDEKACS DELTVYKQV 1560
 LQWADFSGD VTILTMWRPK MPASACVNV YRVVVGESIW KTLTHSNKT NTVLKVLPD 1620
 TTYQVKVQV CLSKAHNTND FVTLRTPEGL PDAPRNQLS LPREAEGVIV GHWAPPIH 1680
 GLIREYIVY SRSGSKMAS QRAASNFTET KNLLVNTLYT VRVAAVTSRG IGWNSDSKSI 1740
 TTIKGVIPP PDHIDSYGE NYLSFTLTME SDIKVNGYV NLFWAFDTHK QERRTLNFRG 1800
 SILSHKVMNL TAHTSYEISA WAKTDLGDSF LAFEHVMTRG VRPPAPSLKA XAINQTAVEC 1860
 TWGTPRNVVY GIFYATSPFD LYRNPKSLTT SLHNKTIVS KDEQYFLVR VVVPYQGPSS 1920
 DVVVVKMIPD SRLPPRHHLV VHTGKTSVVI KWESFYDSD QDLIAIAVK DLIRKTRSY 1980
 KVKSRNSTVE YTLNKLPEGG KYHIIVQLGN MSKDSIKIT TVSLAPDAL KIITENDHVL 2040
 LFWKSLALKE KHPNESRGYE IHMFDSAMNI TAYLGNITDN FFKISNLKMG HNYTPTVQAR 2100
 CLFNQICGE PAILLYDELG SGADASATQA ARSTDVAADV VPILFLILLS LGVGFALY 2160
 KHRRLQSSPT APANSHYSSR LGSAPSSGD DLGEDDEDAP MITGFSDDVP MVIA

Seq ID NO: 79 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 120-755

1 11 21 31 41 51
 CCTGCACTC CCTGCCAGT GTGCGAGGCA GCGTGAAGCT GGGGCTGCT CCCCAGGCC 60
 TCTGGAGCGC ATCTCAGACC TTCTGAGACC TATGTGCTG GCCCCAGCA ACCCGCAACA 120
 TGGCAGATGG GGCAAGAGCC AACCCCAAG GGTTCAAAA GAAGGTGCTG GATAGATGCT 180
 TCTCTGGGTG GAGGGGCCCA CGCTTCGGGG CCTCCTGTCC TTCAAGAACC TCCAGGTCTA 240
 40 GCTCGGTAT GAAGAAGTTC TTCACCGTGG CCATCCTTGC TGCGACGCTT TGTCCACAG 300
 CTCACGCGAG CCTGCTCAAC CTGAAGGCCA TGGTGGAGGC CGTCACAGGG AGGAGCGCCA 360
 TCCTGTCTCT CGTGGGCTAC GGTGCTACT GTGGGCTGG GGGCGTGGC CAGCCCAAGG 420
 ATGAGGTGGA CTGCTGCTGC CACGCCACAG ACTGCTGCTA CCAGGAACCT TTTGACCAAG 480
 GCTGTCAACC CTATGTGGAC CACTATGATC ACACCATCGA GAACAACACT GAGATAGCT 540
 45 CAGTGTGAT CAACAAGACA GAGTGTGACA AGCAGACATG CATGTGTGAC AAGAACATGG 600
 TTCTGTGCTT CATGAACAG AGGTACCGAG AGGAGTACCG TGGCTCTCTC AATGTCTACT 660
 GCCAGGGCCC CACGCCCAAC TGCAGCATCT ATGAACCGCC CCTGAGGAG GTCACTGTGA 720
 GTCAACAATC CCCAGCGCCC CCGGCCCTCT CCTAGAGCCT CTGAGGTTTG AGAGAGAGAG 780
 CGGAGGAGG GTCTGGCTTG GGGACAGAC GAGGTGACAG GAGGGTAGGA CCGAGGCCAG 840
 50 GAGCCTGAGG GTTCTGTGTT GCCTCCTCCC TGGAGCTCTC CAGTGAGGGC TCAGCTCTCA 900
 GAGGACTCAG GAAGGCTTGG GTCTGTGACT CCCCAGGCCA GCGCCAGGCA TGGGTGCTCT 960
 CTGCTGTCTG TTCTGACTG GGTGGGAGGC ACGGAGCTTA TAGGGGCTCT TCCTGAGGGT 1020
 GGCCGGGGAG ACCTGAGAGA GAGGAGGAGG GGCCTCTGAG TGGGGCTCT GTTGTGCGG 1080
 CAGTTTAAAC TCCCGGAGC CTTAGAAAGT CTGAGCCTTA GAAAGTCTGG GCCTGAGCAT 1140
 55 CCAGGCCAG AGCTGATGC ATCCTCGGCC CAAGATCACA GGAAGGCAGA TTGCTGGTCA 1200
 CAAAGCATGG GTTCCGGGAG CCCCTCAGCT GATCCACAG GATGGCCTGG GGTGGTGGCT 1260
 ACTTTGGGCT TGAAGCTCTC CAGGTTTACA CCTAGGGGA TGTGAGTGC TGAAGTCTCC 1320
 CACTGAGGTG GCCATGAGTC GAGCAGGCTC CTGGGCACTG ACAGAGCCAC ACACCAAGT 1440
 AGCCCTCAAG TCTAGCCTCA GAGCAGGCTC CTGGGCACTG ACAGAGCCAC ACACCAAGT 1500
 60 ACACCCCAAG GGCTAATATG GGGACACACA AAAATATGGC CTTCAACACC TACAAGTCTT 1560
 CTCTGTGTCC CCATCGAGC CATGCACATC ACCCAACCC TGCTCTGCCA CACCACTGG 1620
 GTCTGAGGAG CACTCTACC CCGGGCTCC GGGTCCCTGA CAGACACTGC CCTCTGGCC 1680
 TGCACTGGA ATGGCAGCCA GAACACTGGA GGGGACCCA CACCTCTCT CCTCTGGCTG 1740
 TGGATGGGTG TTGCAAGTCC CATCCCTCTT GGCCTGCACC TGGAACAGCA GCCAGAACAC 1800
 65 CGGAGGGGGA CCCACACCTT CTCTCCCTGG GCTGTGGGCA GCGCTCACAA GTCCCATTTG 1860
 TGGGAAGAG GCTGAGGGCT GAGACCCACC TCAGTGAAGA GGGAAACGTA AGCAGGGAGA 1920
 GCATCAAGCG GGGAGGCAGC CTGGAACCTT CTAGAAGAGG GTCAAGTAG GAGGCTACAT 1980
 GGAAGCTTCT AGAAGGCAGT AAGGAACAGG GTGCTGAAGG AGAGGGGAGA AGATGGGAGC 2040
 70 ATGGAGAGAC GAGGTGAGTG ACAGCCACCA GCAGGGACGG GCCTCCAGGC AACACAGAGG 2100
 AGCTGGGGGC CAGGGCCTTA CCGGGCTGGG TTCTGTGTG GGGGCTGGAG CTGGGGCTGA 2160
 AGTGGAGGGG ACCGCCCTGC GGGCCCAAGC ACTGTGTTT CTCCAGGTGC ACCTTACCTT 2220
 CCTCTTACC TGCCCGAGCC CCAACTCAGG GTCACTCAGG TCACCGAGC CAGCCCAACC 2280
 TGCCCGAAAA CCACTGAAGC CACCTCCGC CCGACGTCAA CCGGATCCA CTAGTTTGA

Seq ID NO: 80 Protein sequence:
 Protein Accession #: Bos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
MADGAKANPK GFKKKVLDR FSGWRGPRFG ASCPSRTSRS SLGMMKKFTV AILAGSVLST 60
AHGSLNLKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCCAH DCCYQELFDQ 120
5 GCHPYVDHYD HTIENNTIEV CSDLNKTEDC KQTCMCDKNM VLCLMNQTYR EBYRGFLNVY 180
CQGPPTNCSI YEPPEEVTC SHQSPAPPAP P

```

Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: NM_018136.1
Coding sequence: 38..2218

```

1      11      21      31      41      51
|      |      |      |      |      |
GAAATCTGTA CGAACTATTC AGGCTGCTTT TAGAGGCATG AAAGTTAGAC AAAAATTGAA 60
15 AAATGTATCA GAGGAAAAGA TGGCAGCCAT .TGTTAAACCA TCTGCACCTCT GCTGTTACAG 120
AAGCAAAACT CAGTATGAAG CTGTTCAAAG TGAAGGTGTT ATGATTCAG AGTGGTATAA 180
AGCTTCTGGC TTGCTTGTT CACAGGAAGC AGAGTATCAT TCTCAAAGTA GGGCTGCAGT 240
AACAATTCAA AAAGCTTTTT GTAGAATGGT CACAAGAAAA CTGGAACAC AGAATGTGC 300
TGCCCTACGG ATTCACTTCT TCCTTCAGAT GGCTGTGTAT CGGAGAAGAT TTGTTACGCA 360
20 GAAAAGAGCT GCTATCACTT TACAGCATTA TTTTAGGAGC TGGCAAACCA GAAAACAGTT 420
TTTACTATAT AGAAAAGCAG CAGTGGTTTT ACAAATCAC TACAGAGCAT TTCTGTCTGC 480
AAAACATCAA AGACAAGTCT ATTTACAGAT CAGAAGCAGT GTTATCATT TCAAGCTAG 540
AAGTAAAGGA TTTATACAGA AACGGAAGTT TCAGGAAATT AAAAATAGCA CCATAAAAT 600
TCAGGCTATG TGGAGGAGAT ATAGAGCCAA GAAATATTTA TGTAAAGTGA AAGCTGCCTG 660
25 CAAGATTCAA GCCTGGTATA GATGTTGGAG AGCACACAAA GAATATCTAG CTGTATTAAA 720
AGCTGTTAAA ATTATTCAG GTTGCTTTCT TACCAAACTA GAGAGAACAC GGTTTTGTAA 780
TGTGAGAGCA TCAGCAATTA TCATTACAG AAAATGGAGA GCTATACTTC CTGCAAGAT 840
AGCTCATGAA CACTTCTTAA TGATAAAAAG ACATCGAGCT GCTTGTTTGA TCCAAGCACA 900
TTATAGAGGA TATAAAGGAA GGCAGGTCTC TCTTCGGCAG AAATCTGCTG CTTTGATCAT 960
30 ACAAAAATAT ATACGAGCCA GGGAGGCTGG AAAGCATGAA AGGATAAAAT ATATTGAATT 1020
TAAAAATCT ACAGTTATCC TACAAGCACT GGTGCGTGGT TGGCTAGTAC GAAAAAGATT 1080
TTTAAACAG AGAGCCAAA TTCGACTTCT TCACTTCACT GCAGCTGCAT ATTATCACCT 1140
GAATGCTGTT AGAATTCAAA GAGCCTATAA ACTTTACCTG GCTGTGAAGA ATGCTAACAA 1200
GCAGGTTAAT TCAGTCACTCT GTATTACAG ATGGTTTCGA GCAAGATTAC AAGAAAAGAG 1260
35 ATTTATTGAG AAATATCATA GCATCAAAAA GATTGAGCAT GAAGGTCAAG AATGTCTGAG 1320
CCAGCGAAAT AGGGCTGCAT CAGTAATACA GAAAGCAGTG CGCCATTTTC TCCTCCGTAA 1380
AAAGCGAAA AAATTCACATA GTGGAATCAT TAAAATTCAG GCATTATGGA GAGGCTATT 1440
TTGGAGGAAG AAAATGATT GTACAAAAAT TAAAGCTATA CGACTAAGTC TTCAAGTTGT 1500
TAATAGGAGG ATTCGAGAAG AAAACAAACT CTACAAAAGA ACTGCACCTG CACTTCATTA 1560
40 CCTTTTGACA TATAAGCACC TTTCTGCCAT TCTTGAGGCC TTAACACACC TAGAGGTAGT 1620
TACTAGATTG TCTCCACTTT GTTGAGGAA CATGGCCAG AGTGGAGCAA TTTCTAAAAT 1680
ATTTGTTTTG ATCCGAAAGT GTAATCGCAG TATTCCTTGT ATGGAAGTCA TCAGATATGC 1740
TGTGCAAGTC TTGCTTAATG TATCTAAGTA TGAGAAAAC ACTTCAGCAG TTTATGATGT 1800
AGAAAAATGT ATAGATATAC TATTGGAGCT TTTCAGATA TACCGAGAAA AGCCTGTAA 1860
45 TAAAGTTGCA GACAAGGCG GAAGCATTTT TACAAAAACT TGTGTTTTGT TGGCTATTTT 1920
ACTGAAGACA ACAATAGAG CCTCTGATGT ACAGAGTAGG TCCAAAGTTG TTGACCGTAT 1980
TTACAGTCTC TACAACTTA CAGCTCATAA ACATAAAATG AATACTGAAA GAATACCTTTA 2040
CAAGCAAAAG AAGAATCTCT CTATAAGCAT TCCTTTTATC CCAGAAACAC CTGTAAGGAC 2100
CAGAATAGTT TCAAGACTTA AGCCAGATTG GGTTTTGAGA AGAGATAACA TGGAGAAAT 2160
50 CACAAATCCC CTGCAAGCTA TTCAAAATGGT GATGGATACG CTTGGCATTG CTTATTAGTA 2220
AATGTAAACA TTTTCAGTAT GTATAGTGT AAGAAATATT AAAGCCAATC ATGAGTACGT 2280
AAAGTGATT TTGCTCTCTG GTTACAAGTT TTAATATCTG ACTTTGTTTT AAAAAACAT 2340
AAACTGTTCA TTACATCTTT CATTTTTATC ATTTATAGTT TTATGCATGT AATAAACTAA 2400
TATGTCATAA GATG

```

Seq ID NO: 82 Protein Sequence
Protein Accession #: NP_060606.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MKVRQKLKNV SEEKMAAIVN QSALCCYRSK TQYEAQVSEQ VMIQEWYKAS GLACSQEAAY 60
HSQSRAAVTI QKAFCRMVTR KLETQKCAAL RIQFFLQMAV YRRRFVQQRK AAITLQHYFR 120
TWQTRKQPLL YRKAADVLLQ HYRAFLSAKH QROVYLQIRS SVIIIQARSK GFIIQKRFQE 180
65 IKNSTIKIQA MWRRYRAKRY LCKVKAACKI QAWYRCWRAH KEYLAVLKAV KIIQGCFFTK 240
LERTRFLNVR ASAIIIQRKW RAILPAKIAH EHFLMIKRHR AACLIQAHYR GYKGRQVSLR 300
QKSAALLIQK YIRAREAGKH ERIKIEFKK STVILQALVR GWLVRKRFLE QRAKIRLLHP 360
TAAAYYHLNA VRIQRAYKLY LAVKNANKQV NSVICIQRFW RARLQEKRFI QKYHSIKKIE 420
HEGQECLSQR NRAASVIQKA VRHPLLRKKQ EKFTSGIIKI QALWRGVSWR KKNDCCTIKA 480
70 IRLSLQVVRN EIREENKLYK RTALALHYLL TYKHLAILE ALKHLEVVTR LSPLCENMA 540
QSGAISKIPV LIRSCNRSIP CMEVIRYAVQ VLLNVSKYEK TTSAVYDVEN CIDILLELLQ 600
IYREKPNKV ADKGGSIPTK TCCLLAILLK TTNRASDVRS RSKVVDRIYS LYKLTAKHKH 660
MNTERILYKQ KKNSSISIPP IPETPVRTRI VSRLPDQWVL RRDNMEEITN PLQAIQMVMD 720
TLGIPY

```

Seq ID NO: 83 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095

1 11 21 31 41 51
 1 TTCTCCCGCA ACCTTCCTCT CGCTCCCTCC CGTCCCCCCC AGCTCCTAGC CTCGACTCC 60
 5 CTCCCCCCT CACGCCCGCC CTCTCGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT 120
 TTCTGTCTCT CTCGCTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGTCTCT 180
 TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCAAGTT CACTCTGTCT CTCCTACTAT 240
 CTCTGCCCCC CTCTATCTCT GATACACAG CTGACCTCAT TTCCCGATAC CTTTTCCCCC 300
 CCGAAAGTA CAACATCTGG CCGCCCCCAG CCGGAAGACA GCCCGTCTCT CTTGGACAAT 360
 10 CAGACGAATT CTCCCCCCC CCCCAGGATC AAAAGCCATC CCCCCGCTCT GCCCGTCTG 420
 ACATTGGGCC CCGCGACTC GGCCAGAGCG GCGTGGCAG AGGAGTGTCC GGCAGGAGG 480
 CCAACGCCCG CTGTTGGGTT TGGGACACGC AGCAGGAGG TGGGCGGCG COTCGCCGGC 540
 TTCCAGACAC CAATGGGAAT CCCAATGGG AAGTCGATGC TGGTGTCTCT CACCTTCTTG 600
 GCCTTGCCTT CGTGTGCTAT TGCTGCTTAC CCGCCAGTG AGACCTGTG CCGCGGGGAG 660
 15 CTGTGGGACA CCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA 720
 AGCGTGTGA GCCGTGCGAG CCGTGGCATC GTTGGAGAGT GCTGTTTCCG CAGCTGTGAC 780
 CTGGCCCTCC TGGAGACGTA CTGTGTATCC CCGCCCAAGT CCGAGAGGGA CGTGTGAGC 840
 CCTCCGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCCAATAT 900
 GACACCTGGA AGCAGTCCAC CCAGCGCCTG CCGAGGGGCC TGCTGCTCTT CTTGCGTGCC 960
 20 CGCGGGGTC ACCTGCTCGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACCTCACCGT 1020
 CCGCTGATTG CTCTACCCAC CCAAGACCCC GCCACCGGG GCGCCCCCCC AGAGATGGCC 1080
 AGCAATCGGA AGTGAAGCAA ACTGCGCAA GTCTGCAGCC CCGCGCCACC ATCTGCAGC 1140
 CTCTCTCTGA CCAAGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200
 CCGCTGGGG CTCTCTCTGA CCGAGTCCCC GTGCCCGGCC TCCCGGAAC AGGCTACTCT 1260
 25 CTGCGCCCC CTCCATGGG CTGAGGAAGC ACAGCAGCAT CTTCAAAATC GTACAAATC 1320
 GATTGGCTTT AAACACCTTT CACATACCTT CCCCC

Seq ID NO: 84 Protein Sequence
 Protein Accession #: NP_000603.1

30 1 11 21 31 41 51
 1 MGIPMGKSM LLLTFLAFAS CCIAAYRPSE TLGGELVDT LQFVCGDRGF YFSRPASRVS 60
 RSRGIVEEC CFRSCDLALL ETYCATPAKS BRDVSTPPTV LPDNFPYRPV GKPFQYDTWK 120
 35 QSTQRLRRGL PALLRARRGH VLAKELEAPR EAKRHRPLIA LPTQDPAHGG APPEMASNRK 180

Seq ID NO: 85 DNA sequence
 Nucleic Acid Accession #: XM_092643.1
 Coding sequence: 1-5352

40 1 11 21 31 41 51
 1 ATGACTGAAG CCATTACAGA AGCAGCAGTA GCCTCAAGTG AGGAGGTGTC AGAGGAAAGA 60
 45 GACGACCTGG GGCCTCTTGA ATTACATGAC AGTGGTACCT TTCAACAAGT CGTGAACCTT 120
 CTGGACATCA TTGACAGCGA GTCAGCAAAG ACGGACACAA CAGGGGACAG CCTTGACATG 180
 CGGAAGACCC TGCCCTCGGT GATAATCATG GAGAAGGCCA CCAGTGAGCC TTCTGTAGTG 240
 ATAAACACTC TCATCCGCTG CCTGCAGGTG CCAGAGATTT CCACCCAGCG CAAGGTCAAC 300
 ATTTACAACA TCCTCCAGGA CATCATCCAG CAGGAGGGGG AGCTGGAGGA GCAGTGCCTG 360
 50 CAGAGGCTGG TGCCATTGCG CTCGAAGGAG ATGAGGGAGA TCCAGAGATG GGAGGGCTAT 420
 ATGAAGGCAG AGGTGGCCAG CGACACACTG GTGGCTCTGT CCGAAACCA CTTCAAGCTT 480
 GTCATGTAGC AGCTGCAGCA CCACCTCAAG CCCCTCAACC TCACTGATGA ATTTGTATC 540
 ATCACACTGG CCAAGCTGGC CAACGGCAAT GTGTTTGAAT TCATGCCATA CATGGGCATC 600
 ACCCTGGCTA CCATATTAC CATGCTGAGA CTGCGCAATG AAGCCCAAGT ACGCCAGCG 660
 55 ATCTGCAGTG CCATGGAGAC CTTCTGTGAG ACGGTGCAGT TTTATCTGAA GCACCTGGAG 720
 GAGAGCGTGT ACCCGTGAT GACTGAGGAG GAGTTTGGCC TGAAGGTGTT CCCCATGTAT 780
 CGCTACTTCG TGACAGTGTG GCTGAGGCAC TACAACCCCG AGGTGAAGCT GGGGTCATC 840
 AAGTCCCTGA AGCCCATGCT GGGCTCTCTT CTGCCCAAG ATGACCTGCG GGAGCAGGTC 900
 TACGACTACA TCCCTCTGCT GCTGGCGGAG TACCAGGGCA GTCTGGAGGT CTTGAGGCG 960
 60 ATCTTGAAC TGTCAGTCAC CACCAACACC CCTGTCCCC AAATGCAAGT ACACACCATT 1020
 TTACAGAAC TGCAAGTCCA GGTGTGCAAC AAGGCCCGG CCCAGCATCA GTACAGCAGC 1080
 CAGAATCTGA TGGAGATGTT GCATGCTTTC GTAGCCCTTG CTGCTCTCTA CCCCAGGAG 1140
 CTGATGAAGT TCTTCTCTAG CCAGATGGAG ACAAAACAAG AGGCCGTCG CGTGGGGACT 1200
 CTGAATCTGA TTAGGGCTAT AGTGAGCGCA GATGAGCCCA GGTGAGTAT CAGGGCCATC 1260
 65 TACCTGGCTA TCCGGGTAGT CAAGAACACC ATCTCTGATA CCGGTCCAA GGTGAGGATG 1320
 GCTATTCTCC ACATCATTTG GCAGTTGGCT CTCTGTGGCT ACCAGGAGAG AATCAAAGGC 1380
 TGGGGCTCTA AGTACCTGTC TGTGCAGCTG ACCTTATCCA CCTACAACT GACAAATGCG 1440
 CGGGAGAAGT TTTATCAGAG GGAATGGAG GAGAGGATGG TCCACAAAGT CACCATGGAC 1500
 ACTGTGAAGA TCATTACCTC TTCTGTCACT GGGATGACCA CCGAGTTTGT GGTGAGGCTG 1560
 70 CTGTGCTACA TCATGGAGAC AGACTACGTG GAAGCTTTGA CTCTATCTG TATCAGCTC 1620
 ACAAACTGCG CAGAACACCA GCTCCATGGC CAGGATGTGG ATGTACAGGT GGCTGGCAAG 1680
 AGCAGGCAAG TGGACCTGCC TGCACTCAG AAGCTGTGCG CCGCTCTCTT GGTGCTGATG 1740
 TCATCACTT ACAAGGGGGA GGGTCTGGG ATAGCCATGC TCAACCTCTT GAGGACCTG 1800
 AGCCAGAGCA TGCACCTCT CATGGCCGAC ATGTGGGAGC TGGAGATTGC GCTACTGCTC 1860
 75 CGGTACCTCG AAGAATATC TGAGTTCACT TGGGATCAGA AAGCCTGGGA AGACAAGCTG 1920
 ATTCAGTTTC TCGAAACTC CCTCAAGAAG ACCCGGGGGT CTAGCTGGAG CTTGCGCTTT 1980
 AGTAAAGAGC TGAACAACCA GATTGCGAGC TTGACAGCC CCTCTCTGGA GAAGGCTTTT 2040
 CTGTACCGGG CTTGGGCTT CACCTTGGCC ACAGGCTGG AGGCCAGCAA GGTGAGGCTC 2100
 CTGCTGTGAG AGCTGCTGTA CAAGACGGAC TACAGCAATG ACTTTGACAG CGAGGGTGTG 2160

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

ATTATGTGCT TTGGCCTGTG TGCCCGGGGC CAGGTAAAAA CGGTGCTGAA TGTGCTTCAT 2220
 GACTTCGAGG AGAGGATCCA GGAGTCAGAG CAGTCCTGGC AGATCAGTGC TTGGCGGAAG 2280
 GACCATCCCT GGAGGCGGGA GACAGTGAAA AGTGCCCTCA TGGTGATGTA TAGCTGCGTG 2340
 GCCTCCTACT GCCACCCCA GTTGCTCCTC AACCTGCTGG ACAGCCCAT CACGCTAAG 2400
 ATCATTACCC ATTATGTCAG CAGCTGCCAG GACATCTGTC TCAAAATGGC CTTCATGAAG 2460
 AGTGTGTGTC AGGTATACCA GGCCATCAAC AACATCAAGG ACCTGGAGGA CTTCACCTTT 2520
 GCCCAGAAGA CACTCTTAC CAGCATTATA GTGGCGGTCA TCAAGGCAGA ACCGACTGAC 2580
 AACCTGGTTT CTCAGTGCG AGCCTTGCGG ATGGAGGCC TCTCGCACCT GAGCAAGCTG 2640
 AAGCCTTTCT ACTCCACAGA GGAACACAGT GAGCTGATGG ATATCAGCAT ACATTCTGTA 2700
 ATTTCTCTCC AACTCCCAGG AGAGGACAAT GAGTCCATTA AGACCTGTGA TGCAATGCC 2760
 CTGAGCTCCC TGGAGCAGCT GATGGAGAGC CTCTGCAGA GGCAGCTGGA CCCCAAGGGG 2820
 CTGCAGAGA TGGTGACGCT CCTGGAAGAG TGGATCTTGT CGGAGAAAGA ATGGGAGCGG 2880
 GAAAAGGCCG TGAGCTCCA TCTCTATCTC ATGTGGATT TGTCCACAG CACTGCTGTC 2940
 TGTATCCACC TAAAGCTGGG GCAGTTTGGC ACAATGGTGG GACTCATTGC CCGTGCACC 3000
 TGTGATGCCC ATCAAGAAGC CCGCATGGCC TCAATGAATG TCCTGTCCAG CCTGCTAGAT 3060
 CTTCACGCAA GCCAGACCTG CTCTTGTGG GGCCTTTCCA AGCAGAAGGA GCTTGAGAAA 3120
 TGTAAAGGGG ACCTCTCAG CACAGATGTG GAGAAGATCT TCTGTGCATC CTCCAGAATC 3180
 GCCAAGGTGG TCTGCATGGA GTTAGCTGC GATGAGGTGG TCTCGCTCAT CCAGAAGCTC 3240
 TGGCAGAAC CAAGGCGCAT GAACCTGCAG CATGACAAGG CCTCTGTGAC CTGGATAGCC 3300
 TTCTCTCTCC AGATGCGGCG CAAGGAGCTG GAGGACAAGG TGGCCGAGAT CCTGAGTGCC 3360
 ATCCTGGTGC ACCTGCGGCT GGTGGACCAC CCAGAGGTGC GGCCTTCTCT CATTCAGGCG 3420
 ATCTCTGCTC TGGCGACCA CCACAGGAG ACCATCTCA CATCGCTCCT GAGGAGGCGA 3480
 CTGCCATGAG AGAGCCACCT GGCAGAGGTG TGGCTGGCAG TGTGGAGAA CGTGCCCTTC 3540
 GCCCGGACCA TGCTCCACAG CCTGATGGGC CGGCTGCAGT CACGGCTCAG CCCGAGAATC 3600
 AGTGCCACCT CCAAGGTGGA CATCTGGCGC CTGGCTGGG TGGACCCCTT GATGACCTTG 3660
 TGCAACATCC ACCTTCTCAT TCAGAAGCTG GATGAGAATG ACAAGCTCCC GGACTTCTCT 3720
 CCTGACCTCA TCTACACCTC CTGCTGCAG CTGGAAAGCA GCCACCGACC AGAGGCGGCC 3780
 CCGCCGGTCT TGAAGATGTG GAAGCTGGTC CACACCACTC CTCTGCCGGA GGAGATGAAC 3840
 CTGCAAGAGT GCTCTCGAGG GCGGCTCACT ATCAAGTCCA TGCAGCTCTT GTTCAAGAGA 3900
 GTCAAGAGCC AGCACCTGCG ACATACCTTG GACGAGCAGG CAGTGTGGGA CCTCTGCAG 3960
 GAGCGCGGGA CATTCCTGGA GGTGTGAGC CTGCTGGCCA GGCTGTGCAT GCAGCACTG 4020
 GAGGGCCACA GGCAGAGGCT GGCAGAGCTG GTGCTCAGGG GCATGGACTC AGAAGTCTTG 4080
 AGCTGCCGCA TCAGCAGCAC AGCGGTCTGC GTGGAAATGA GGCACCGGTT CATGAGCGGC 4140
 CCAGTCTGTT ACCAGGAGAA GCTGCTGAAG CCGGCAGCTT TGCTGCTGGA GAAGGTGCC 4200
 GACCAGGAGG AAGACGAGGC CCTGCGGCTG CTGTCCCTGC GCGCCCTCG CAACATGGCC 4260
 CTGGCGGCC CCAAGAGGT GAAGCAGTAC CGGAAGGTCT TGCTGGAGAA GTGCTGGGC 4320
 CCCCTGAGG AGCCCGTGAG CAACAGCGTG ACTGCCGAGG GCATGGAGGC CCTGACCAAG 4380
 ATCTGGCTG AGCTCCGGA AGGGGATGTG GGTCTCTCT TCGACGCCAT GTCTGAGCAG 4440
 TGCAAGATCT TCTTCGACAA CGAGAGCGAG CTGCTGCGTC TGAAAGCCTT CATCTCTTT 4500
 GGAAGGCTGG CAAGGCTGGT CGGATGTCC AAGAAGCATT TCTTCAAGG GGAGGTGAAG 4560
 AAGGCTGGA TCCCTCTCAT GCTGCATCC CAGGACCCCT GCTCCAATGC AGCCCAAGTA 4620
 AGATACATCC TGGGCTTGT GTCCAGTCT GGGGCCCGCT GTTCCCGAG GAAACAGGTC 4680
 CTGCGGTCTG CTGATCGGCT CTGATGGCT ACCATGTTTC AGTGTGTGCA CTCTGGGGC 4740
 TGGAAAGTCCC TGGAGCATCC CTCAGGGCCA AGTGATACCG CTACTGATGA CAAGATGACC 4800
 GTTTTCAGA CAACCATGTG CTCCATCCTG ACTCGGAAAA AGCCGCTGT TCTCTACCGC 4860
 TTCTTGCTAG AAACAATGGC CTATGTTAAA AATAACTTGT CAAGAATCAG AATCGCTGCT 4920
 TGCAACTTGG CAGGAATTAT TATGAAGCAG ATGTCTACAC ATTATCTGAA AAAGCTGSAC 4980
 TTCCAGCAT TACGGAATTC CTCCAGGAA CTACAGCTGG ACCCGATCC CGGGCCACT 5040
 GGCCCAAGG GTCCGAAACT AGCTTTGTGT CTTCACCTGG AGTTCATCCA CACGACTGCT 5100
 GACAGCGTGC CTAAGGCCAG GCACTGTGCC AAGCGAGCAG GTAACACAGG ACTTCCAAAC 5160
 TGTTCACAGT CCACTGCCA AAGGAATTC CCAATCCGGG TCCCATCAAC AGGAGAGAGC 5220
 TGCTATGCTG TCCAAATCC AACCCTGCT AAAGCCTTCT CTGGAACAGT GGTCTTCAA 5280
 CTGTTTGTG GAGCAATGG TGACTTGATT TCCTGCCAG TGATAAAGAG TATTGCTGCT 5340
 AAACAAGCT GA

Seq ID NO: 86 Protein sequence:
 Protein Accession #: XP_092643.1

60
 65
 70
 75

1 11 21 31 41 51
 MTEAITEAAV ASSEEVSEER DDLGPLLHD SGTFFQVVNL LDIIDSESAK TDTTGAGLDM 60
 RKTLASVIIM EKATTEPSVV INTLIRCLQV PEISTQRKVN IYNIQDIIQ QEGELEEQCV 120
 QRLVAIASKE MREIPMEBGY MKAEVASDTL VALSRNHPSL VMYELQHHLK PLNLTDEFVI 180
 ITLAKLANGN VFEPMPYMG I TLATIFTMLR LANEAKIRQA ICSAMETPCE TVQFYLKHL 240
 ESVPVMTTEE EPALKVPFMY RYFVTVWLRH YNPEVKLGVI KSLKPLMLGLL LFNDDLREQV 300
 YDYIPLLLAE YQGSLEVLQ ILELSVTINT PVPQMLQHTI FTELEVQVCN KAPAQHQYSS 360
 QNLMMVHCF VALARSYPKE LMKFFFSQME TNKEAVRVGT LNLIRAIVSA DEPRMSIRAI 420
 YLAIRVVKNT ISDTRSKVRM AILHIIGQLA LCGYQERIKG WGLKYLVSQ LSTYKLTNR 480
 REKFYQRDLE ERMVHKVTMD TVKIIITSSVS GMTTFEWFVRL LCYIMETDYY EALTPIICSL 540
 TNLAEHLQHG QDVDSVAGK SRQVDLPAPQ KLLARLLVLM SSPYKGBGRG IAMLNLLRTL 600
 SQSIAPSMAD MWLEBIALIV RYLEEHTFT WDQKAWEDKL IQPLRNSLKK TRGSSWSRL 660
 SKELNNQIAS FDSPLSKGFP LYRALGFTLA TGLEASKVEV LLELLYKTD YSNDFDSEGV 720
 IMCFGLCARG QVKTVLNVLIH DFEERIQESE QSWQISAWRK DHPWRRETVK SALVMVYSCV 780
 ASYCHPQLLL NLVDSPIITAK IHHYVSSCQ DICLKMAMFK SVVQVTKAIN NIKDLEDHP 840
 AQKTTLSII VAVIKAEPTD NLVSPVRALA MEALSHLSKL KPFFYSTBENS ELMDISHSV 900
 ISLQLPGEON ESKITLYANA LSSLEQLMES LLQRLDPKFG LQEMVQLLEK WILSEKEWER 960
 EKAIVSLHLYL MWIYVHSTAV CIHLKIQFQG TMVGLIAPCT CDHQRTRMA SMNVLSLLD 1020
 LEASQTCSLN GPSKQKELEK CKGLDQSTDV EKIPASSRI ARVVMQEFSC DEVVSLIQKL 1080

5 CENTGAMNLQ HDKASVTWIA FFLQMRKEL EDKVAEILSA ILVHLPVVDH PEVRRLLIDG 1140
ILLLAHHHQE TILTSLLRQP LPMESHIAEV NLAVSENVPF ARTMLHSLMG RLQSRILSPRI 1200
SATSKADIWR LAADVPLMTL CTIHLLIQKL DENDKLDPDL PDLIYTLILLQ LGSSHRPEAA 1260
PPVLKMKLV HTTPLEEMN LQRCRGRVT IKSMQLLFKR VKSQAHLAHL DEQAVWDLQ 1320
DGGTFLEGVS LLARLCMQHV EGHQRRLAEL VLRGMDSEVL SCRISSTAVC VEMHRFRMSG 1380
PVLVQEKLLK PAALLLEKGA DQSEDEALRV LSLRALGNMA LGAPKKVKQY RVLLEKCLG 1440
PLREPVNSV TAEGMEALTK ILAELREGDV GSSFDAMSEQ CRIFPDNESE LLRLKAPILF 1500
GKLARVVMS KKHFFKGEVK KAWIPLMLHS QDPCSNAQV RYILGFVSQS GARCSPRKQV 1560
10 LGSAGSACMA TMFQCVHFWG WKSLEHPSGP SDTATDDKMT VFQTTMCSIL TRKKPAVLRY 1620
FLLTMAVYK NNLRSIRIAA CNLAGIIMQK MSHYLLKLD FPALRNSLQE LQLDPDPGPT 1680
GPKGRKLALC LHSEFIHTHA DSVPKARHCA KRAGKPLGN CSQSNQQRNS PSGVPSTGES 1740
CYAVQNPTRA KAFSGTVVFK LFCGANGDLI SCPVIKISIAA KQA

15 Seq ID NO: 87 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
20 CACTTCTCCC TCTCCTTAGT TCTCCGGTAA CCAAACCTTC TCTCGTTATA TACCAATGA 60
TAAACCAAAA GTAATGTTGT ACAGGTTAAA GATTCAAAAC AAACCATAGC AACTGAAACA 120
GGGTATCAGG ACGCAAATGC TTGGCTGGAA TGGATTAAAC ATTCTGTGTC AGGCTAAACA 180
AAAGCGCCTG TTACACTTGT GTGACAGGCA GGCCAGAGAC CCAAATTGTT CCCTTTCCAC 240
TTGGGTGGTC CTCTCACAGA CCGGCGCATGA CTTGTGTGGT AGCTCTCTTC CAGAACCCCA 300
CAGCCTGGGG TGGTGAGTCA TGCAAGACTC TTTCACTGCT GTTCCCTGAG GTCAAGAGCC 360
25 CTGCAGGTCA GCCCTGAGGA CTATCCGGCC TCCAGCCCTT GATGTTAACT TCACCTCATG 420
CCTTTCAAGG CAGGGGAAA AGTTAGCAIT CCTTGGAGAC TTAACAGGGT GCAGTGAAAC 480
CAGGCCCTTT GAAGAGCTTA CCAATCAGTC TGCCCTTGTT CATCCCGAG CAGATGTGTG 540
GTGGTATTGC TGGGAGTAC TGCTGGGTAC TCTGCCAAGT AATTAGAGCA GCACCTCATG 600
30 TCTAGTCCAA CTGGCCATCC CTTTCAACCT AGCATTCTGT CAATATGATA AAAAAAATG 660
TAAAGAAGTG CCTCACGTGG GTCCTTGACC CCCATGTTTA TATAAACT ATTGGGTCT 720
ATGAGGAGAA CCCGATGA

35 Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..759

1 11 21 31 41 51
40 ATGCAGGAAG AAACAGGCTG GCAGCTTGGG GAAAGGATTC TTACATACCA CGGCGACCAG 60
GTAACCTGTG GCACAGACCC AGAAGAAAGT AGAAAAATA GTTTTGGAGG AAACCTCATT 120
GTGAACACAC CTCACCAAGT CAGAACTATC CTAAGTCAGA AAGCAGAAAG GTGCTTACT 180
GACTCCAGAA TCTTAAAGTA TGAGGCTATT CTCTTAGAAA AAGATGATT AACATTAAAC 240
ACTGATAATT CACTTAAACC AGCAGGTTTC CTAACAGGGG ATCTATATCA AAAGAGAGAG 300
45 CACACATGTT TAGTTTAAAT TAATTACCAT ACAAAGGTCC GACCAGACCT AGGAGAAACT 360
CCCTTCAGGA CCGGACAACA CTTTATAGAT GGTTCCTCCC AGGTGATAGA GGGAAAAAGA 420
TACAAATGGT ATTCAAGTAT TGATAGAGAA ACTCTTGTA AATAGAGTT AGGAAAAATTG 480
CTAAATAATT GGTCTGCTCA AACATGTGAG CTGTTTGAC TCAGCCAAGC CTTAAAGGAC 540
TTACAGAAAC AGGAAGGAAC CATCTATACA GATTCTAAGT ACGCCTTTGG AGTGGCTCAT 600
50 ACATTGTGAA AAATTGTGAC TGAACGAGGT CTTATTAATA GCAATGCGCA AGACTTGGTC 660
CATAAGGAAT TAATCACCCA AGTATTAAT AACCTTCAGC TGCCAAAAGA AACAGCTATT 720
GACCATGTCC CCGGACACCA AAAAGGCTT TCTTTTAA

55 Seq ID NO: 89 Protein Sequence
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
60 MQEETGWQLG ERILTYHQDQ VTLCTDPEES RKISFGNLI VNTPHQVRTI LSQKAERWLT 60
DSRILKYEAI LLEKDDLTLT TNSLNPAGF LTGDLVQKRE RTCLVLINXH TKVRPDLGET 120
PFRTGQHFID GSSQVIEGKR YNGYSVIDRE TLVEIELGKL FNNWSAQTC LPAISQALKD 180
LQNEQETIYT DSKYAFGVAR TFGKIWTERG LINSKQDLV HKELITQVLT NLQLPKETAI 240
DHVPGHQKSL SF

65 Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

1 11 21 31 41 51
70 AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
TCTCTGAGA GAGGCGGCG CACCCGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC 180
CTAATATGCG GCTGCGGCTG CTTGTGTCCG CGGAGTCTCT GCTGGTGGCT CTCCTGCCCT 240
75 GCCCGCATG CAGGCGGCTC CTGAGCGCGG GCGCGGTCCC GGGAGCTCGG CAGGCGCGG 300
AGCACCTCA GCCCTTGGAT TTCTTCCAGC CGCCGCGCGA GTCCGAGCAG CCCAGCAGC 360
CGCAGGCTCG GCGCGTCTG CTCGCGATGG GAGAGGAGTA CTTCTCCGCG CTGGGGAAAC 420
TCAACAGAG CCCGCGGCT CCGCTTCCG CCGCTCTCC GCTCTCGGCC GGAGGCAGCG 480
GCAGCGGCC TTCCCGCGAA CAGGCGACCG CCAACTTTT CCGCTGTGTG CTGCAGCAGC 540

5
10
15
20
25
30
35
40
45
50

```
TGCTGCTGCC TCGCGCTCG CTGACAGCC CCGCGGCTCT CGCGGAGCGC GCGCTAGGA 600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCTCGGA TCTCACCTTC CACCTCCTCC GGGAAAGTCTT GGAATGGCC AGGGCCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
GTGCGTTTGG CCAAAAAGAA TCTGCATTGA GCACAAAAAA AATTAAAAAA AATACAGTAT 840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA 960
GCAGCAACAC AATGTTATTCT GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAAAGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTGTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAAAGT
```

Seq ID NO: 91 Protein Sequence
Protein Accession #: NP_000747.1

1 11 21 31 41 51
| | | | |
20 MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGSG RPSPEQATAN FFRVLLQQLL 120
LPRRSIDSPA ALAERGARNA LGGHQEPAPER ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180
AQAHSNRKL MEIIGK

Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

1 11 21 31 41 51
| | | | |
30 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTCTC TCTAAGGATG 60
GCCCAGAAGG AGAAGCTCTTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
AGCACCTGCG CCCAGCGAGT CCTCCGGAAG GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
35 AGTGGGACAC CCGACATCTT AACCGCGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300
CCTCTGGGCA AAGGCAAGTT TGGAAAAGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
ATCCTGGCGC TCAAGGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
CTGGCAGAG AGATCGAAAT CCAGGCCAC CTGCACCATC CCAACATCCT GGTCTCTAC 480
40 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG 600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATCA CAGAGACATA 660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGCTGG 720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCCTGA CTACCTGCCC 780
CCAGAGATGA TTGAGGGGCG CATGCACAA TGAAGAGTGG ATCTGTGGTG CATTGGAGTG 840
45 CTTTGTCTAG AGCTGTGTTT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
TATCGCCGCA TCGTCAAGGT GGAACCTAAG TTCCCGCCTT CTGTGCCAC GGGAGCCAG 960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCTT GGCCAGGTTC 1020
TCAGCCACCC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCTCTCCCT TGCCCTTCAA 1080
TCTGTGCCT GATGTTCCT GTCACTTCACT CGSGTGCGTG TGTTTGTATG TCTGTGTATG 1140
50 TATAGGGGAA AGAAGGGATC CTTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
TTAATAAAG CTGAAGCTTT TTGT

Seq ID NO: 93 Protein Sequence
Protein Accession #: NP_004208

1 11 21 31 41 51
| | | | |
55 MAQKENSYPW PYGRQTAPSG LSTLPQVRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
SSGTPDILTR HPTIDDPBIG RPLGKGFN VYLAREKXSH FIVALKVLFK SQIEKEGVEH 120
60 QLRREIEIQA HLHHPNILLR YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180
MEELADALMY CHGKVIHRD IKPENLLGL KBELKIADFG WSVHAPSLRR KTMCGTLDYL 240
PPMIEGRMH NEKVDLWICG VLYCYELLVGN PPFESASHNE TYRRIVKVDL KPPASVPTGA 300
QDLISKLLRH NPSERLPLAQ VSAHPNVRAN SRRVLPPSAL QSVA

Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

1 11 21 31 41 51
| | | | |
70 GGCACGAGCG AGTCTCTGTC TCTCTGCCAA CGCGGCCCGG ATGGCTTCCC AAAACCGCGA 60
CCCAGCCGCG ACTAGCGTGC CCGCGGCCCG TAAAGGAGCT GAGCGAGCG GGGGCGCGC 120
CCGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA 180
75 TAAAGGGAAT TCTGCTCTCC CTGAATCAGA CAACCTTTTC AAATGGGTAG GGACCATCCA 240
TGGAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCTCCAG 300
TGGCTACCCT TACAATGCGC CCACAGTGAA GTTCTCTCAG CCCTGCTATC ACCCCAACGT 360
GGACACCCAG GGTAAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA 420
TGTCAGGACC ATCTGCTCTCT CCATCCAGAG CCTTCTAGGA GAACCAACA TTGATAGTCC 480

CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCACCA GCTTTTAAGA AGTACCTGCA 540
AGAAACCTAC TCAAGCAGG TCACCAGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC 600
CTTGTGTCGT CTTTAAATTT TTTCTTAGA TGGTCTGTCC TTTTGTGAT TTCGTATAG 660
GACTCTTTAT CTTGAGCTGT GGTATTTTGT TTTTGTTTT GTCTTTTAAA TTAAGCCTCG 720
GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCCTT TTTTAAAAAA AAAAAAAA 780
AAA

Seq ID NO: 95 Protein Sequence
Protein Accession #: NP_008950.1

1 11 21 31 41 51
MASQNRDPAA TSVAARAKGA EPSGGAARGP VGKRLQOELM TLMMSGDKGI SAPPESDNLF 60
KMWGTIHGAA GTVYEDLRYK LSLFPPSGYP YNAPTVMKFLT PCYHPNVDTQ GNICLDILKE 120
KWSALYDVRT ILLSIQSLLG EPNIDSPLENT HAAELWKNPT AFKKYLQETP SKQVTSQEP 179

Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1 11 21 31 41 51
AGAACGGCTT CCGCGGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG 60
AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
CCGAAGGTCC TGAAGATAC TGCTCTTTGG TGTAAATAAC TTGATATGTA CTGGCTTCCT 180
GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACCT ACCTGACCAT 240
TTTGTATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300
TAGCCCTGTC TATTCAATTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC 360
AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTTAAAGAA AGTGCGAAGC GCTTTTGGGA 420
ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
CCTGTTACAG ATGCTTTCTA TTCCGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
TACGAGCTGG CTTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC 600
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTGTCTGG 660
AGCATTTGCT CTTTGTATTA CATATATGCT CATTTGAAAT AATAATTATT TTGCGGTAGA 720
CACTGCCTCT GCTATAGCTA TTGCCCTTGT GACATTTGGC ACTATGTATC CCATGAGTGT 780
GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATGTGTC AGTTGGACAA 840
ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTATAGAA GTCCGAAATG AACATTTTGT 900
GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA 960
TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTTAGTGT CTACTCTAAC 1020
TGTTCAAATT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC 1080
CAATGTCTTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
ATTTAAACACT CTGGGAAAA ATGTGAACCC AGTTATTCTT CTAACACAC AAACAAGGCC 1260
TTATGGTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
TGGAGTTCCA GGAATGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
TAGATATGGA ACTAATAATA GAATTTGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440
TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAAT TTGCATTGAC 1500
TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560
TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCCCTGTA AATGTTAAAG 1620
GCTTTAAATA GGCTTCCTTT AGAAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680
GTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTCTTT TCCGAGACGG AGTCTTGCTC 1800
TGCCACTGTG CCGGCCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC 1860
CTTAGTTTTT GTTTTGTTTT GTTTTTTGAG ATGGAGTCTC ACTCTGTGCC CCAGGCTGGA 1920
ATGCAAGTGGC ATGATCTCAG CTCACCTGCA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC 1980
TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCCC AGCTAATTTT 2040
TGTATTTTAA GTAAAGACCG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG 2100
ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160
CCTGGCCGAT ATTTCTTTA ATGAAATTTA TAAATATGCT TCTTGARTAA TACACATTTT 2220
GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT 2280
AATTGCTAAA TTTTCTTTG AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAAA 2340
TTTTTAGCAG AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400
GATTTTGTGT AAAGTTTCTC TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 97 Protein Sequence
Protein Accession #: BAB70980.1

1 11 21 31 41 51
MGTHLFRKP QRSFFGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60
TAYTYLTIPT LFLSLMCLIS YWVTLRKPSV VYSFGFERLE VLAVFASTVL AQLGALFILK 120
ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLSIKRNKP AYVSEAASTS WLQEHVADLS 180
RSLCGIIPGL SSIFLPRMNP FLVIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF 240
GTMYPMSVYS GKVLQQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH 300
VRIRRDANQ MVLAHVTRNL YTLVSTLTQV IFKDDWIRPA LLSGFVAANV LNFSDHHVIP 360
MPLLKGTDDL NPVTSTPAKP SSPPEFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420
SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GYNRIGQPR P

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
5 1 11 21 31 41 51
| | | | |
ATGGACTTAA CCAATGCTTC ACAATACCA AGAAAAAAT ATTCAATGT GATAAATATA 60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA 120
AGACCTTTCA AATGTATAGA ATGTGGCAA GCTTTTAACA AGTTTCAAC CCTTACTACA 180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC 240
10 AACTGGTCTC CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA 300
TGTGAAGAAT GTGGCAAAGC CTCAACTGG TCCTCATACC TTACTGCATA TAAGATAACT 360
CATACTAGAG AGAAACCCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG 420
AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT 480
15 GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTG A
```

Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..531

```
20 1 11 21 31 41 51
| | | | |
ATGGACTTAA CCAATGCTTC ACAATACCA AGAAAAAAT ATTCAATGT GATAAATATA 60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA 120
25 AGACCTTTCA AATGTATAGA ATGTGGCAA GCTTTTAACA AGTTTCAAC CCTTACTACA 180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC 240
AACTGGTCTC CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA 300
TGTGAAGAAT GTGGCAAAGC CTCAACTGG TCCTCATACC TTACTGCATA TAAGATAACT 360
CATACTAGAG AGAAACCCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG 420
30 AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT 480
GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTG A
```

Seq ID NO: 100 Protein Sequence
Protein Accession #: FGENESH predicted

```
35 1 11 21 31 41 51
| | | | |
MDLTNASQIP RKYPNVINI GKFFINFQIQ TDIREIREK RPFKCIEOGK AFNKFSTLTT 60
HKKIHTREKP YKCECCGKAP NWSSYLTIHK RIHTGEKLYK CEECGKAFNW SSYLTAAYKIT 120
40 HTREKPKYKCE ECGKAPKYSS NLTHKIIHT GEHLYKCEEC GKAFNHAACF FVILKI
```

Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_032589.1
Coding sequence: 147-422

```
45 1 11 21 31 41 51
| | | | |
GGCAGAGGCT CTGTATTGTC AAATAGGCTT CCCACTTGGC AGGGGCGGTC TTGTCCACTC 60
GTTTCTGTAA ACATGGGTGG CAAAAGAGA AGATGGAGCT GCCATTAGA ACATGCCTAA 120
TCCAGCTTTC ATCTTGCTGA GCAAAAATGA AGGAGCCTGG ACCCAACTTT GTTACTGTGA 180
50 GAAAGGGTCT TCATTCACTC AAGATGGCAT TTGTTAAGCA CCTACTGCTG GAGTGCAGTG 240
GTTCAATCAC GGATCACTGC AGCCTCCACC TCCAGTTTCA AGAAATCTTC ATGTCTCAGC 300
CTCTGAGCA GCTAGGATTA CAGACAAACC TTGGAATCA AGAAAGTTCT GGAATGATGA 360
AGCTGTTTAT GCCAAGACCG AAGTGCTGTC CCCAGTATGA GTCCATTGAG TTATGCGCGT 420
55 GACAATTTTC TTGGAATCCC TTTTATTGTT TAGTTCTCAC TTGTTTCCAT ATTTAGTGAA 480
TGTACATTTA ATTGCAAAGC TGTCATTAAT AAAAATCTTT ATAGTACCTC ACTGCAC
```

Seq ID NO: 102 Protein sequence:
Protein Accession #: NP_115978.1

```
60 1 11 21 31 41 51
| | | | |
MKEPGPNFVT VRKGLHSFRM APVHLLLEC SGSITDHCSL HLPVQEILMS QPPEQLGLQT 60
65 NLGNQESSGM MKLFMPRPKV LAQYESIQFM P
```

Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_014501.1
Coding sequence: 60..737

```
70 1 11 21 31 41 51
| | | | |
GGCGGACCGA AGAACGCAGG AAGGGGGCCG GGGGGACCCG CCCCAGGCGC GCCGACGCCA 60
TGAAGTCCAA CGTGGAGAAC CTACCCCGCG ACATCATCCG CTGGGTGTAC AAGGAGGTGA 120
CGCACTGAC CGCAGACCCA CCCGATGGCA TCAAGGTCCT TCCCAACGAG GAGGACCTCA 180
75 CGGACCTCCA GGTCAACCATC GAGGGCCCTG AGGGGACCCC ATATGCTGGA GGTCTGTTCC 240
GCATGAAACT CCTGCTGGGG AAGGACTTCC CTGCCTCCCC ACCCAAGGSC TACTTCCTGA 300
CCAAGATCTT CCACCCGAAC GTGGGCGCCA ATGGCGAGAT CTGCGTCAAC GTGCTCAAGA 360
GGGACTGGAC GGCTAGAGCTG GGCATCCGAC ACGTACTGCT GACCATCAAG TGCCTGCTGA 420
```

TCCACCTAA CCCCAGTCT GCACTCAACG AGGAGGCGGG CCGCTGCTC TTGAGAACT 480
AOGAGGAGTA TGCGGCTCGG GCCCGTCTGC TCACAGAGAT CCACGGGGGC GCCGCGGGC 540
CCAGCGGAG GCGCGAAGCC GGTGCGGCCC TGGCCAGTGG CACTGAAGCT TCCTCCACCG 600
ACCTGGGGC CCCAGGGGGC CCGGAGGGG CTGAGGGTCC CATGGCCAAG AAGCATGCTG 660
GCGAGCGGA TAAGAAGCTG GCGGCAAGA AAAAGACGGA CAAGAAGCGG GCGCTGCGGG 720
CGCTGCGGG GCTGTAGTGG GCTCTCTTCC TCCTTCACCC GTGACCCCAA CCTCTCCTGT 780
CCCTCCCTC CAACTCTGTC TCTAAGTTAT TTAATATATG GCTGGGGTCG GGGAGGGTAC 840
AGGGGCACT GGGACCTGGA TTGTGTTTTC TAAATAAAGT TGGAAAAGCA

10 Seq ID NO: 104 Protein Sequence
Protein Accession #: NP_055316.1

1 11 21 31 41 51
15 MNSNVENLPP HIIRLVYKEV TTLTADPPDG IKVFPNEEDL TDLQVTIEGP EGTPTYAGGLF 60
RMKLLLGKDF PASPPKGYFL TKIFHPNVGA NGEICVNVLK RDWTAELGIR HVLLTIKCLL 120
IHPNPESALN EEAGRLLEN YEYAARARL LTEIHGGAGG PSGRABAGRA LASGTBASST 180
DPGAPGGPG AEGPMAKKHA GERDKKLAAL KKTDKKRALR ALRRL

20 Seq ID NO: 105 DNA sequence
Nucleic Acid Accession #: NM_005101
Coding sequence: 76..573

25 1 11 21 31 41 51
CGGCTGAGAG GCAGCGAACT CATCTTTGCC AGTACAGGAG CTTGTGCGGT GGCCACACAGC 60
CCACAGCCCA CAGCATATGG CTGGGACCTG ACGGTGAAGA TGCTGGCGGG CAACGAATTC 120
CAGGTGTCCC TGAGCAGCTC CATGTCGGTG TCAGAGCTGA AGGCGCAGAT CACCAGAAG 180
ATTGGCGTGC ACGCTTTCCA GCAGCGTCTG GCTGTCCACC CGAGCGGTGT GGCGCTGCAG 240
GACAGGGTCC CCCTTGCCAG CCAGGGCCTG GGCCCTGGCA GCACGGTCTT GCTGGTGGTG 300
GACAAATGCG ACGAACTCTT GAGCATCCTG GTGAGGAATA ACAAGGGCCG CAGCAGCACC 360
TACGAGGTCC GGCTGACGCA GACCGTGCC CACCTGAAGC AGCAAGTGAG CGGGCTGGAG 420
GGTGTGCAGG ACGACCTGTT CTGGCTGACC TTCGAGGGGA AGCCCTGGA GGACCACTC 480
35 CGCTGGGGG AGTACGGCCT CAAGCCCCTG AGCACCGTGT TCATGAATCT GCGCTGCGG 540
GGAGGCGGCA CAGAGCCTGG CCGGCGGAGC TAAGGGCCTC CACCAGCATC CGAGCAGGAT 600
CAAGGGCCGG AAATAAAGGC TGTGTAAGA GAAT

40 Seq ID NO: 106 Protein Sequence
Protein Accession #: NP_005092

1 11 21 31 41 51
45 MGNDLTVKML AGNEFQVSL SSMVSSELKA QITQKIGVHA FQQLAVHPS GVALQDRVPL 60
ASQGLGPGST VLLVVDKDE PLSILVRNKK GRSSTYEVRL TQTVHLKQQ VSGLEGVQDD 120
LFWLTFBKP LEDQLPLGEY GLKPLSTVPM NLRLRGGGTE PGGRS

50 Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 1..1161

1 11 21 31 41 51
55 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGTTGT TGGGGCTGGA GTTTATCTTT 120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTTGAAA 180
TCCAGCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
CGTTGCTGA TGACTACTA TGTGGGCGT TCAGACTGGA AGTTTGGGA CATCCCTTGC 300
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAOGGTG 360
60 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
AATTGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC 480
CACTCTCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGTT CCTCTGCCC 600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
65 GACCGCATG CCAAGATCAA GAGAGCCATC ACCITCATCA TGGTGGTGGC CATGCTCTTT 720
GTATCTGCT TCCTTCCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
TGGGCAAGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGGTTCTT TATCACTCTC 840
AGCTTCACTC ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
70 TTCCCAACT TCTTCTCCAC TTGATCAAC CTCACAGGGG ACCCAACAA AACAGAGGC 960
CCAGATAATA ACCGAGCAC GAGCGTCGAG GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1020
GCTCCAGAGG CGTTAATGGC CAACTCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080
ACCTCAAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACACAGCAT TCTGGAGAAA 1140
CAGTTGGGAT GTTCATCGA G

75 Seq ID NO: 108 Protein Sequence
Protein Accession #: NP_006009.1

1 11 21 31 41 51

5 MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PVVLGLEPIF GLLGNGLALW IFCFHLKSWK 60
SSRIFLFLNLA VADFLLIICL PFVMDYYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIFLTIV 120
VAVDYFRFV HPHHALNKIS NWTAAIISCL LMGITVGLTV HLLKKLLIQ NGPANVCISF 180
SICHTFRWHE AMFLLEFLLP LGIILFCSAR IISLRQRQM DRHAKIKRAI TFMVVAIVF 240
VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SPTYMNSMLD PVVYFSSPS 300
FPNFFSTLIN RCLQRKMTGE PDNNRSTVE LTGDPNKTRG APEALMANSQ EPWSPSYLGP 360
TSNNHKKKGH CHQEPASLEK QLCCIE

10 Seq ID NO: 109 DNA sequence
Nucleic Acid Accession #: NM_005030.2
Coding sequence: 63..1874

15 1 11 21 31 41 51
GGCAGGAGG AGCGGTGCGG AGGCTCTGCT CGGATCGAGG TCTGCAGCGC AGCTTCGGGA 60
GCATGATGTC TGCAGTGACT GCAGGGAAGC TGGCACGGGC ACCGGCCGAC CCTGGGAAAG 120
CCGGGTCCCG CGGAGTTGCA GCTCCCGGAG CTCCGGCGGC GGCTCCACCG GCGAAAGAGA 180
TCCCGGAGGT CCTAGTGGAC CCACGCAGCC GCGGGCGCTA TGTCCGGGCG CGCTTTTGG 240
20 GCAAGGGCGG CTTTGCCAAAG TGCTTCGAGA TCTCGGACGC GGACACCAAG GAGGTGTTCC 300
CGGGCAAGAT TGTGCCTAAG TCTCTGCTGC TCAAGCCGCA CCAGAGGGAG AAGATGTCCA 360
TGAAATATC CATTACCCG AGCCTCGCCC ACCAGCACGT CGTAGGATTC CACGGCTTTT 420
TCGAGGACAA CGACTTCGTG TTCGTGGTGT TGGAGCTCTG CCGCCGGAGG TCTCTCCTGG 480
AGCTGCACAA GAGGAGGAAA GCCTTGACTG AGCCTGAGGC CCGATACTAC CTACGGCAAA 540
25 TTGTGCTTGG CTGCGAGTAC CTGCAACGAA ACCGAGTTAT TCATCGAGAC CTCAAGCTGG 600
GCAACCTTTT CCTGAATGAA GATCTGGAGG TGAATAAGG GGATTTTGGG CTGGCAACCA 660
AAGTCGAATA TGACGGGGAG AGGAAGAAGA CCTGTGTGG GACTCCTAAT TACATAGCTC 720
CCGAGGTGCT GAGCAAGAAA GGGCACAGTT TCGAGGTGGA TGTGTGGTCC ATTGGGTGTA 780
TCATGTATAC CTGTGTAGTG GGCACACCAT CTTTTGAGAC TCTTTGCCTA AAAGAGACCT 840
30 ACCTCCGGAT CAAGAAGAAT GAATACAGTA TTCCCAAGCA CATCAACCCC GTGGCCCGCT 900
CCCTCATCCA GAAGATGCTT CAGACAGATC CCACTGCCCC CCCAACCAAT AACGAGCTGC 960
TTAATGACGA GTTCTTTACT TCTGGCTATA TCCCTGCCCG TCTCCCCATC ACCTGCCTGA 1020
CCATTCCACC AAGGTTTTTC ATTGCTCCCA GCAGCCTGGA CCCAGCAAC CGGAAGCCCC 1080
TCACAGTCTC CAATAAAGGC TTGAGAGAAC CCCTGCTGTA CGGTCCCCGG GAAAAAGAAG 1140
35 AACCAGTGGT TCGAGAGACA GGTGAGGTGG TCGACTGCCA CCTCAGTGAC ATGCTGCAGC 1200
AGCTGCACAG TGTCAATGCC TCCAAGCCCT CGGAGCGTGG GCTGGTCAGG CAAGAGGAGG 1260
CTGAGGATCC TGCCTGCATC CCCATCTTCT GGGTCAGCAA GTGGTGGGAC TATTGGGACA 1320
AGTACGGCTC TGGGTATCAG CTCTGTGATA ACAGCGTGGG GGTGCTCTTC AATGACTCAA 1380
CAGCCCTCAT CCTCTACAAT GATGGTGACA GCCTGCAGTA CATAGAGCGT GACGCGACTG 1440
40 AGTCCTACCT CACCGTGAGT TCCCATCCCA ACTCCTTGAT GAAGAAGATC ACCCTCCTTA 1500
AATATTTCCG CAATATCATG AGCGAGCACT TGTGAAGGC AGGTGCCAAC ATCAGCGCGC 1560
GCGAAGGTGA TGAGCTCGCC CGGCTGCCCT ACCTACGGAC CTGGTTCCGC ACCCGCAGGG 1620
CCATCATCCT GCACCTCAGC AACGGCAGCG TGCAGATCAA CTCTCTCCAG GATCACACCA 1680
45 AGCTCATCTT GTGCCCACTG ATGGCAGCGG TGACCTACAT CGACGAGAAG CGGAGCTTCC 1740
GCACATACCG CCTGAGTCTC CTGGAGGAGT ACGGCTGCTG CAAGGAGCTG GCCAGCCGGC 1800
TCCGCTACGC CCGCACTATG GTGGACAGC TGCTGAGCTC ACGCTCGGCC AGCAACCGTC 1860
TCAAGGCTCT CTAATAGCTG CCCTCCCTC CGGACTGGTG CCTCCTCAC TCCCACCTGC 1920
ATCTGGGGCC CATACTGGTT GGCTCCCGGG GTGCCATGTC TGCAGTGTGC CCCCAGCCCC 1980
CGGTGGCTGG GCAGAGCTGC ATCATCCTTG CAGGTGGGGG TTGCTGTGTA AGTTATTTT 2040
50 GTACATGTTT CAGGTGTGGT TCTACAGCCT TGTCCCTCCT CCGCTCAACC CCACCATATG 2100
AATTGTACAG AATATTTCTA TTGAATTCGG AACTGTCTT TCCTTGGCTT TATGCACATT 2160
AAACAGATGT GAATATTTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

55 Seq ID NO: 110 Protein Sequence
Protein Accession #: NP_005021.2

60 1 11 21 31 41 51
MSAAVTAGKL ARAPADPGKA GVPVGAAPGA PAAAPPAKEI PEVLVDPRSR RRYVRGRFLG 60
KGGFAKCFEI SDADTKEVFA GKIVPKSLLL KPHQREKMSM BISIHRSLAH QHVVFHGF 120
EDNDFVFFVL ELCRRRLLE LHKRRKALTE PEARYYLRLQI VLGCQYLHRN RVIHRDLKLG 180
NLFLNEDLEV KIGDFGLATK VEYDGERKKT LCGTPNYIAP EVLSKKGHSE EVDVWSIGCI 240
65 MYLLVKGKPP FETSCLKETY LRIKNEYSI PKHINPVAAS LIQKMLQTD TARPINELL 300
NDEFTSGYI PARLPITCLT IPRFSAIAPS SLDPSNRKPL TVLNKGLNLP LPERPREKEE 360
PVVRETGEVV DCHLSMLQ LHSVNASKPS ERGLVRQEEA EDPACIPIW VSKWVDYSDK 420
YGLGYQLCDN SVGLFPNDST RLILYNDGDS LQYIERDGE SYLTVSSHNP SLMKKITLLK 480
YFRNYMSEHL LKAGANITPR EGDELARLPY LRTWFRTRSA IILHLSNGSV QINFFQDHTK 540
70 LILCPLMAAV TYIDEKRDFR TYRLSLLEEY GCCKELASRL RYARTMVDKL LSSRSASNRL 600
KAS

75 Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

1 11 21 31 41 51
TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60

5 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGCGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 10 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAT 300
 AAAGGACAAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 15 GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGGAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 20 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAATATACA TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCTATAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTTCA TAACCAAAT AGCAGCACCG GTCTTAATTT 1140
 TAGTGTTCCT AACCTTTTAT CATGTAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 25 TGACTTTTT GTTTGTATCC GTTTGTATAA ATGATAGCAA TATCTGGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACCTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTCAATG CTATATACTG TAAATTTAG GTATACCTCA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTT TCTCTAATAA ACTACCACAA CCTTCTTTTT TAAAAAAA AAA

Seq ID NO: 112 Protein Sequence
 Protein Accession #: NP_005400.1

30 1 11 21 31 41 51
 MSVKGMIAL AVILCATVVQ GPFMFKRGR LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

35 Seq ID NO: 113 DNA sequence
 Nucleic Acid Accession #: NM_001110.1
 Coding sequence: 470..2716

40 1 11 21 31 41 51
 GAATTCGAGG ATCCGGGTAC CATGGGCGGC GGCAGGCCTA GCAGCACGGG AACCGTCCCC 60
 CGCGCGCATG CGCGCGCCCC TGAAGCGCCT GGGGGAACGG TATGGGCGGG AGGTAGGGGC 120
 GCGGCTCCGC GTGCGCATTTG GGTGCCCCGG CGTCACGTGG TGAGGAAGGA GCGGAGGTC 180
 45 TGAGTTTCGA GGGAGGGGGG GAGAGAAGAG GGAACGAGCA AGGGAAGGAA AGCGGGGAAA 240
 GGAGGAAGGA AACGAACGAG GGGGAGGGAG GTCCCTGTTT TGGAGGAGCT AGGAGCGTTG 300
 CCGGCCCTTG AAGTGGAGCG AGAGGGGAGT GCTTCGCGGT TTCTCCTGCC AGGGGAGGTC 360
 CCGGCTTCCC GTGGAGGCTC CGGACCAAGC CCCTTCAGCT TCTCCCTCCG GATCGATGTG 420
 CTGCTGTTAA CCGTGAGGGA GCGCGCGGCG GCGGCAGCGG CAGCGGAAGA TGTGTGTTCT 480
 50 GAGAGTGTTA ATTCTGCTCC TCTCTGGGCG GCGGGGATG GGAGGTCAGT ATGGAATCC 540
 TTTAAATAAA TATATCAGAC ATTATGAAGG ATTATCTTAC AATGTGATT CATTACACCA 600
 AAAACACGAG CGTGCCAAAA GAGCAGTCTC ACATGAAGAC CAATTTTAC GTCTAGATT 660
 CCATGCCCAT GGAAGACATT TCAACCTACG AATGAAGAGG GACACTTCCC TTTTCAGTGA 720
 TGAATTTAAA GTAGAAACAT CAAATAAAGT ACTTGATTAT GATACCTCTC ATATTACAC 780
 TGGACATATT TATGTGAAG AAGGAAGTTT TAGCCATGGG TCTGTTATTG ATGGAAGATT 840
 55 TGAAGGATTC ATCCAGACTC GTGGTGGCAC ATTTTATGTT GAGCCAGCAG AGAGATATAT 900
 TAAAGACGGA ACTCTGCCAT TTCACCTCTG CATTATCAT GAAGATGATA TTAACATACC 960
 CCATAAATAC GGTCTCAGG GGGGCTGTGC AGATCATTCA GTATTGAAA GAATGAGGAA 1020
 ATACCAGATG ACTGGTGTAG AGGAAGTAAC ACAGATACTT CAAGAAGAAC ATGCTGCTAA 1080
 TGTGCCAGAA CTCTGAGGA AAAAAAGTAC AACTTCAGCT GAAAAAATA CTGTGAGCT 1140
 60 TTATATTCAG ACTGATCATT TGTTCCTTAA ATATTACGGA ACACGAGAAG CTGTGATTGC 1200
 CCAGATATCC AGTCATGTTA AAGCGATTGA TACAATTTAC CAGACCAAG ACTTCTCCGG 1260
 AATCCGTAAC ATCAGTTTCA TGGTGAAACG CATAAGAATC AATACAACCT CTGATGAGAA 1320
 GGACCTTACA AATCCTTTCC GTTTCCTAAA TATTGTTGTG GAGAAGTTTC TGAATTGAA 1380
 65 TTCTGAGCAG AATCATGATG ACTACTGTTT GGCTATGTC TTCACAGACC GAGATTTTGA 1440
 TGATGGCGTA CTTGGTCTGG CTTGGGTGG AGCACCTTCA GGAAGCTCTG GAGGAATATG 1500
 TGAATAAAGT AACTCTATT CAGATGGTAA GAAGAAGTCC TTAACACTG GAATTATTAC 1560
 TGTTCAGAAC TATGGGTGAT CCCCATGTA TTCTGGAACA GAGTGACAC CAGGAGAATC 1620
 AGTTGGACAT AACTTTGGAT CCCCATGTA TTCTGGAACA GAGTGACAC CAGGAGAATC 1680
 70 TAAGAATTG GGTCAAAAG AAAATGGCAA TTACATCATG TATGCAAGAG CAACATCTG 1740
 GGACAACTT AACACAATA AATTCTCACT CTGTAGTATT AGAAATATAA GCCAAGTTCT 1800
 TGAGAAGAAG AGAAACAAT GTTTTGTGTA ATCTGGCCAA CCTATTGTG GAAATGGAAT 1860
 GGTAGAACAA GGTGAAGAAT GTGATTGTGG CTATAGTGAC CAGTGTAAG ATGAATGCTG 1920
 CTTGATGCA AATCAACAG AGGGAAGAAA ATGCAAACTG AAACCTGGGA AACAGTGCAG 1980
 75 TCCAAGTCAA GGTCTTGTG GTACAGCACA GTGTGCTTTC AAGTCAAAG CTGAGAAGTG 2040
 TCGGATGAT TCAGACTGTG CAAGGGAAGG AATATGTAAT GGCTTCACAG CTCTCTGCCC 2100
 AGCATCTGAC CCTAAACCAA ACTTCACAGA CTGTAATAGG CATACACAAG TGTGCATTAA 2160
 TGGGCAATGT GCAGGTTCTA TCTGTGAGAA ATATGGCTTA GAGGAGTGA CGTGTGCCAG 2220
 TTCTGATGGC AAAGATGATA AAGAATTATG CCATGTATGC TGTATGAAGA AAATGGACCC 2280

5 ATCAACTTGT GCCAGTACAG GGTCTGTGCA GTGGAGTAGG CACTTCAGTG GTCGAACCAT 2340
 CACCCTGCAA CCTGGATCCC CTTGCAACGA TTTTAGAGGT TACTGTGATG TTTTCATGCG 2400
 GTGCAGATTA GTAGATGCTG ATGGTCTCTT AGCTAGGCTT AAAAAAGCAA TTTTATGTC 2460
 AGAGCTCTAT GAAAAATTG CTGAATGGAT TGTGGCTCAT TGGTGGGCG TATTACTTAT 2520
 GGGGAATTGCT CTGATCATGC TAATGGCTGG ATTTATTAAG ATATGCACTG TTCATACTCC 2580
 AAGTAGTAAT CCAAGTTGCG CTCTCTCTAA ACCACTTCCA GGCACCTTAA AGAGGAGGAG 2640
 ACCTCCACAG CCATTTCAGC AACCCGAGCG TCAGCGGCCG CGAGAGAGTT ATCAAAATGGG 2700
 ACACATGAGA CGCTAACTGC AGCTTTTGCC TTGGTTCTTC CTAGTGCCTA CAATGGGAAA 2760
 10 ACTTCACCTC AAGAGAAAC CTATTAAGTC ATCATCTCCA AACTAAACCC TCACAAGTAA 2820
 CAGTTGAAGA AAAAATGGCA AGAGATCATA TCCTCAGACC AGGTGGAATT ACTTAAATTT 2880
 TAAAGCTGA AAATTCGAAT TTGGGGTGG GAGGTGGAAA AGGAACCCAA TTTTCTTATG 2940
 AACAGATATT TTTAACTTAA TGGCACAAAG TCCTAGAATA TTATTATGTG CCCCGTGTTC 3000
 CCTGTCTTC GTTGCTGCAT TTTCTTCACT TGCAGGCAAA CTGGCTCTC AATAAACTTT 3060
 15 TACCACAAAT TGAATAAAT ATATTTT TCACTGCCAA TCAAGGCTAG GAGGCTCGAC 3120
 CACCTCAACA TTGGAGACAT CACTTGCCAA TGTACATACC TTGTTATATG CAGACATGTA 3180
 TTTCTTACGT ACACGTACT TCTGTGTGCA ATTGTAAACA GAAATTGCAA TATGGATGTT 3240
 TCTTGTATT ATAAATTTT TCCGCTCTTA ATTAATAAAT ACTGTTTAAAT TGACATACTC 3300
 AGGATAACAG AGAATGGTGG TATTCAGTGG TCCAGGATTC TGTAAATGCTT TACACAGGCA 3360
 20 GTTTTGAAAT GAAATCAAT TTACCCCATG GTACCCGGAT CCTCGAATTC

Seq ID NO: 114 Protein Sequence
 Protein Accession #: NP_001101.1

25 1 11 21 31 41 51
 | | | | |
 MVLLRLVILL LSWAAGMGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRAK RAVSHEDQFL 60
 RLDFAHGRH FNLRMKRDTS LFSDEFKVT SNKVLDDYDTS HIYTGHIYGE EGSFSGHSVI 120
 DGRFEGFIQT RGGTFYVEPA ERYIKDRITLP FHSVIYHEDD INYPHKYGPQ GGCADHSVFE 180
 30 RMRKYQMTGV EEVQIPQEE HAANGPELLR KKRRTSAEKN TCQLYIQTDH LFFKYGTRE 240
 AVIAQISSHV KADITTYQT DFGGIRNISP MVKRIIRINT ADEKPTNPF RPFNIGVEKF 300
 LELNSEQNHD DYCLAYVPTD RDPDDGVGL AWVGAPSGSS GGICEKSKLY SDGKKKSLNT 360
 GIITVQNYGS HVPKVSHT FAHEVGHNFG SPHDSGTBCT PGESKHLGQK ENGNVIMYAR 420
 ATSGDKLNHN KFSLCSIRNI SQVLEKKRNN CFVESGQPIC GNGMVEQGE CDGYSQDCK 480
 35 DECCFDANQP BGRCKLKPQ KQCSFSPQGPC CTAQCAFPSK SEKCRDSDC AREGICNGFT 540
 ALCPASDPKP NPTDCNRHTQ VCINGQCAGS ICEKYGLEEC TCASSDGKDD KELCHVCCMK 600
 KMDPSTCAST GSVQWSRHFS GRITITLQPGS PCNDFRGYCD VPMRCRLVDA DGFLARLKA 660
 IFSPRLVENI AEWIVAHWA VLLMGIALIM LMAFGIKICS VHTPSSNPKL PPKPLPLPTL 720
 KRRRPPQPIQ QPQRQRPRES YQMGHMRR

Seq ID NO: 115 DNA sequence
 Nucleic Acid Accession #: NM_000577.2
 Coding sequence: 41-520

45 1 11 21 31 41 51
 | | | | |
 GGCACGAGGG GAAGACCTCC TGTCCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CGGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
 GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCGCGA TACTTGCAAG GAACAAATGT 180
 CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 50 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
 CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCTGCC CCGTTGGTT 420
 CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
 CGTCATGGTC ACCAAATCTT ACTTCCAGGA GGAAGAGTAG TACTGCCAG GCCTGCCTGT 540
 55 TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCGCTGCCCC AGGGCTCCCG 600
 GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCAGAAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTCGCC 780
 TCTGCATTCA GGATCAAAAC CCGACCACCT GCCCAACCTG CTCTCTCTT GCCACTGCT 840
 60 CTTCTCCCTT CATTCCACCT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGAGGTT 960
 TTTAAGGGTT TGTGGAATAA GAAAATTAGG ATTTCTATGAT TTTTCTTTT CAGTCCCGT 1020
 GAAGGAGAGC CTTTCATTG GAGATTATGT TCTTTGGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCTGCAAT TTGTGAATG ATGGTGAAG TAAGTGGTAG CTTTCCCTT CTTTCTTCT 1140
 65 TTTTCTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCAT 1200
 ATTTTCTTTT TCCTTTTAAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCACGCTG 1260
 CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC 1320
 TCTATCAGA AGTTCTCAG CTCCTAAGGC TCTGAGCAAA TGTGCTCCT GGGGTTCTT 1380
 TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTAGCATGT AGAGCTTCTG GCACTTGGAG 1440
 70 ACTGTATGA AAGATGGCTG TGCCTCTGCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCAAGCA CTAAGCTCG 1560
 CTCTTGGCAG GACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAA GCCTAAAAAA AAAAAA 1680
 75 AAAAAA

Seq ID NO: 116 Protein Sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNVLE EKIDVVPPIEP 60
 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSNRK QDKRFAPIRS DSGPTTSFES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 GCACTTTAGC TCAGTGATGG ATTTTAAGAA CGATTACACC TGTCGCCTGT GGTCTGACTC 60
 CAGGCACTCG CGTCAGGTAC TTCTGCTCCA GGATAGCTTT ATGAATTGCT CTGACAGCAT 120
 CATCAATGGT TCCTTTTCGTG CGCTTGGCTT TATTTCATGAG GCTCAGGTGCG GGGAAAGACT 180
 GATGGTCCAC TGTGACAGCA AGACAGGTAA TGCAAAATACG GATTTCATCT GGGTGGGTCC 240
 AGATAACAGA CTGCTAGAGC CGGATAAAGA GATGGAAAAC TTTTACGTGT TTCACAAATGG 300
 AAGTCTGCTT ATAGAAAGCC CTCGTTTGA GGATGCTGGA GTGTATTCTT GTATCGCAAT 360
 GAATAAGCAA CGCCTGTATA ATGAACTGT GGACGTCACA ATAAATGTGA GCAATTCAC 420
 TGTAAAGCAGA TCCCATGCTC ATGAGGCATT TAACACAGCT TTTACCACTC TGTGCTGCTG 480
 CGTGGCCAGT ATCGTTTGG TACTTTTGT CCTCTATCTG ACTCCATGCC CCTGCAAGTG 540
 TAAACCAAG AGACAGAAAA ATATGCTACA CCAAGCAAT GCCCATTCAT CGATTCTCAG 600
 TCCTGCCCC GCTAGTGATG CCTCCGCTGA TGAACGGAAG GCAGGTGCAG GTAAAAGAGT 660
 GGTGTTTTTG GAACCCCTGA AGGATACTGC AGCAGGGCAG AACGGGAAAG TCAGGCTCTT 720
 TCCACGCGAG GCAGTGATAG CTGAGGCGAT CCTAAAGTCC ACGAGGGGGA AATCTGACTC 780
 AGATTCAATC AATTCAGTGT TTTCTGACAC ACCTTTTGTG GCGTCCACTT AA

Seq ID NO: 118 DNA sequence
 Nucleic Acid Accession #: AB032989.1
 Coding sequence: 1..1316

1 11 21 31 41 51
 CCCATTCCTT GCCCAGTTAC ACAGCACTAC TGGACCTCAG TCACAACAAC CTGAGCCGCC 60
 TGCAGGCGCGA GTGGACCCCG ACGGCGCTGA CCCAACTGCA CTCCTCTGCTG CTGAGCCACA 120
 ACCACCTGAA CTTCATCTCC TCTGAGGCGT TTCCCGCGT ACCCAACCTG CGCTACCTGG 180
 ACCTCTCCTC CAACAGAGCTG CGTACACTGG ATGAGTTCTT GTTCAGTGAC CTGCAAGTAC 240
 TGGAGGTGCT GCTGCTCTAC AATAACCACA TCATGGCGGT GGACCGGTGC GCCTTCGATG 300
 ACATGGCCCA GCTGCAGAAA CTCTACTTGA GCCAGAACCA GATCTCTCGC TTCCCTCTGG 360
 AACTGGTCAA GGAAGGAGCC AAGCTACCCA AACTAACGCT CCGTGGATCT TCTTCTAACA 420
 AGCTGAAGAA CTGCGCATTG CCTGACCTGC AGAAGCTGCC GGCGTGGATC AAGAAATGGGC 480
 TGTACCTACA TAACAACCCC CTGAACCTGC ACTGTGAGCT CTACCAGCTG TTTTCACACT 540
 GGCAGTATCG GCAGCTGAGC TCCGCTGATG ACTTTCAAGA GGATCTGTAC TGCATGAACT 600
 CCAAGAGAGT GCACATATGC TTCAACCTGA GTTTCCTCAA CTGTGGCGAG TACAAGGAGC 660
 GTGCTCGGGA GGCCCACTG GGTGACACCT TGATCATCAA GTGTGACACC AAGCAGCAAG 720
 GGATGACCAA GGTGTGGGTG ACACCAAGTA ATGAACGGGT GCTAGATGAG GTGACCAATG 780
 GCACAGTGAG TGTGCTCTAA GATGGCAGTC TTCTTTTCCA GCAGGTGCAG GTGAGGAGC 840
 GTGGTGTGTA TACCTGCTAT GCCATGGAG AGACTTTCAA TGAGACACTG TCTGTGGAAT 900
 TGAAAGTGCA CAATTTACAC TTGCAAGGAC ACCATGACAC CCTCAACACA GCCTATACCA 960
 CCCTAGTGGG CTGTATCCTT AGTGTGCTCC TGTCTCTCAT ATACCTATAC CTCACCCCTT 1020
 GCGGCTGCTG GTGCCGGGTG GTAGAGAAGC CTTCAGGACA TCAAGGAGAC AGCCTCAGCT 1080
 GTTTTGACCG CGGGGTGGCT TTCTTGAAC CTGCTGAGCC TGGGCAAGGGT CAAACCGGCA 1200
 AGCTCAAGCC AGGCAACACC CTGCCAGTGC CTGAGGCCAC AGGCAAGGGC CAAAGGAGGA 1260
 TGTGCGATCC AGAATCAGTC AGCTCGTCT TCTCTGATAC GCCCATTTGT GTGTGAGCAG 1320
 GATGGGTGG TGGGGAGATT CTGCCCCAGG AGAGGTAATG CACCCCTGAA GGATATGAGG 1380
 GGATGGAAGA GAGGGCTGGC TGCCCCAAGG AATGGATTCC TCCTGACCTC AAGGGAATTG 1440
 GTCCAGGTA CAACAGAGAG CAAGACCCCA AACAGGGCGT GGCTGCCACG ATTTTCAAT 1500
 GGGGGTATAT TAATCTCTAG GCAAAATGCTA CACCCGTACC CAAAGCCCTG CCAATTCTCA 1560
 GTGTGGTAGA GGAAGAGAAG CATGCTGAG TTGGATGGGA ATGAGGAAGG AGTGAGGGA 1620
 AGAACAGATT CCTTAACTT TCATGAGGTC ATCCCTAGCT CCTTAAGAGA AAAACATTTA 1680
 GAAAAAATAA TTTTCTCTAT CTCTGCCAC CCACACCTGT GATGTTGTGT GTGTTGGGGG 1740
 AGCTTCCACA GGAGCCACAC TGGGGAAGAG CTGTAGTATC TTCTTTGTGT AGCAAGTCAA 1800
 ACTTACAGC TGGGGAAGTT GAAAACTTT GGAATATGAG TCAGGAAAAG GCTGAGACCT 1860
 CAATCGGTAA CAATTTCCCA AAGCTGTTGT AAGACTTTGC ATTAAGCCCT TTCTTTTCTC 1920
 TGATGTGCC TGGGTGGATG GATCTTTGCA GGAGCCTGGC CTGCTGCTT TTAGTTACAA 1980
 CAGCAATGTG GGAATGTGTA TCTGTGCTT GTCTGGGAC CAATGGCACA GAGGTTATA 2040
 GCATGAACCTG AAGGGTCCAT GTACAGCAT AGGTGCCAGC ACGAACTTG TAGATGGGGG 2100
 GTGAATTTCA GATAGGCTAA TTCCCTGGTT GGTGAAACCC TTGGTTAGTA TTTGATTCCC 2160
 AGCATCTGTG TGTAGGCCA GAGTGGGGG TGCTGAAGGC AGAGCTTTTA TGGATGCTG 2220
 CCAAGAGCT GGTACATGGG CCCACTCAC GATAGAAGGA TGAAGGTAAA TCAGCCTCTA 2280
 TTATGTAGCA TCCAGCTGGA CCTAGCTGAT TCTCAATGTA TGCCATCTCT TCATCCAGTC 2340
 TCCTTATCAA GCTCAGGTGG GATTCTGAAT TTTCCCTAAT ATGCTGCTCT GTAAAGGGAG 2400
 GAGTCCAAGA AAGCCTGGCC CCAGCTGGCT TAGAGTAGGC TTGGCGATAG TGAATATCCA 2460
 GTATATATCT CCTCTGTGT GACAAGGTTG CCTTGCTCCT CTCAGAGATA CCACCTCTGC 2520
 TGCAGAGTCA AAGCATGGGG TTTTGACAT AGAAGGGTTG GAATTTGGGTG GTCTCTACCC 2580
 CAGAAATGCA ATTTGGAGTG CAGCTTCAAG TTTCTGCCCTC TCCACAGATT CCAGGCAATC 2640
 CTGAAGCAGA GATAATCAGT AGTACTAAAC TTTTCAGAGG GGAGTTCTGC CACCCCATTC 2700

CTCACATCGAG AGGTCTTTGC AGTTGTGGTT GTGAGGCCAG AGSAACTTAA GAAGAATGAG 2760
 CTCACATTC CATTCCATCC AAGGTTGCAG AATACCTTGA GTATGGAGAT GACCGATCCC 2820
 TTAAACCTTT CCCTTTGACT ATACTGCATG CCCTGTGAGT GGCTGCTCTG AGCTTTGGCG 2880
 GGGGATGAGC AGGGTGAAGG TGAAAATGTT CTCTGATGTT GGTTTTCTT AGTGCTCTCT 2940
 5 CTCTCCACG TTTCTAGTCC ATTGGAAGTT CTCCAGATCC TCTAGATTTC TGACCTCTTT 3000
 TTACATTCTA AGAGGTGTCA TTTACCTGTG GGTGAGGGGC TTGAGGGGCC TGACTATTAA 3060
 GCTTCTTATT ATGATTGGGG AAGGGGACTC AACATCTTCC CCTTGTCTGG TCCTGGGAAC 3120
 TCAAGACTGC TGTCCATCCT TTATTAGTAA CCTAGTTTGG TTGAGAGAGA GGTGCAGCAT 3180
 10 TTCCCTCAAG TACCTGCATG CTCATAGGTA TGCATGCTTA TAGGTATGCA TGCACACCAG 3240
 CACCTTGAAT TCCACCAGGA CAGTGAATCT GTAGTCCCA TTAATGATAC TCTCAGAAATG 3300
 GTCTCCACCA ATGTGCACAA CTTCATGCAC ACAATTGTAT TCCTCTTTAG GAGAGACAGT 3360
 GACCATGCCA GGCTCTTCAA ATACACACTC CTGTATTTTC ATTTCTGAAC TCCTGAAGC 3420
 TTACCCACA TCTCCATGGC ACTGAATCAC TTTTCTGCCC AGGCTGGAGT TAGAAGAACC 3480
 15 ATGGGTGAA GGCTTTGGGA GAAGAGGTGG TAAGGAGCTA CCTGGTCTT TGGACTCCTC 3540
 AGAAACCTCC CGTGAAGACT ATATATATGA GCAATATATG AGCAATTAAG ATAGAAGTAG 3600
 GTCATTGAAG GACTCAGAAG GAAACTGGCA AGGGGCTAAG TAGCTGTGAG CTGCTCTTCC 3660
 TGTAACTGT CTTGAGGAGA GAAAAGTTGT CTTGATTAT TCCAGAGACT CTTGAGAAAT 3720
 TTGTTACTGG AGCTATAGGA ACTAGGACTC CCTCCTCAGA CTCATCAGGA AATCTGGGAA 3780
 20 AATCTCATCT CCATGCTGCA GTCTCCCGC TTGGCACCAT CTAGGGCTCT GAAGATCTTT 3840
 AAATGAGCGG TTAATGAAG CAGGCCCTCT GGGGCATCGT GATGGAGCTC CTGAGGACTG 3900
 GGAGGGCCGT TTTCTTCATA ATTCCTACCC AGTTTAGGGA ATGAGAAAAG GCCCTGTGGC 3960
 TCTTAAGTCT CTTGACTATA TCCACTAGTT TGGCCTTGAG TTTGAGACAC CTGGTAGATG 4020
 TACCTGGCTG CCTACCAAG AGATTGATT TGTTCCTTCC CGTGGTTTCA GGTGATAGAA 4080
 CCCAAGGATA GCTTTTAAAT TGGAGAATTG AATAATCAGC ATATGTAAAG GCACTAGAAC 4140
 25 CCTGTGTTGA AACTGCCAG GTGTGGGTAT AAGAAAAGGC CGAGAGATCA CCACCTCCTC 4200
 TTACCTTACC CCACCCCAT AAACCAGACA TGTCTCCAG GAAGCAGGTG TCCCTGGACA 4260
 CAGAGGATGA CAGGGCTCTA CAATCTGTGT AATTATTATT ATTATTATTA TTTGTATT 4320
 ATGGGGCCCA AGAAGGGGGC CAGGAGAGGG TACACCCAG CTGGGAGAG CAAAGCAGAT 4380
 30 GGATCCAGTT TCTGTGTGT TCTTACCTCT GTACTTCCTC GTAGCTCTGC TGACAAAGCA 4440
 AGCAGGCCCT CCGTGTCCAA GACCCCATTC CTCCCACTTG TGTACACCTA GGCTGGCAAA 4500
 TCTTGGAGCC TCTGGGCTCT GAAAACTAGA CAATGATCAT TAAACCTGGC TTGAGTCTCT 4560
 GTTCTGGC

Seq ID NO: 119 Protein Sequence
 Protein Accession #: BAA86477.1

1 11 21 31 41 51
 | | | | |
 40 HSLPSYALL DLSHNNLSRL RAEWTPTRLT QLHSLLLSHN HLNFISSSEAF SPVFNLRYL 60
 LSSNQLRLTD EPLFSDLQVL EVLLLYNNHI MAVDRCAFDD MAQLQLLYLS QNQISRPFLE 120
 LVKEGAKLPK LTLDDLSSNK LKNLPLPDQL KLPWIKNGL YLHNNPLNCD CELYQLFSHW 180
 QYRQLSSVMD FQEDLYCMNS KKLHNVNFLS FLNCGEYKER AWEAHLGDTL IIKCDTKQQG 240
 MTKVWVTPSN ERVLDEVING TVSVSKDGLS LFPQQVQVEDG GVYTCYAMGE TFNETLSVEL 300
 45 KVINFTLHGH HDTLNTATYT LVCGLSVVL VLIYLYLTPC RCNCRGVEKP SSHQGDLSLS 360
 SMLSTTPNHD PMAGGDKDDG FDRRVAFLEP AGPGQQQNGK LKPGNTLPVP EATGKGQRMM 420
 SDPESVSVF SDTPIV

Seq ID NO: 120 DNA sequence
 Nucleic Acid Accession #: NM_005071
 Coding sequence: 9..1703

1 11 21 31 41 51
 | | | | |
 55 GATAGACCAT GAGCAGCCAT GGCAACAGCC TGTTCCTTCG GGAGAGCGCG CAGGGCTCGG 60
 GCGGGTGGG CTGGCTGCAG CGGCTGCAGG AAAGCCTGCA GCAGAGAGCA CTGCGCACGC 120
 GCCTGCGCCT GCAGACCATG ACCCTCGAGC ACGTGCCTGG CTTCCTGCGC CGAAACGCCT 180
 TCATTCTGCT GACGGTCAGC GCGGTGGTCA TTGGGGTCAG CTGGGCTTT GCCCTGCGCC 240
 CATATCAGCT CACCTACCGC CAGATCAAGT ACTTCTCTTT TCCTGGAGAG CTTCGTATGA 300
 60 GGATGCTGCA GATGCTGGTG TTACCTCTCA TTGTCTCCAG CCTGGTCACA GGTATGGCAT 360
 CCTGGACAA CAAGGCCACG GGGCGGATGG GGATGCGGGC AGCTGTGTAC TACATGGTGA 420
 CCACCATCAT CGCGGCTTTC ATCGGCATCC TCATGGTCA CACATCCAT CCCGGGAAGG 480
 GCTCCAGCT GGGGCTGCAC CGGAGGGGCC GGATCGAGAC CATCCCCACA GCTGATGCC 540
 TCATGGACCT GATCAGAAAT ATGTTTCCAC CAAACCTTGT GGAGGCCCTG TTTCAACAGT 600
 TCAAGACGCA GTACAGCAGC AGGGTGGTAA CCAGGACCAT GGTGAGGACA GAGAACGGGT 660
 65 CTGAGCCGGG TGCTTCCATG CCTCTCCAT TCTCAGTGA GAACGGAACC AGCTTCTCTG 720
 AAAATGTCAC TCGGGCTCTG GGTACCTTGC AGGAGATGCT GAGCTTTGAG GAGACTGTAC 780
 CCGTGCCTGG CTCGCGCAAT GGCAATCAAG CCCTGGGCTT CGTGGTCTTC TCTGTGGCCT 840
 TTGGGCTGCT CATGTGTGCG ATGAAACACA AGGGCAGAGT CCTCAGGGAC TTCTTCGACA 900
 70 GCCTCAATGA GGCTATTATG AGGCTGGTGG GCATCATTAT CTGGTATGCA CCTGTGGGCA 960
 TCTGTTCCT GATTGCTGGG AAGATTCTGG AGATGGAAGA CATGGCCGTC CTGGGGGGTC 1020
 AGCTGGGCAAT GTACACCTTG ACCGTATCG TGGGCCTGTT CCTCATGCC GGCATTGTCC 1080
 TTCCCTCAT CTACTTCCTC GTCACTCACC GGAACCCCTT CCCCTTCATT GGGGGCATGC 1140
 TACAAGCCCT CATCACCGCT ATGGGCACGT CTTCCAGCTC GGCAACGCTG CCTCATCCTC 1200
 75 TCCGCTGCT GGAGGAGGCG CTGGGTGTGG ACCGCCCAT CACCAGGTTT GTCCTGCCCG 1260
 TGGGCGCCAC GGTCAACATG GATGGCACTG CCCTCTACGA GGCCTGGCT GCCATCTTCA 1320
 TTGCTCAAGT TAACAATAC GAGCTCAACC TGGGTGAGAT CACAACCATC AGCATCACGG 1380
 CCACGACAGC CAGTGTGGG GCTGCTGGCA TCCCCAGGC GGGTCTGGTC ACCATGGTCA 1440
 TTGTGCTTAC GTGCTGCGC TTGCCACCG AAGACATCAC GCTCATCATC GCCCTGGACT 1500

GGTTCCTTGA CCGGCTTCGC ACAATGACCA ACGTACTGGG GGAICTCAATT GGAGCGGCCG 1560
 TCATCGAGCA CTTGTCTCAG CGGGAGCTGG AGCTTCAGGA AGCTGAGCTT ACCCTCCCCA 1620
 GCCTGGGGAA ACCCTACAAG TCCCTCATGG CACAGGAGAA GGGGGCATCC CGGGGACGGG 1680
 GAGGCAACGA GAGTGTATG TGAGGGGCTT CCAGCTCTG

Seq ID NO: 121 Protein Sequence
 Protein Accession #: NP_005062

1 11 21 31 41 51
 | | | | |
 MSSHGNSLFL RESGQRLGRV GWLQRLQESL QQRALRTRLR LQTMTEHLVL RFLRRNAFIL 60
 LTVSAVVIGV SLAFALRPYQ LTYRQIKYFS FPGELLMRML QMLVLPPLVS SLVTGMASLD 120
 NKATGRMGMR AAVYVMVTI IAVFIGILMV TIHPGKGSK EGLHREGRIE TIPTADAFMD 180
 LIRNMFPNPN VEACFKQFKT QYSTRVVTRT MVRTEGSESE GASMPPPPSV ENGTSFLENV 240
 TRALGTIQEM LSFETVPVP GSANGINALG LVVFSVAFGL VIGGMKHKGR VLRDPFDSLNL 300
 EAIMRLVGII IWFAPVGLF LIAGKILEME DMAVLGGQLG MYTLTVIVGL FLHAGIVLPL 360
 IYFLVTHRNP PFFIGGMLQA LITAMGTSSS SATLPITPRC LEEGLGVDRR ITRFVLVPGA 420
 TVNMDGTALY EALAAIFIAQ VNNYELNLGQ ITTISITATA ASVGAAGIPQ AGLVTMWIVL 480
 TSVGLPTEDI TLIIAVDWFL DRLRTMTNVL GDSIGAAVIE HLSQRELEIQ EAEELTLPISLG 540
 KPYKSLMAQE KGASRGRGGN ESAM

Seq ID NO: 122 DNA sequence
 Nucleic Acid Accession #: NM_031966.1
 Coding sequence: 178..1479

1 11 21 31 41 51
 | | | | |
 ACGAACAGGC CAATAAGGAG GGAGCAGTGC GGGGTTTAAA TCTGAGGCTA GGCTGGCTCT 60
 TCTCGGCGTG CTGCGGCGGA ACGGCTGTTG GTTCTGCTG GTTGTAGGTC CTTGGCTGGT 120
 CGGGCCTCCG GTGTTCTGCT TCTCCCGCTG GAGCTGCTGC CTGGTGAAGA GGAAGCCATG 180
 GCGCTCCGAG TCACCAAGGAA CTCGAAAATT AATGCTGAAA ATAAGCGGAA GATCAACATG 240
 GCAGGCGCAA AGCGGCTTCC TACGGCCCTT GCTGCAACCT CCAAGCCCGG ACTGAGGCCA 300
 AGAACAGCTC TTGGGACAT TGGTAACAAA GTCACTGAAC AACTGCAGGC CAAATATGCT 360
 ATGAAGAAAG AAGCAAAACC TTCAGCTACT GGAAAAGTCA TTGATAAAAA ACTACCAAAA 420
 CCTCTTGAAA AGGTACCTAT GCTGGTGCCA GTGCCAGTGT CTGAGCCAGT GCCAGAGCCA 480
 GAACCTGAGC CAGAACCTGA GCGCTGTAAA GAAGAAAAAC TTTCGCTGTA GCCTATTTTG 540
 GTTGATATCG CCTCTCCAAG CCCAATGGAA ACATCTGGAT GTGCCCTGCG AGAAGAAGAC 600
 CTGTGTACAG CTTTCTCTGA TGTAAATCTT GCAGTAAATG ATGTGGATGC AGAAGATGGA 660
 GCTGATCCAA ACCTTTGTAG TGAATATGTG AAAGATATTT ATGCTTATCT GAGACAACCT 720
 GAGGAAGAGC AAGCAGTCAG ACCAAAATAC CTACTGGGTC GGAAGTCAC TGGAAACATG 780
 AGAGCCATCC TAATTGACTG GCTAGTACAG GTTCAAATGA AATTCAGGTT GTTGCCAGGAG 840
 ACCATGTACA TGACTGTCTC CATTATTGAT CGGTTTCATG AGAATAATTG TGTGCCCAAG 900
 AAGATGCTGC AGCTGGTTGG TGTCACTGCC ATGTTTATATG CAAGCAAATA TGAAGAAATG 960
 TACCCCTCAG AAATTGGTGA CTTTGCTTTT GTGACTGACA ACACCTTATC TAAGCACCAA 1020
 ATCAGACAGA TGGAAATGAA GATTCTAAGA GCTTTAAACT TTGGTCTGGG TCGGCTCTTA 1080
 CCTTTGCACT TCCTTCGGAG AGCATCTAAG ATTGGAGAGG TTGATGTGCA GCAACATACT 1140
 TTGGCCAAAT ACCTGATGGA ACTAATATG TTGGACTATG ACATGGTGCA CTTTCTCTCT 1200
 TCTCAAATTG CAGCAGGAGC TTTTTCCTTA GCACTGAAA TTTCTGGATA TGGTGAATGG 1260
 ACACCAACTC TACAACATTA CCTGTCTAT ACTGAAGAAT CTCTTCTTCC AGTTATGCCAG 1320
 CACCTGGCTA AGAATGTAGT CATGGTAAAT CAAGGACTTA CAAAGCACAT GACTGTCAAG 1380
 AACAAGTATG CCACATCGAA GCATGCTAAG ATCAGCACTC TACCACAGCT GAATTCTGCA 1440
 CTAGTTCAAG ATTTAGCCAA GGCTGTGCA AAGGTGTAAC TTGTAAACTT GAGTTGGAGT 1500
 ACTATATTTA CAAATAAAAT TGGCACCATG TGCCATCTGT AAAAAAAAAA AAAAAAAAAA 1560
 AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 123 Protein Sequence
 Protein Accession #: NP_114172.1

1 11 21 31 41 51
 | | | | |
 MALRVTRNSK INAENKAKIN MAGAKRVPTA PAATSKPGLR PRTALGDIGN KVSEQLQAKM 60
 PMKKEAKPSA TGVVIDKKLP KPLEKVPMLV PVPVSEPVPE PEPEPEPEPV KEEKLSPEPI 120
 LVDITASPSM ETSGCAPAE DLQAFSDVI LAVNDVDAED GADFNLCSEY VKDIYAYLRQ 180
 LEESEQVRPK YLLGREVTGN MRALIDWLW QVQMKFRLQ ETMYMTVSII DRFMQNNCVP 240
 KKMQLVGVGT AMPIASKYEE MYPPEIGDFA FVTDNTYTKH QIRQMEMKIL RALNFGLRP 300
 LPLHFLRRAS KIGESVDVEQH TLAKYLMELT MLDYDMVHFP PSQIAAGAF C LALKILDNGE 360
 WPTTLQHYLS YTESLPLVM QHLAKNVVMV NQGLTKHMTV KNKYATSKHA KISTLPQLNS 420
 ALVQDLAKAV AKV

Seq ID NO: 124 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 13-1424

1 11 21 31 41 51
 | | | | |
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCCTGTA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGTTG TGAAGATAC 120

5 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGGAT 300
 GTCCATCATT TCAGGGAAAT GCCAGGGGGG CCGTATGGA GGAAACATTA TATCACCTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGA 420
 GCTTTCCAAG TATGAGTAA TGTTACCCCT TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 GCTGACATTT TGGTGGTTTT TGCCCGTGGG GCTCATGGAG ACTTCCATGC TTTTATGGC 540
 AAAGGTGAA TCCTAGCCCA TGCTTTTGGG CTGGATCTG GCATTGGAGG GGATGCACAT 600
 10 TTCCATGAGG ACGAATTCCT GACTACACAT TCAGGAGGCA CAAACTTGTG CCTCACTGCT 660
 GTTCACGAGA TTGGCCATTG CTTAGTCTT GGCCATTCTA GTGATCCAAA GGCCTGAATG 720
 TTCCCCCCTT ACAAATATGT TGACATCAAC ACATTTCCGC TCTCTGCTGA TGACATACGT 780
 GGCAATCAGT CCGTGTATGG AGACCCAAA GAGAACCAAC GCTTGCCAAA TCCTGACAT 840
 TCAGAACGAG CTCTCTGTGA CCCCATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 15 AGTGTAAATT TAAATTTCTT CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 GAAATTTAAG CCAGAAATCA AGTTTTCTT TTTAAAGATG ACAAATACTG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTT TCCTAATCTT 1140
 GTGAAAAAAT TTGATGCAGC TGTTTTAAAC CCACGTTTT ATAGGACCTA CTCTTTGTGA 1200
 GATAACAGT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCTCGG TTATCCAAA 1260
 20 CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 AACAAATCTT ACTATTCTT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380
 CGTATCACA AACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAAAT GTGTAATTAA 1440
 TGGTTTTGT TACTTCATT CAGCTAATA AGTATTATT GCATATTGCT TATGCTCTCA 1500
 25 GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAAAT TTTTCAATT TGAATACTT AATTGTCCAT TCTTGCTTGA 1620
 CTCTACTATT AAGTTTGAAT ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCTTAA CATCCTTGGG CTGAGAAAT ATACTTACTT CTGGCATAAC 1740
 TAAATAAAG TATATATATT TTGGCTCAA TAAATTG

Seq ID NO: 125 Protein sequence:
 Protein Accession #: Eos sequence

35 1 11 21 31 41 51
 MKFLILLILL ATASGALPLN SSTSLKXNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RGVDPDVHVF REMPGGPVNR KHYITYRINN 120
 YTFDMNRDGV DYAIRKAPQV WSNVTLKFS KINTGMADIL VVFARGAHGD PHAFDGGKGI 180
 LAHAFPGPSG IGGDAHFDEED EFWTTHSGGT NLFLTAVHEI GHSGLGLGHS DPKAVMPEPTY 240
 40 KYVDINTFRL SADDIRGIQS LYGDPKFNQR LPNPDNSEFA LCDPNLSFDA VTTVGNKIPF 300
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLPKDD KYNLISNLRP 360
 EPNYPKSIHS PGFPNFKKI DAAVFNPRFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
 NFOGIGPKID AVFYSNKY YFPQGSNQFE YDFLLQRITK TLKSNWFGC

Seq ID NO: 126 DNA sequence
 Nucleic Acid Accession #: NM_000077.2
 Coding sequence: 272..742

50 1 11 21 31 41 51
 CCCAACCTGG GGGCACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GGCCTCCCTT TGCCTGGAAA GATACCGCGG TCCCTCCAGA 120
 GGATTTGAGG GACAGGCTCG GAGGGGCTC TTCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTACACAGAG GGTGGGGCGG ACCCGGTGCG CTCGGCGGCT GCGGAGAGGG 240
 55 GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGCGGGGGA GCAGCATGGA 300
 GCCTTCGGCT GACTGGCTGG CCAAGGCCGC GCGCGGGGT GGGGTAGAGG AGGTGCGGGC 360
 GCTGTGGAGG GCGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
 GGTCTGATG ATGGGCAAGC CCGGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480
 CAACCTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGCAC GACGCTGCCG GGGAGGGCTT 540
 60 CCTGGACAGC CTGTGTGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCGCTG 600
 GGGCGGTCTG CCCCTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCCTCAGAC ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCAGT CACGGAAGGT CCTACAGGCG CACAACCTGC CCCGCCACAA CCCACCCGCG 840
 65 TTTGCTAGTT TTCATTTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
 AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCACTG TGTGGAGTT TTCTGGAGTG 1020
 AGCACTCAGC CCCTAAGCGC ACATTCTATG GGGCATTCTT TGCAGCCTC GCAGCCTCCG 1080
 GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAC TAGGG AAGCTCAGG GGGTTACTGG 1140
 70 CTTCCTCTGA GTCACACTGC TAGCAATGG CAGAACCAAA GCTCAATAA AAATAAAATA 1200
 ATTTTCATTG ATTCATC

Seq ID NO: 127 Protein Sequence
 Protein Accession #: NP_000068.1

75 1 11 21 31 41 51
 MEPAAGSSME PSADWLATAA ARGVEEVRA LLEAGALPNA PNSYGRRPQ VMMGSAARVA 60
 ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAEE 120

LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 128 DNA sequence
Nucleic Acid Accession #: NM_058196.1
Coding sequence: 104..421

5

1 11 21 31 41 51
| | | | |
10 TGTGTGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC GGTATGCGG 60
GCCCCACCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
CCGAGTGGCG GAGCTGTGTC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCCGCCAC 180
TCTCACCGCA CCGGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
GCACCGGGCC GGGCGCGCGC TGGACGTGCG CGATGCCTGG GGCGTCTGCG CCGTGGACCT 300
GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CGGGGGGCAC 360
15 CAGAGCGAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG 420
AAGAAACAG AGAGGCTCTG AGAAACCTCG GAAAACTTAG ATCATCAGTC ACCGAAGGTC 480
CTACAGGGCC ACAACTGCCG CGGCCACAA CACCCCGCTT TCGTAGTTT TCATTAGAA 540
AATAGAGCTT TAAAAAATGT CCGCTCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAA AGAAAAACAC 660
20 CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACCTCAGC CCTAAGCGCA 720
CATTCAATGT GGCATTCTTT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTTCATGACA 780
AGCAATTTGT GAACTAGGGA AGCTCAGGGG GGTTACTGGC TTCTCTTGAG TCACACTGCT 840
AGCAATGGC AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCCTC

25

Seq ID NO: 129 Protein Sequence
Protein Accession #: NP_478103.1

30

1 11 21 31 41 51
| | | | |
MMGSGARVAE LLLLHGAEPN CADPATL/TRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
RLPVDLAEL GHHRDVARYL RAAAGGTRGSN HARIDAAEGP SDIPD

35

Seq ID NO: 130 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272..646

1 11 21 31 41 51
| | | | |
40 CCCAACCTGG GCGGACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCCGAGC ACTCGCTCAC GCGTCCCCT TGCTGGAAA GATACCGCGG TCCCTCCAGA 120
GATTTGAGG GACAGGGTCG GAGGGGGCTC TTCGCCACG ACCGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTACCCAGAG GGTGGGGCGG ACCGCTGCG CTGCGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
GCCGCGGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCGCG 360
45 GGGTCCGGTA GAGGAGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
TAGTTACCGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCAGCGGGAG CAGGGGATGG 480
CGGGCAGCTC TGGAGGACGA AGTTTGACAG GGAATTGGA TCAGGTAGCG CTTGATTCT 540
CCGAAAAAG GGGAGGCTTC CTGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC 600
TCCTGGCGAC GCCTCGGGG CTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
50 ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAG 720
TCATGATGAT GGGCAGCGCC GAGTGGCGG AGCTGCTGCT GCTCCAGCGC GCGGAGGCCA 780
ACTGCGCGCA CCCCCTCACT CTCACCGAC CCGTGACGA GCTGCCCCG GAGGGCTTCC 840
TGGACACGCT GGTGGTGTCT CACCGGGCCG GGGCGCGGCT GGAAGTGGC GATGCTTGG 900
GCCGTCTGCC CGTGACCTG GCTGAGGAG TGGGCCATCG CGATGTGCA CGGTACCTGC 960
55 GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCC CATAGATGCC GCGGAAGGTC 1020
CCTCAGACAT CCCCAGTTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
CATCAGTCAC CGAAGGTCTT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
CGTAGTTTTT ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCTTTTAA CGTAGATATA 1200
TGCTTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
60 TGTAAAAAAG AAAAACACCG CTTCTGCTT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTCTTTC GAGCCTCGCA GCCTCCGGAA 1380
GCTGTGAGCT TCATGACAAG CATTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCT 1440
CTCTTGAGTC ACACCTGCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAAATT 1500
TTCATTCACT CACTC

65

Seq ID NO: 131 Protein Sequence
Protein Accession #: NP_478104.1

70

1 11 21 31 41 51
| | | | |
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL EAGALPNAPN SYGRRPIQVG 60
RRSAAGAGDG GRWRTKFAG ELESASISL RKGRLPGEF SEGVNHRPP PGDALGANET 120
KEEE

75

Seq ID NO: 132 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163..684

1 11 21 31 41 51
| | | | | |
CCTCCCTACG GCGCCCTCCG GCAGCCCTTC CCGCGTGC GC AGGGCTCAGA GCGTTCCGA 60
GATCTTGGAG GTCGGGTGG GAGTGGGGT GGGGTGGGG TGGGGGTGAA GGTGGGGGC 120
5 GGGCGCGCTC AGGGAAGGCG GGTGCGCGCC TCGCGGGCG AGATGGGCAG GGGCGCGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGCGAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
GGGCGCGCAG CGGCTGCGA GCTCGGCCCT GGAGGCGCG AGAACATGTT GCGCAGGTTT 300
TTGGTGACCC TCCGATTG GCGCGCGTGC GGCGCGCGC GAGTGAGGTT TTTGTTGGTT 360
10 CACATCCCCG GGCCTACGCG GAGTGGGCA GCGCCAGGG GCGCGCGCG TGTGGCCCTC 420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAG CGCTTCTTAG AAGACCAGGT 480
CATGATGATG GGCAGGCGCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA 540
CTGCGCGCAG CCCGCCACTC TCACCGGACC CGTGCAAGAC GCTGCCCGGG AGGGCTTCCT 600
GGACACGCTG GTGGTGTG AC CGGGCGCG GGCGCGGCTG GACGTGCGCG ATGCTGGGG 660
15 CCGTCTGCCG GTGGACCTG CTGAGGAGCT GGGCCATGCG GATGTCGCAG GGTACCTGCG 720
CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCG ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCGATTGAA AGAACAGAG AGGCTCTGAG AACCTCGGG AACCTTAGAT 840
CATCAGTCAC CGAAGTCTCT ACAGGGCCAC AACTGCCCGC GCCACAACCC ACCCGCTTT 900
CGTAGTTTTT ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTAA CGTAGATATA 960
20 TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAAACACCG CTCTGCGCTT TTTACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCGCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCTCGCA GCCTCCGGAA 1140
GCTGTGCGAC TCATGCAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTA CTGCTT 1200
CTCTTGAGTC ACATGCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAAATT 1260
TTCATTCATT CACTC

Seq ID NO: 133 Protein Sequence
Protein Accession #: NP_478102.1

30 1 11 21 31 41 51
| | | | | |
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AELGPGGGE NMVRRFLVTL RIRACGPFR 60
VRVFPVHIPR LTGEWAAPGA PAAVALVLM LRSRLGQQP LPRRPHDDG QRPSSGAAAA 120
PRRGAQLRRP RHSHPTARR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

35 Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 1..1077

40 1 11 21 31 41 51
| | | | | |
ATGGGGTTCA ACTTGACGCT TGCAAAATTA CCAATAACG AGCTGCACGG CCAAGAGAGT 60
CACAAATTCA GCAACAGGAG CGACGGGCCA GGAAAGAACA CCACCTTCA CAATGAATTT 120
GACACAATTG TCTTGGCCGT GCTTTATCTC ATTATATTTG TGGCAAGCAT CTGTCTGAAT 180
45 GGTTTAGCAG TGTGGATCTT CTTCACATT AGGAATAAAA CCAGCTTCAT ATTCTATCTC 240
AAAAACATAG TGGTTGCAGA CCTCATAATG ACGCTGACAT TTCCATTTCC AATAGTCCAT 300
GATGCAGGAT TTGGACCTTG GTACTTCAAG TTTATTCTCT GCAGATACAC TTCAGTTTGT 360
TTTTATGCAA ACATGTATAC TTCCATCGTG TTCCTTGGGC TGATAAGCAT TGATCGCTAT 420
CTGAAGGTGG TCAAGCCATT TGGGACTCT CGGATGTACA GCATAACCTT CACGAAGGTT 480
TTATCTGTTT GTGTTTGGGT GATCATGGCT GTTTTGTCTT TGCCAAACAT CATCCTAACA 540
50 AATGGTCAGC CAACAGAGGA CAATATCCAT GACTGCTCAA AACTTAAAG TCCTTTGGGG 600
GTCAAATGCG ATACGCGAGT CACCTATGTG AACAGCTGCT TGTTTGTGGC CGTGTCTGGT 660
ATTCTGATCG GATGTTACAT AGCCATATCC AGGTACATCC ACAAATCCAG CAGGCAATTC 720
ATAAGTCAGT CAAGCCGAAA GCGAAAACAT AACCAAGACA TCAGGTTGT TGTGGCTGTG 780
TTTTTTACCT GCTTTCTACC ATATCACTTG TGCAGAATTC CTTTACTTT TAGTCACTTA 840
55 GACAGGCTTT TAGATGAATC TGCAAAAAA ATCCTATATT ACTGCAAGA AATTACACTT 900
TTCTGTCTG CGTGTAAATG TTGCCTGGAT CCAATAAATT ACTTTTTCAT GTGTAGGTCA 960
TTTTCAAGAA GGCTGTTCAA AAAATCAAAT ATCAGAACCA GGAGTGAAAG CATCAGATCA 1020
CTGCAAGTG TGAGAAGATC GGAAGTTCGC ATATATTATG ATTACACTGA TGTGTAA

60 Seq ID NO: 135 Protein Sequence
Protein Accession #: NP_076404

65 1 11 21 31 41 51
| | | | | |
MGFNLTLAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWIFPHI RNKTSFIFYL KNIVVADLIM TLTFPPRIVH DAGFGPWYFK FILCRYTSVL 120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSTPTKV LSVCVWVIMA VLSLPIIILT 180
NGOPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRPQ 240
70 ISQSSRRKRK NQSIRVVVAV FFTCFLPYHL CRIPFTFSL DRLLDESAQK ILIYCKEITL 300
FLSACNVCLD PIIFYFMCRS FSRRLPKKSN ITRSESIRS LQSVRRSEVR IYDYTDV

Seq ID NO: 136 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

75 1 11 21 31 41 51
| | | | | |

5
 10
 15
 20
 25
 30

```

ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAAAG 120
CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACTGCTT CATTCAGAGC 180
CTTTTTCGCT TCCTGGAGCA CCGGGCATG CGACGTGGCG GCCAGGCCCT GAAGCTGCCC 240
TCCCCGCGGC GGGGCTCGGT GGCATGTGCG ATTGCCGCGT ACCAGGAGGA CCCTGACTAC 300
TTGCGCAAGT GCCTGCGCTC GCGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
GTGGTGGGAT GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
GGCGGCGACG AGCAGGCGCG CTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
GGTGAGACCG AGGCGAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
AGCACCTTCT CGTGCATCAT GCAGAA GTGG GGAGGCAAGC GCGAGGT CAT GTACACGGCC 600
TTCAAGGCCC TCGGCGATTG GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
GATCCAGCCT GCACCATCGA GATGCTTGA GTCTGGAGG AGGATCCCCA AGTAGGGGGA 720
GTCGGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC 780
GTGCGGTACT GGTGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840
CAGTGATTA GTGGGCCCTT GGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900
GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
ACAGAGACCC CCACTAAGTA CCTCGGTGG CTCAACAGC AAACCCGCTG GAGCAAGTCT 1080
TACTTCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140
TACGAGTCAG TGTGTCAGGG TTTCTTCCCC TTCTTCCTCA TTGCCACGGT TATACAGCTT 1200
TTCTACCGGG GCGGCATCTG GAACATTCTC CTCTTCCTGC TGACGGTGCA GCTGGTGGGC 1260
ATTATCAAGG CCACCTACGC CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTCTGTGCC 1320
CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGGCCA AGATCTTTCG CATTGCTACC 1380
ATCACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGA CTTCTATGGC 1440
CTCATTCCTG TGTCCATCTG GGTGGCAGTT CTCTGGGAG GGTCTGGCTA CACAGCTTAT 1500
TGCCAGGACC GTTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACTGTAT 1560
GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
AAGAACCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA
  
```

Seq ID NO: 137 Protein Sequence
Protein Accession #: NP_005320.1

35
 40
 45

```

1 11 21 31 41 51
| | | | |
MPVQLTTALR VVGTSFLPALA VLGGILAAYV TGYQPIHTEK HYLSFGLYGA ILGLHLLIQS 60
LFAFLEHRRM RRAGQALKLP SPRRGSVALC IAAQEDPDY LRKCLRSAQR ISFPDLKVVM 120
VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNPFHEAGE GETEASLQEG MDRVRDVVRA 180
STFSCIMQKW GSKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
VGGDVQILNK YDSWISPLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMV RNSLLQGFLE 300
DWHYQKPLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQQRWSKS 360
YFREWLYNSL WFKHKLHWMY YESVVTGFFP FFLIATVIQL FYRGRINNIL LFLLTVQLVG 420
IIKATYACFL RGNAEIMFMS LYSLLYMSSL LPAKIFAIAI INKSGWGTSG RKTIVVNFPG 480
LIPVSIWVAV LLGGLAYTAY CQDLFSETEL AFLVSGAILY GCVWVALLML YLAIIARRCG 540
KKPEQYSLAF AEV
  
```

Seq ID NO: 138 DNA Sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

50
 55
 60
 65

```

1 11 21 31 41 51
| | | | |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
GACGGGGCAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCAG GGGGCAATGC 180
TGGCGGGCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGCGC CAGGGGCAGC 240
AAGGGCCTCG GGGCGGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGCGC CGGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA 360
CCTGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCCA CCGCTTCCCC TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTCCC TGTGTATGTG GATCACGCAG TGCTTCTGTC CCGTGTTTT 600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCT GCGCGCCCTT CCTAGGTGAT 660
GCCTCTCTCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCTG GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA 780
  
```

Seq ID NO: 139 Protein Sequence
Protein Accession #: NP_001318.1

70
 75

```

1 11 21 31 41 51
| | | | |
MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEIARRSLA QDAPPLPVFG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLVPV LAQPPSGQRR 180
  
```

Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: Bos sequence

Coding sequence: 53..459

```

1      11      21      31      41      51
5      |      |      |      |      |
      CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGAGC CATGCAGGCC 60
      GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
      CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
      GGTCCCAGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
      CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG 300
10     GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
      ATCAGCTCCT GTCTCCAGCA GCTTTCCTTG TTGATGTGGA TCACGCAAGT CTTTCTGCC 420
      GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
      TAGGTATGTC CTCCTCCCTC AGGGAATGGT CCCAGCAGA GTGGCCAGTT CATTGTGGGG 540
15     GCTGTATTGT TTGTCGTGG AGGAGGACGG CTTACATGTT TGTTCGTGA GAAAATAAAG 600
      CTGAGCTA

```

Seq ID NO: 141 Protein Sequence
Protein Accession #: Eos sequence

```

20     1      11      21      31      41      51
      |      |      |      |      |
      MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
      PRGPHGGAAS AQDGRCPGGA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLMLMWITQC 120
25     FLPVFLAQAP SQGRR

```

Seq ID NO: 142 DNA Sequence
Nucleic Acid Accession #: NM_130467.2
Coding sequence: 246..638

```

30     1      11      21      31      41      51
      |      |      |      |      |
      AGGCAGAGCT CTGCAAGGAG AGGTGTGTGC TTCGTTCITT CCGCCATCTT CGTCTTTCC 60
      AACATCTTCG TTCCTTCTCA CTGACCGAGA CTCAGCCGGT AGGTCTGCAG AGTGGTCTTC 120
35     CTGGTAATTT AGTTGTGAGT GAATGTGTGG AGGAGCCAGC GGGCTTAGGA CAGGTCTCTGT 180
      GGCACAGTCC GTGGCTTTGA GGGAAAAGGG CCTCGCGGTG GTCCCTCCGCC TTCCCCCAGG 240
      TCGTGATGCA GCGCGCATGG GCCCGTAATC GTGGCTGGGC TGGAACGAGG GAGGAAGTGA 300
      GAGATATGAG TGAGCATGTA ACAAGATCCC AATCCTCAGA AAGAGGAAAT GACCAAGAGT 360
40     CTTCCCAGCC AGTTGGACCT GTGATTGTCC AGCAGCCCAC TGAGGAAAAA CGTCAAGAAG 420
      AGGAACCAAC AACTGATAAT CAGGGTATTG CACCTAGTGG GGAGATCAAA AATGAAGGAG 480
      CACCTGTCTG TCAAGGGACT GATGTGGAAG CTTTCAACA GGAAGTGGCT CTGCTTAAGA 540
      TAGAGGATGC ACCTGGAGAT GGTCTGATG TCAGGGAGGG GACTCTGCCC ACTTTTGATC 600
      CCCTAAAGT GCTGGAAGCA GGTGAAGGGC AACTATAGGT TTAACCAAG ACAATGAAG 660
45     ACTGAAACCA AGAATATTGT TCTATGCTG GAAATTGAC TGCTAACATT CTCTTAATAA 720
      AGTTTTACAG TTTTC

```

Seq ID NO: 143 Protein Sequence
Protein Accession #: NP_569734

```

50     1      11      21      31      41      51
      |      |      |      |      |
      MSEHVTRSQS SERGNDQESS QPVGPIVQQ PTEEKQEEE PPTDNQGIAP SGEIKNEGAP 60
      AVQGTDEAF QQELALLKIE DAPGDGPDVR EGTLPFTDPT KVLEAGEGQL

```

Seq ID NO: 144 DNA Sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

```

60     1      11      21      31      41      51
      |      |      |      |      |
      GGCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCCT CCGGACTCTT TTCTCTTAC 60
      TGAGATTCAI CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCTAGA 120
      CCAAGGCGCT ATGTACAGCC TCCTGAAATG ATTGGGCCTA TCGCGCCGA GCAGTTCAGT 180
      GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT 240
65     GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
      GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGTAT 360
      GGGCAGGAGG TGAACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAG 420
      CAATCAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCTTA TGTGGAAT 480
70     TTGTCATTA AAATCTCCC AATAAGCTT TACAGCCTTC TGCAAAA

```

Seq ID NO: 145 Protein Sequence
Protein Accession #: NP_001467.1

```

75     1      11      21      31      41      51
      |      |      |      |      |
      MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAQEGE 60
      DEGASAGQGP KPEADSQEQG HPQTGCCECD GPDGQEVDPF NPEEVKTPEE GEKQSQC

```

Seq ID NO: 146 DNA Sequence
Nucleic Acid Accession #: NM_005562
Coding sequence: 90..3671

5	1	11	21	31	41	51	
	ACAGCGGAGC	GCAGAGTGTAG	AACCAACCAAC	CGAGGCGCGC	GGCAGCGACC	CCTGCAGCGG	60
10	AGACAGAGAC	TGAGCGGCCC	GGCACCGCCA	TGCCTGCGCT	CTGGCTGGGC	TGCTGCCTCT	120
	GCTTCTCGCT	CCTCCTGCCC	GCAGCCCGGG	CCACCTCCAG	GAGGGAAGTC	TGTGATTGCA	180
	ATGGGAAGTC	CAGGCAGTGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GGTAATGGAT	240
	TCCGCTGCCT	CAACTGCAAT	GACAACTACT	ATGGCATTTCA	CTGCGAGAAG	TGCAAGGAATG	300
	GCTTTTACCG	GCACAGAGAA	AGGGACCGCT	GTTTGCCCTG	CAATTGTAAC	TCCAAGGTT	360
15	CTCTTAGTGC	TCGATGTGAC	AACCTGAGAC	GGTGCAGCTG	TAAACCAAGT	GTGACAGGAG	420
	CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGTCTAC	GGATGCGGGG	TGCACCCCAAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TACTGAGAGA	ACGCTGTGAT	AGGTGTCTGAT	600
	CAGGTTACTA	TAATCTGGAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGTCTATG	660
20	GGCATTACAG	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTCATCAAGA	TGTTGATGCG	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
	AATGGTCAAG	CGCCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGGCTGTCTC	900
	TTGACTAGCC	TGAGTACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
25	GTGCTGGTCT	ACGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAACTCTAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTG	1200
	TCTCTGGAGC	CCAGCACCC	TGGGTTGAAC	AGTGTATATG	TCCTGTTGGG	TACAAGGGGC	1260
30	AATCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTC	AGCGAGACTG	GGGCCTTTTG	1320
	GCACCTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCGTG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTTCAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GSTTTCTACA	1440
	ACGATCCGCA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
	CAGTGTAGCC	CGAGACGGAG	GAGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCGGGTG	1560
35	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGAGCCC	CTTTGGTGAA	CATGCCCCAG	1620
	TGAGGCTCTG	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCGGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
	ACCAAGTGCAA	AGCAGGCTAC	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
	GAGCTGTCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGGAAGT	GATGGCACTT	1860
40	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTG	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAAATG	1980
	AGGCCCTGAT	TTCAAAAGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTTCA	2100
	AAGGTGTCTAG	CAGTCCCTT	GGTCTCCAGT	TGGCCAAAGT	GAGGAGCCAA	GAGAACAGCT	2160
45	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCGGGCT	CTGGGAAAGT	2220
	AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCCTGC	CTCAGACCCG	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CATGAGCAA	CTGACAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
50	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGTAGC	CCGACCGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CACCTAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCCCTTCAG	GTGGGAAGAG	2700
	CAAAAGAGAT	CAAAACAAA	CGGATTCAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
55	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAAATGAGAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAAGCTGAA	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
60	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CCTGAAATTC	TCCAGTGAGA	TTGAAACAGGA	GATTGGGAGT	CTGAACTTGG	3180
	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	GTGAGATGAG	GGAGGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCGAT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAAGC	3360
65	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCCTGCAT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTCAGA	GCTGGAAGAG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGG	GAACTATTAG	GACAACTGCT	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
70	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTGGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTCAGC	TGACCCCATT	CCTGATCCCA	TGGCCAGGTG	GTTGCTTTAT	3840
	TGCACCATAC	TCTTTGCTCT	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCAAGGCAG	3960
75	ATGTTTGCTT	CATAATAGTC	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTTCTTGA	GTAATGTGAC	TAAAGGAAAA	AACITTGACT	TTGCCACAGG	4080
	ATGAAATTCT	TCTTAATGTC	AGAAACAGAT	GCAACCCAGT	CACACTGTGG	CCAGTAAAAA	4140
	ACTATTGCTT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200

5 ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTGAGAGTG 4260
 AGGACCTGTA AGGCAGGCCC ATTCAGAGCT ATGGTGCTTG CTGGTGCCCTG CCACCTTCAA 4320
 GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC 4380
 ATTTTATTA AAGCATTTC TACCAGCAAA GCAAATGTTG GGAAGATATT TACTTTTTCG 4440
 GTTTCAAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAATTT CTCTAGATTT 4500
 ATTAGTCCTA ATTCATCTCT ACTTTTCGAA CACCAAAAAT GATGCGCATC AATGTATTTT 4560
 ATCTTATTTT CTCAATCTCC TCTCTCTTC CTCCACCCAT AATAAGAGAA TGTTCCTACT 4620
 CACACTTCAG CTGGGTCACA TCCATCCCTC CATTTCATCT TCCATCCATC TTTCCATCCA 4680
 10 TTACTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG 4740
 GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800
 AGCATTTTTA AAAATAAAAT TTAACCTTAC AAACCTTGTT TGTCAACAAGT GGTGTTTATT 4860
 GCAATAACCG CTGTGTTTGC AACCTCTTTC CTCAACAGAA CATATGTTGC AAGACCCCTC 4920
 CATGGGGGCA CTTGAGTTTT GGCAGGCTG ACAGAGCTCT GGGTGTGCA CATTTCCTTG 4980
 15 CATTCAGCT GTCACCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
 TAACACAGT GGAATTTGCT GGAGGAACCA GAGGCACCTC CACCTTGGCT GGAAGACTA 5100
 TGGTGTGCC TTGCTTCTGT ATTTCTTGG ATTTCTCTGA AAGTGTTTTT AAATAAGAA 5160
 CAATTGTTAG ATGCC

20 Seq ID NO: 147 Protein Sequence
 Protein Accession #: NP_005553

1 11 21 31 41 51
 25 MPALWLGCCL CFSILLPAAR ATSRREVDCD NGKSRQCIFD RELHROTNGG FRCLNCNDNT 60
 DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCPKPGVTG ARCDRLPGPF 120
 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGKN 180
 PEGCTQCFY GHASACRSSA EYSVHKITST FHQDVGDKWA VQRNGSPAKL QWSQRHQDV 240
 30 SQAQLRDPVY FVAPAKFLGN QQVSYGQSL FDIYRDRGR HPSAHDVILE GAGLRITAPL 300
 MPLGKTLPCG LTKTYTFRIN EHPNNWSPQ LSYFEYRRL RNLTLALIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWE QCICPVGYKG QFCODCASGY KRDSARLGPF GTCIPCNCQG 420
 GGACDPDGD CYSGDENDPI ECADCPIGFY NDPHDPSCSK PCPCNNGFSC SVMPEDEVV 480
 CNNPCPGVTG ARCELADGY PGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLEK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGRSDGT CVCKPGFPGP 600
 35 NCEHGAFSCP ACYNQVKIOM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL 660
 QDILRDAQIS BGASRLSLGQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHEV SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSVRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLG 900
 40 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREBFL 960
 QVDNRKAEE EAMKRLSYIS QKVSASDKT QQAERALGSA AADAQRAKNG AGEALISSE 1020
 IEQIGSLNL EAVNTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
 AQKVDTRAKN AGVTIQDTLN TLDGLLHLM QPLSVDEEGL VLLBQKLSRA KTQINSQLRP 1140
 MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL BQQ

45 Seq ID NO: 148 DNA Sequence
 Nucleic Acid Accession #: NM_021048.2
 Coding sequence: 327..1436

1 11 21 31 41 51
 50 GGCAACGAGG AGAAGCGAGG TTCTCGTTCT GAGGGACAGG CTGAGATCG GCTGAAGAGA 60
 GCGGGCCAG GCTCTGTGAG GAGGCAAGGG AGGTGAGAAC CTGCTCTCA GAGGGTGACT 120
 CAAGTCAACA CAGGGAACCC CTCTTTTCTA CAGACACAGT GGGTCGAGG ATCTGACAAG 180
 55 AGTCCAGGTT CTCAGGGGAC AGGGAGAGCA AGAGGTCAAG AGCTGTGGGA CACCACAGAG 240
 CAGCACTGAA GGAGAAGACC TGCCTGTGGG TCCCATCTCG CCAAGTCTCT CCCCACTCC 300
 CACCTGCTAC CCTGATCAGA GTCATCATGC CTCGAGCTCC AAAGCGTCAG CGCTGCATGC 360
 CTGAAGAAGA TCTTCAATCC CAAAGTGAGA CACAGGGCCT CGAGGGTGCA CAGGCTCCCC 420
 TGGCTGTGGA GGAGGATGCT TCATCATCCA CTTCACACAG CTCTCTTTT CCATCCTCTT 480
 60 TTCCCTCCTC CTCTCTTTC TCCTCCTCCT CCGCTATCC TCTAATACCA AGCACCCAG 540
 AGGAGGTTTC TGCTGATGAT GAGACACCAA ATCCTCCCCA GAGTGCTCAG ATAGCCTGCT 600
 CCTCCCCCTC GGTGTTGCT TCCCTTCCAT TAGATCAATC TGATGAGGGC TCCAGCAGCC 660
 AAAAGGAGGA GAGTCCAAGC ACCCTACAGG TCCTGCCAGA CAGTGAGTCT TTACCCAGAA 720
 GTGAGATAGA TGAAGAGGTG ACTGATTGG TGCAGTTTCT GCTCTTCAAG TATCAATGA 780
 65 AGGAGCCGAT CACAAAGGCA GAAATACTGG AGAGTGTCAT AAAAAATTAT GAAGACCACT 840
 TCCCTTTGTT GTTTAGTGAA GCCTCCGAGT GCATGCTGCT GGTCTTTGGC ATTGATGTAA 900
 AGGAAGTGGA TCCCACTGCG CACTCCTTTG TCCTTGTCAC CTCCCTGGGC CTCACCTATG 960
 ATGGGATGCT GAGTGATGTC CAGAGCATGC CCAAGACTGG CATTCTCATA CTTATCCTAA 1020
 GCATAATCTT CATAGAGGGC TACTGCACCC CTGAGGAGGT CATCTGGGAA GCACTGAATA 1080
 70 TGATGGGGCT GTATGATGGG ATGGAGCACC TCATTATGG GGAGCCACAG AAGCTGCTCA 1140
 CCCAAGATTG GGTGCAGGAA AACTACCTGG AGTACCGGCA GGTGCTTGGC AGTGATCTCT 1200
 CACGGTATGA GTTCTGTGG GGTCCAAGGG CTCTAGCTGA AATTAGGAAG ATGAGTCTCC 1260
 TGAAATTTTT GGCCAAGGTA AATGGGAGTG ATCCAAGATC CTCCCACTG TGGTATGAGG 1320
 AGGCTTTGAA AGATGAGGAA GAGAGAGCCC AGGACAGAAT TGCCACCACA GATGATACTA 1380
 75 CTGCCATGCG CAGTCAAGT TCTAGCGCTA CAGGTAGCTT CTCTACCCCT GAATAAGATA 1440
 AGACAGATTG TTCAGTGTG TTTAAAAGGC AAGTCAAATA CCACATGATT TTACTCATAT 1500
 GTGGAATCTA AAAAAA AAAA

Seq ID NO: 149 Protein Sequence
Protein Accession #: NP_066386.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA FLAVEEDASS STSTSSSFPS SFPSSSSSSS 60
      SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDGSS SQKEESPSTL 120
      QVLPDESLEP RSEIDEKVTD LVQPLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS 180
      BCMLLVFGID VKEVDPTGHS FVLVTSGLT YDGLMSDVQS MPKTGILILI LSIIFIEGYC 240
10     TPBEVIWEAL NMMGLYDGMH HLIYGEPRKL LTQDHWQENY LEYRQVPGSD PARYEFLNGP 300
      RAHAEIRKMS LLKFLAKVNG SDPRSFLWY EALKDEBER AQDRIATTDD TTAMASASSS 360
      ATGSFSYPE

```

Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12..398

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGACAGC CCTGGCTGTG GCTACAGGGC 60
      CAGCCCTTAC CCTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120
      TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
      ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
      TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
25     ACAACGCTGC ACCCACCOCG ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
      TGAGCCTCTCT GGGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
      TCAATGCTTCT CTTCCCTTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
      GGGTGGCAGG AGCCCCAGGC TGAGGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
      CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
30     ACAGAGGATG CAGCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
      GATTTCACAC TCCTTCTGTT TTGTGCGGT TTATTTTGTA CTCAAATCTC TACATGGAGA 720
      TAAATGATT AAAC

```

Seq ID NO: 151 Protein Sequence
Protein Accession #: NP_003686

```

35     1      11      21      31      41      51
      |      |      |      |      |      |
      MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK 60
40     KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
      AVILAPSL

```

Seq ID NO: 152 DNA Sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

```

45     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCTCTGCC TCTGTGTGCA TGTCCGTTCC 60
50     GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
      GAACATGTCC GGTCTAAGAC CAAGGTTCTT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
      AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
      CACCTTACCC TGAAGTGGT GAAGCCAGT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300
      TCAGGTGATG AGGCAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGCCACAA 360
55     GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
      AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
      TTAATCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
      AGGGGTCAA AAGCTTATTT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600
      TCCCAAATT AATGAGAATG AGATCAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA 660
60     AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
      TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

```

Seq ID NO: 153 Protein Sequence
Protein Accession #: NP_006389.1

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      MAPNASCLCV HVRSEEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
70     RSLSSYGIDK EKTITLTKV VKPSDEELPL FLVESGDEAK RHLQVRRSS SVAQVKAMIE 120
      TKTGIIPETQ IVTNCKRLE DGKMMADYGI RKGNNLFLAS YCIGG

```

Seq ID NO: 154 DNA Sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74..2788

```

75     1      11      21      31      41      51
      |      |      |      |      |      |
      GTGGGTCAAG TGAACCACTT TTCGCGCGAA ACCTGGTTGT TGCTGTAGTG GCGGAGAGGA 60

```

TCGTGGTACT GCTATGGCGG AATCATCGGA ATCCTTCACC ATGGCATCCA GCCCGGCCCA 120
 GCGTGGGOGA GGCAATGATC CTCTCACTC CAGCCCTGGC CGAAGCTCCC GGCGTACTGA 180
 TGCCTTCACC TCCAGCCCTG GCCGTGACCT TCCACCATTT GAGGATGAGT CCGAGGGGCT 240
 CCTAGGCACA GAGGGGCCCC TGGAGGAAGA AGAGGATGGA GAGGAGCTCA TTGGAGATGG 300
 CATGGAAGG GACTACCGCG CCATCCCAAG GCTGGACGCC TATGAGGCCG AGGGACTGGC 360
 TCTGGATGAT GAGGACGTAG AGGAGCTGAC GGCCAGTCAG AGGGAGGCAG CAGAGCGGGC 420
 CATGCGGCAG CGTGACCGGG AGGCTGGCGG GGGCTTGGGC CGCATGCGCC GTGGGCTCCT 480
 GTATGACAGC GATGAGGAGG ACGAGGAGCG CCCTGCCCGC AAGCGCCGCC AGGTGGAGCG 540
 GGCCACGGAG GACGGCGAGG AGGACGAGGA GATGATCGAG AGCATCGAGA ACCTGGAGGA 600
 TCTCAAAGC CACTCTGTGC GCGAGTGGGT GAGCATGGCG GGCCCCCGGC TGGAGATCCA 660
 CCACCGCTTC AAGAACTTCC TGGCAGCTCA CGTCGACAGC CACGGCCACA ACGTCTTCAA 720
 GGAGCGCATC AGCGACATGT GCAAAGAGAA CCGTGAGAGC CTGGTGGTGA ACTATGAGGA 780
 CTTGGCAGCC AGGGAGCAGC TGCTGGCCTA CTTCTGCCT GAGGCACCGG CGGAGCTGCT 840
 GCGATCTTT GATGAGGCTG CCCTGGAGGT GGTACTGGCT ATGTACCCCA AGTACGACCG 900
 CATCACCAAC CATCTCCATC TCCGCACTTC CCACCTGCCT CTGGTGGAGG AGCTGCGCTC 960
 GCTGAGGCAG CTCGACTCTA ACCAGCTGAT CCGCACCAGT GGGGTGGTGA CCAGCTGCAC 1020
 TGGGCTCTCG CCCCACTAGC GATGGTCAA GTACAACTGC AACAACTGCA ATTTCTGCTC 1080
 GGGTCTTTTC TGCCAGTCCC AGAACCAGGA GGTGAAACCA GGCTCCTGTC CTGAGTGCCA 1140
 GTGCGCCGCG CCCTTTGAGG TCAACATGGA GGAGACCATC TATCAGAACT ACCAGCGTAT 1200
 CCGAATCCAG GAGAGTCCAG GCAAAGTGGC GGCTGGCGCG CTGCCCCGCT CCAAGGACGC 1260
 CATTCTCTCC GCGAGTCTGG TGGACAGCTG CAAGCCAGGA GACGAGATAG AGCTGACTGG 1320
 CATCTATCAC AACACATATG ATGGCTCCCT CAACACTGCC AATGGCTTCC CTGTCTTTGC 1380
 CACTGTCTAT CTAGCCAACC ACGTGGCCAA GAAGGACAA CAGGTGTCTG TAGGGGAACT 1440
 GACCGATGAA GATGTGAAGA TGATCACTAG CCTCTCCAAG GATCAGCAGA TCGGAGAGAA 1500
 GATCTTTGGC AGCATTGCTC CTTCCATCTA TGGTCATGAA GACATCAAGA GAGGCTGGC 1560
 TCTGGCCCTG TTCGAGGGGG AGCCCAAAA CCCAGGTGGC AAGCACAAGG TACGTGGTGA 1620
 TATCAACCGT CTCTTTGTGG GAGACCCCTG CACAGCGAAG TCGCAGTTTC TCAAGTATAT 1680
 TGAGAAAGTG TCCAGCCGAG CCACTCTTAC CACTGGCCAG GGGCGCTCGG CTGTGGGCTC 1740
 CACGGCGTAT GTCCAGCGCG ACCCTGTCTG CAGGGAGTGG ACCTTGGAGG CTGGGGCCCT 1800
 GGTCTGGGCT GACCGAGGAG TGTGTCTCAT TGATGAATTT GACAGATGA ATGACCGAGA 1860
 CAGAACCCAG ATCCATGAGG CCACTGGAGCA ACAGAGCATC TCCATCTCGA AGGCTGGCAT 1920
 CGTCACTCTC CTGACGGCTC GCTGCAOAGT CATTCCTGCC GCCAACCCCA TAGGAGGGCG 1980
 CTACGACCCC TCGCTGACTT TCTCTGAGAA CGTGACCTC ACAGAGCCCA TCATCTCAAG 2040
 CTTTGACATC CTGTGTGTGG TGAGGGACAC CGTGGACCCA GTCCAGGACG AGATGCTGGC 2100
 CCGCTTCGTG GTGGGCGAGC ACGTCAGACA CCACCCAGC AACAGGAGG AGGAGGGGCT 2160
 GGCCAAATGG AGCGCTGCTG AGCCCGCCAT GCCCAACAGC TATGGCGTGG AGCCCTGTCC 2220
 CCAGGAGGTC CTGAGGAAGT ACATCATCTA CGCCAAGGAG AGGGTCCACC CGAAGCTCAA 2280
 CCAGATGGAC CAGGACAAGG TGGCCAAGAT GTACAGTGAC CTGAGGAAAG AATCTATGGC 2340
 GACAGGCAGC ATCCCCATTA CGGTGCGCGCA CATCGAGTCC ATGATCCGCA TGGCGGAGGC 2400
 CCACGCGCGC ATCCATCTGC GGGACTATGT GATCGAAGAC GACGTCAACA TGGCCATCCG 2460
 CGTGATGCTG GAGAGCTTCA TAGACACACA GAAGTTTACG GTCATGCGCA GCATGCGCAA 2520
 GACTTTTGCC CGCTACCTTT CATTCGCGCG TGACAACAAT GAGCTGTTC TCTTCTACT 2580
 GAAGCAGTTA GTGGCAGAGC AGGTGACATA TCAGCGCAAC CGCTTTGGGG CCCAGCAGGA 2640
 CACTATTGAG GTCCCTGAGA AGGACTTGGT GGTAAAGGCT CGTCAGATCA ACATCCACAA 2700
 CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCG ACGACCTGAA 2760
 AAGGAAATG ATCCCTGAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCTTGGGA 2820
 TTCTGTGTTG GGGTGGTTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAACCTCGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 TGTTTGTTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTGGCCAGTG 3000
 TGTCTTACTT GGTGTCTGAA CATCTTGCCA CCTCGAGTG CTTTGTCTCC ACTCAGTACC 3060
 TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCGTGTGGT TTAGGTGTTA GCCTTCTTAC 3120
 ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAGTTG CGATTTCAGG CTGCTTTTGC 3180
 TGCCTTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CCTGCAGGTT 3240
 TCTGTGCCCC TGTGTTGGA GAGGGCACGA CAGTGCCAGC GCAGCGTCTT GGGCTCTCTA 3300
 GTGCGAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCAAT CGGTTTGGTT TCTGTAGTTT 3420
 TAATTTTAA TAAAGTTGAA TAAATATATA AAAAAAAAA AAAAA

Seq ID NO: 155 Protein Sequence
 Protein Accession #: AAH17490.1

1 11 21 31 41 51
 | | | | |
 65 MAESSESFTM ASSPAQRRR NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE 60
 GPLEEEEDGE ELIGDGMERD YRAIPELDAY EAEGALALDE DVEELTASQR EAAERAMRQR 120
 DREAGRLGR MRRGLLYDS EDEEREPARK RRQVERATED GEEDEEMIES IENLEDLKGH 180
 SVREWSMAG PRLEIHRFPK NFLRTHVDH GHNVFKERIS DMCKENRESL VVNVEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 HLNQLRTSG VVTSTGVLF QLSMVKYNCN KCNVLGPFC QSQNQEVKPG SCPEQCSAGP 360
 70 FEVNMETIY QNYQIRIQE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGLMTAN GFPPFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEIFAS 480
 IAPSIYGHED IKRKLALALP GGEPKPNPGK HKVRGDINVL LGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGQ ASAVGLTAYV QRHPVSREW LEAGALVLAD RGVCLIDEFD KMNDQRTSI 600
 HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 75 CVVRDVTDPV QDEMLARFVV GSHVRHHPN KEEEGLANGS AAEPAAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEBAHARI 780
 HLRDYVIEDD HMRVIRVMLE SFIDTQKFSV MRSMRKTFR YLSFRDNDNE LLLFILKQLV 840
 AEQVTVQRNR FGAQQDTIEV PEKDLVDKAR QINIHNLASF YDSELFMRNK FSHDLKRM 900

LQQF

Seq ID NO: 156 DNA Sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

5
10
15
20
25
30
35
40
45

1	11	21	31	41	51	
GGCAGCAGTA	GGGGTGGCGG	GTCAGTGCTG	CTCGGGGGCT	TCTCCATCCA	GGTCCCTGGA	60
GTTCTTGGTC	CCTGGAGCTC	CGCACTTGGC	GCGCAACCTG	CGTGAGGCAG	CGCGACTCTG	120
GCGACTGGCC	GGCCATGCCT	TCCCGGGCTG	AGGACTATGA	AGTGTGTAC	ACCATTTGGCA	180
CAGGCTCCTA	CGGCCGCTGC	CAGAAGATCC	GGAGGAAGAG	TGATGGCAAG	ATATTAGTTT	240
GGAAAGAACT	TGACTATGGC	TCCATGACAG	AAGCTGAGAA	ACAGATGCTT	GTTTCTGAAG	300
TGAATTTGCT	TOGTGAACTG	AAACATCCAA	ACATCGTTCTG	TTACTATGAT	CGSATTATTG	360
ACCGGACCAA	TACAACACTG	TACATTGTAA	TGGAATATTG	TGAAGGAGGG	GATCTGGCTA	420
GTGTAATTAC	AAAGGGAACC	AAGGAAAGGC	AATACTTAGA	TGAAGAGTTT	GTTCTTGGAG	480
TGATGACTCA	GTTGACTCTG	GCCCTGAAGG	AATGCCACAG	ACGAAGTGAT	GGTGGTCATA	540
CCGTATTGCA	TGCGGATCTT	AAACCAGCCA	ATGTTTTCTT	GGATGGCAAG	CAAAACGTCA	600
AGCTTGGAGA	CTTTGGGCTA	GCTAGAATAT	TAAACCATGA	CACGAGTTTT	GCAAAAACAT	660
TTGTTGGCAC	ACCTTATTAC	ATGTCCTCTG	AACAAATGAA	TGCAATGTCC	TACAATGAGA	720
AATCAGATAT	CTGTGATTG	GGCTGCTTGC	TGTATGAGTT	ATGTGCATTA	ATGCCTCCAT	780
TTACAGCTTT	TAGCCAGAAA	GAACTCGCTG	GGAAAATCAG	AGAAGGCCAA	TTGAGGCGAA	840
TTCCATACCG	TACTCTGAT	GAATTGAATG	AAATTATTAC	GAGGATGTTA	AACTTAAAGG	900
ATTACCATCG	ACCTTCTGTT	GAAGAAATTC	TTGAGAATCC	TTTAATAGCA	GATTTGGTTG	960
CAGACGAGCA	AAGAAGAAAT	CTTGAGAGAA	GAGGGCGACA	ATTAGGAGAG	CCAGAAAAAT	1020
CGCAGGATTC	CAGCCCTGTA	TTGAGTGAGC	TGAAACTGAA	GGAAATTCAG	TTACAGGAGC	1080
GAGAGCGAGC	TGTCAAAGCA	AGAGAAGAAA	GATTGGAGCA	GAAAGAACAG	GAGCTTTGTG	1140
TTCTGTAGAG	ACTAGCAGAG	GACAACTGG	CTAGAGCAGA	AAATCTGTTG	AAGAACTACA	1200
GCTTGTCTAA	GGAACGGAAG	TTCTGTCTC	TGGCAAGTAA	TCCAGAACTT	CTTAATCTTC	1260
CATCTTCAGT	AATTAAGAA	AAAGTTTCA	TCAGTGGGGA	AAGTAAAGAG	AACATCATGA	1320
GGAGTGAGAA	TTCTGAGAGT	CAGCTCACAT	CTAAGTCCAA	GTGCAAGGAC	CTGAGAAAAA	1380
GGCTTCAAGC	TGCCAGCTG	CGGGCTCAAG	CCCTGTGAGA	TATTGAGAAA	AATTACCAAC	1440
TGAAAAGCAG	ACAGATCCTG	GGCATGCGCT	AGCCAGGTAG	AGAGACACAG	AGCTGTGTAC	1500
AGGATGTAAT	ATTACCAACC	TTTAAAGACT	GATATTCAAA	TGCTGTAGTG	TTGAATACTT	1560
GGCCCATGTA	GCCATGCTTT	TCTGTATAGT	ACACATGATA	TTTCGGAAAT	GGTTTACTG	1620
TTCTTCAGCA	ACTATTGTAC	AAAATGTTCA	CATTTAATTT	TTCTTTCTTC	TTTTAAGAAC	1680
ATATTATAAA	AAGAATACTT	TCTTGGTTGG	GCTTTTAATC	CTGTGTGTGA	TTACTAGTAG	1740
GAACATGAGA	TGTGACATTC	TAAATCTTGG	GAGAAAAAAT	AATATTAGGA	AAAAAATATT	1800
TATGCAGGAA	GAGTAGCACT	CACTGAATAG	TTTTAAATGA	CTGAGTGGTA	TGCTTACAAT	1860
TGTCATGTCT	AGATTTAAAT	TTTAAGTCTG	AGATTTTAAA	TGTTTTTGAG	CTTAGAAAAA	1920
CCAGTTAGAT	GCAATTTGGT	CATTAAATACC	ATGACATCTT	GCTTATAAAT	ATTCCATTGC	1980
TCTGTAGTTC	AAATCTGTTA	GCTTTGTGAA	AATTCATCAC	TGTGATGTTT	GTATTCITTT	2040
TTTTTTTCTG	TTTAACAGAA	TATGAGCTGT	CTGTCAATTA	CCTACTTCTT	TCCCACTAAA	2100
TAAAAGAAAT	CTTCAGTTA					

Seq ID NO: 157 Protein Sequence
Protein Accession #: NP_002488.1

50
55
60

1	11	21	31	41	51	
MPSRAEDYEV	LYTIGTGSYG	RCQKIRKSD	GKILVWKELD	YGSMTAEKQ	MLVSEVNLLR	60
ELKHPNIVRY	YDRIIDRTNT	TLYIVMEYCE	GGDLASVITK	GTKEROVLDE	EFVLRVMTQL	120
TLALKECHRR	SDGGHTVLHR	DLKPNVFLD	GKQNVKLGDP	GLARILNHD	SFARTFVGTP	180
YYMSPEQMNR	MSYNEKSDIW	SLGCLLYELC	ALMPPPTAFS	QKELAGKIRE	GKFRIPYRY	240
SDELNEIITR	MLNLKDYHRP	SVEEILENPL	IADLVADQBR	RNLERRGRQL	GEPEKSDSS	300
PVLSELKLKE	IQLQERERAL	KAREERLEQK	EQELCVRERL	AKDLARAEN	LLKNYSLLKE	360
RKFLSLASNP	ELLNLPSVVI	KKKVHFSGES	KENIMRSNS	ESQLTSKSKC	KDLKRLHAA	420
QLRAQALSDI	EKNYQLKSRQ	ILGMR				

Seq ID NO: 158 DNA Sequence
Protein Accession #: Eos sequence

65
70
75

1	11	21	31	41	51	
TGAGTTTGCC	CCCTTACCCC	CATCCAGTG	AATATTTGCA	ATTCTAAAG	ACGTGTTTTG	60
ATTGTCACAC	CTGGGTGGGG	AACATGCTAC	TGGCATCTAA	TGCATAGAGG	GCAGTAATGC	120
TGCTAAACAT	CTTTCAACGC	ACAGGACAGA	GCCCCACAAA	AGAGAAATAT	CTAGCCCCAA	180
ATGTCCATAA	CAGTCTGTGT	GAGAAAACCT	ACCGCAGGAT	CTTACTGGGC	TTCATAGGTA	240
AGCTTGCTCT	TGTTCTGGCT	TCTGTAGATA	TATAAAATAA	AGACACTGCC	CAGTCCCTCC	300
CTCAACGCTC	CGAGCCAGGG	CTCAAGGCAA	TTCCAATAAC	AGTAGAATGA	ACACTAAATA	360
TTGATTTCAA	AATCTCAGCA	ACTAGAAGAA	TGACCAACCA	TCCTGGTTGG	CCTGGGACTG	420
TCCTAGTTTT	AGCATTGAAA	GTTTCAGGTT	CCAGGAAAGC	CCTCAGGCCT	GGGCTGCTGG	480
TCACCCTAGC	AGCTGAGGGA	CTCTTCAATA	CAGAAATAGT	CTTTGTGCAC	TGGAGATGAA	540
TATACTTTAA	TTTGTAACAT	GTGAAAACAT	CTATAAACAT	CTACTGAAGC	CTGTTCTGTC	600
TGCACCGACA	TTTTCAATTGA	GTACGGATTC	TTCTCACCAG	ATACAGCTGC	TCTACAACCT	660
TCGAGGGCTG	GTATAAAACCT	AGCTTTTACC	TATTTTAAAT	AATTACATGA	ATAGTAAAAA	720
CTGGATTAA	CCCATGATTC	GGGTATTTTC	AATTTCTTGG	GGAGCTTAGA	GGAOGGACAA	780
ATAAAAAGAT	TATTTCAACA	TCAAATATAY	GCTATTGTGT	ACATATGAAG	ATAACCACAT	840

ATATGTATAA ATTCCACGGT ACTTTTTCAG AATACTATAA AATCCAACAG AAAAAAATAG 900
CATTTACTAT

5 Seq ID NO: 159 DNA Sequence
Nucleic Acid Accession #: E08 sequence
Coding sequence: 264..782

	1	11	21	31	41	51	
10	CCCTGCTCCA	GTACACACCG	GAAGCTGACT	GGTCCACGCA	CAGCTGAAGC	ATGAGGAAAC	60
	TCATCGCGGG	ACTAATTTTC	CTTAAAATTT	AGACTTGAC	AGTAAGGACT	TCAACTGACC	120
	TTCTCTCAGAC	TGAGAAGCTG	TTCCAGTATA	TACATCAAGT	CACTGAGATC	TCCAGCACCC	180
	TGCGCGTGCG	ACTACTGAGA	GACGAGGTGC	CAGGGTGGTT	CCTGAAAGTG	CCTGAGCCCC	240
	AACCTATCAG	CAAGGAGCTC	ATCATGCTGA	CAGAAGTCAT	GGAGGTCTGG	CATGGCTTAG	300
15	TGATCGGGGT	GGTGTCCCTC	TTCTGTCAGG	CCTGCTTCCT	CACCGCCATC	AACTACCTGC	360
	TCAGCAGGCA	CATGGCCAC	AAGAGTGAAC	AGATACTGAA	AGCGGCCAGT	CTCCAGGTTC	420
	CCAGGCCACG	CCCTGGCCAC	CATCATCCAC	CTGCTGTCAA	AGAGATGAAG	GAGACTCAGA	480
	CAGAGAGAGA	CATCCCAATG	TCTGATTCCC	TTTACAGGCA	TGACAGGAC	ACACCTCAG	540
	ATAGCTTGA	TAGCTCTGCG	AGTTCGCCTC	CTGCCTGCCA	GGCCACAGAG	GATGTGGATT	600
20	ACACACAAGT	CGTCTTTTCT	GACCTGGAG	AACTAAAAAA	TGACTCCCCG	CTGGACTATG	660
	AGAACATAAA	GGAAATCACA	GATTATGTCA	ATGTCAATCC	AGAAAGACAC	AAGCCAGTT	720
	TCTGGTATT	TGTCACCCCT	GCTCTGTCTG	AGCCAGCGGA	ATATGATCAA	GTGGCCATGT	780
	GAATTCACAA	TATTTTAAAT	GGGTCACAGT	TCTCTATGGA	TTCTTACATT	TAATTTGTAG	840
	GGAAATGCCA	TTTTTCCCCC	TTAAACAAGG	CATGGGGCTC	ACAAGTCTAT	GGAGACAGGC	900
25	CAAAAAGAA	GTGGAGAAGA	AAACTGATAA	ATACACAGAG	GTCCCTCAAG	CCCATGGACT	960
	CCTGGTCTGT	ACCCAAAAAA	GCTGTTCTGT	CCTCAAAAC	AAAAACAAGG	CTTGGCTGGG	1020
	AAAACAGGCC	AATGCCCCCG	CAAGAAAGGT	TGAGATCAGA	TGTTAGGAAG	AACTTTCAGG	1080
	TAAAGTATGA	GAACATATGA	GTCCATCAGC	AGAGATAGTA	GTGAAGTCTC	TCCCCAGGGA	1140
30	AAATTTTAAA	AAGGTGGAAT	CAGCTGTTGT	AGAGTTCAT	TTGGCAATCT	CATGGTTAAA	1200
	TGACTTCCCT	TTGAGCTCTT	TAATTATTGG	CAATAAACAA	CTTCTTTAAA	AGTTTTAAAT	1260
	AAAATAGCAA	CCACCACCA					

35 Seq ID NO: 160 Protein Sequence
Protein Accession #: E08 sequence

	1	11	21	31	41	51	
40	MLTEVMEVWH	GLVIAVVSFL	LQACPLTAIN	YLLSRHMAHK	SEQILKAASL	QVPRPSPGHH	60
	HPPAVKEMKE	TQTERDIPMS	DSLYRHDSDT	PSDSLSSSCS	SPPACQATED	VDYTVVVFSD	120
	PGLKNDSDPL	DYENIKEITD	YVNVNPERHK	PSFWYFVNPA	LSEPAEYDQV	AM	

45 Seq ID NO: 161 DNA Sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

	1	11	21	31	41	51	
50	CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
	GACAAGCACA	TGGACTTTTT	TTATAATAGG	AGCAACACTG	ATACTGTGCA	TGACTGGACA	120
	GGAAACAAGC	TTGTGATTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCGTGT	TATTTTTTTT	180
	TCTAATTCTC	TGGTCATCGC	GCCAGTGATC	AAAAACAGAA	AATTTTCATT	CCCTCTCTAC	240
	TACCTGTTGG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTCGCTA	TGTATTCCTG	300
	ATGTTTAAAC	CAGGCCACGT	TTCAAAACT	TTGACTGTCA	ACCGCTGGTT	TCTCGCTCAG	360
55	GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCAACT	TGCTGGTTAT	CGCCGTGGAG	420
	AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
	CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTATG	GGGCGTCCC	CACACTGGGC	540
	TGGAATTGCC	TCTGCAACAT	CTCTGCCCTG	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
	TACCTTGT	TCTGGACAGT	GTCCAACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
60	CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGCTCCGCA	TACAAGTGGG	720
	TCCATCAGCC	CCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
	GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTGACGG	CCTGAACCTGC	840
	AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTCTCTGC	TGCTGGCGCT	GCTCAACTCC	900
	GTCGTGAACC	CCATCATCTA	CTCCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
65	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCTCCACA	1020
	GTCCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
	GTCGTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCTCTC	GGCCACCCA	GTTGATGACT	1140
	GTCTTAGG						

70 Seq ID NO: 162 Protein Sequence
Protein Accession #: NP_036284

	1	11	21	31	41	51	
75	MNECHYDKHM	DFPYNRSNTD	TVDDWTGKTL	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
	FHPFPYLLA	NLAADFFAG	IAYVFLMNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
	LVIIVERHMS	INRMVHSNL	TKKRVTLIL	LVWAIAIFMG	AVPTLGNL	CNISACSSLA	180
	PIYSRSYLVF	WTVSNLMAFL	IMVVYLRIV	VYVKKRTNVL	SPHTSGSISR	RRTPMKLMKT	240

VMTVLGAFVV CWTPLGLVLL LDGLNCRQCG VQHVKNRFL LALLNSVNP IISYKDEDM 300
YGTMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

5

Seq ID NO: 163 DNA Sequence
Nucleic Acid Accession #: NM_020242
Coding sequence: 72..4240

10	1	11	21	31	41	51	
	CAGTCGCGCG	CGGTGCAGTC	GGGAGGTGGA	GGCACCGGCT	GCATTGTTTT	CGGGATCGAG	60
	GGGTGAGGGC	GCTATGGCAC	CGGCTGCAC	AACTGAGTTA	CGCAGCGTGA	CAAAATGGTCA	120
	GTCTAACCAA	CCAAGTAATG	AAGGTGATGC	CATCAAAGTT	TTTGTGCGAA	TTGCTCTCTC	180
	TGCAGAAAGA	TCTGGGTGAG	CTGATGGAGA	GCAGAACTTA	TGCTTATCTG	TGCTGTCTCT	240
15	CACGAGTCTC	CGGCTGCAC	CCAACCTGTA	GCCCAAGACC	TTCAAGTTTG	ATCATGTTGC	300
	AGATGTGGAT	ACCACTCAGG	AATCTGTATT	TGCAACTGTG	GCTAAAAGCA	TTGTGGAGTC	360
	TTGCATGAGC	GGTTATAATG	GTACCATCTT	TGCATATGGA	CAGACTGGCT	CAGGGAAGAC	420
	ATTTACTATG	ATGGGACCAT	CTGAATCTGA	TAATTTTCTT	CATAACCTGA	GAGGAGTAAT	480
	CCCACGAAGT	TTTGAATATT	TGTTTTCTCT	AATTGATCGT	GAAAAGAGAA	AGGCTGGAGC	540
20	TGGAAGAGAT	TTCTTTTGTA	AGTGTTCCTT	TATTGAAATC	TACAACGAGC	AGATATATGA	600
	TCTACTGGAC	TCTGCATCGG	CTGACTGTGA	CTTAAGGGAG	CATATCAAGA	AGGGAGTCTT	660
	TGTTGTGGT	CGGCTGGAGC	AGGTGGTAAC	CTCAGCTGCT	GAAGCCTATC	AGGTGCTGTC	720
	TGGAGGATGG	AGGAATAGAC	GTGTGGCATC	AACATCAATG	AACAGAGAAT	CGTCTAGGTC	780
	TCATGCCGTC	TTTACAATTA	CAATAGAGTC	AATGGAGAAA	AGTAATGAGA	TTGTGAATAT	840
25	ACGGACCTCC	CTGACTCAAC	TGGTGGATTT	AGCAGGATCT	GAAAGGCCAA	AAGATACCCA	900
	TGCAGAGGGG	ATGAGATTGA	AGGAAGCAGG	TAACATAAAT	CGATCATTGA	GCTGCCCTGG	960
	CCAAGTGATT	CCAGCAGATT	TGACGTGGG	TAATGGAAAA	CAGAGACATG	TTTGCTACAG	1020
	AGACTCCAAA	CTTACCTTCT	TACTACGGGA	TTCCCTTGGA	GGTAATGCCA	AAACAGCCAT	1080
	AATTGCAAA	GTTTCATCTG	GATCCAGGTG	TTTGGGGGAA	ACCCTATCAA	CACCTAACTT	1140
30	TGCTCAAGA	GCCAAAGCTG	TTAAAAACAA	GGCAGTAGTA	AATGAAGACA	CCCAAGGAAA	1200
	TGTGAGCCAG	CTCCAAGCTG	AAGTGAAGAG	GCTCAAGAAA	CAACTGGCGG	AGCTTGCTTC	1260
	AGGACAGACA	CCACCAGAAA	GCTTCTTGAC	CAGAGACAAA	AAGAAGACTA	ACTATATGGA	1320
	GTATTTCCAG	GAAGCAATGT	TATTTCTTAA	GAAATCTGAA	CAGGAAAAGA	AGTCTCTGAT	1380
	AGAAAAAGTT	ACCCAAATAG	AAGACCTCAC	CCTCAAAAAG	GAAAAATTTA	TTCAATCTAA	1440
35	TAAATGATT	GTGAAATTC	GAGAGGATCA	AATAATACGC	TTGGAAGAGC	TCCACAAGGA	1500
	ATCCCGGGGA	GGTTTTCTGC	CTGAGGAGCA	GGATCGTTTG	CTCTCAGAA	TAAGGAATGA	1560
	GATTCAAACT	CTGCCAGAAC	AAATAGAGCA	CCACCCAGGA	GTTGCAAAAT	ATGCTATGGA	1620
	AAATCATTCC	CTCAGGGAGG	AGAATAGAAG	ACTGAGATTA	TTAGAGCCTG	TGAAAAGAGC	1680
	TCAAGAAATG	GATGCCACGA	CCATTGCAAA	ACTAGAAAAA	GCTTTCTCTG	AAATAAGTGG	1740
40	CATGGAGAGA	AGTGACAAAA	ATCAGCAAGG	ATTTTCACCT	AAAGCTCAGA	AAGAGCCATG	1800
	TTTGTTCGCA	AACACTGAGA	AGTTAAAAGC	ACAACCTCTG	CAAAATCAGA	CAGAGCTGAA	1860
	TAATTCAAAG	CAAGAAATATG	AGAATTCAAA	AGAATCTTCT	AGGAAAAGGC	AGCTAGAAAT	1920
	GGAAATCAGAG	CTTCAGTCTT	TGCAAAAAGC	GAACCTTAAT	CTTGAAAACC	TTTTGGAAGC	1980
	AACAAAAGCC	TGCAAGCGGC	AAGAAGTTTC	TCAGCTGAAT	AAAAATCATG	CTGAAACACT	2040
45	TAAGATTATA	GCTACACCAA	CCAAGGCCTA	CCAACCTCAT	TCCCGACCGA	TACCAAAATT	2100
	AAGCCCTGAA	ATGGGAAGCT	TTGGCTCTCT	ATACACTCAG	AATTCAGACA	TATTAGATAA	2160
	TGATATATTA	AATGAGCCAG	TTCTCTCTGA	GATGAATGAA	CAAGCTTTTG	AGGCCATTTC	2220
	TGAAGAGCTT	AGAACAGTGC	AGGAACAAAT	GAGTGCTCTT	CAAGCCAAAC	TGGATGAAGA	2280
	AGAGCATAAA	AACCTAAAGC	TTACGACGCA	TGTTGACAAA	CTGGAACATC	ATTCTACCCA	2340
50	AATGCAGGAA	CTTTCTCTAT	CAGAAAAGAT	TGATTGGACC	AAACAGCAGG	AAGAGCTTCT	2400
	CTCACAGTTG	AATGTCTCTG	AAAAGCAGCT	TCAAGAGACT	CAAACTAAAA	ATGACTTTTT	2460
	GAAAAGTGAG	GTACATGACC	TGCGAGTAGT	CCTTCATTCT	GCTGACAAAG	AGCTTTCTTC	2520
	AGTGAAATG	GAATATAGTT	CATTCAAAAC	GAATCAGGAG	AAAGAATTCA	ACAACTTTTC	2580
	TGAAAGACAC	ATGCATGTAC	AGCTTCAATT	AGATAATCTC	AGGTTAGAAA	ACGAAAAGCT	2640
55	GCTTGAGAGC	AAAGCCTGCC	TACAGGATTC	CTATGACAA	TTACAAGAAA	TAATGAAATT	2700
	TGAGATTGAC	CAACTTTCAA	GAAACCTCCA	AAACTTCAAA	AAAGAAAATG	AAACTCTGAA	2760
	ATCTGATTCT	AATAATTGGA	TGGAGCTTCT	TGAGGCAGAA	AAAGAACGCA	ATAACAAATT	2820
	ATCATTACAG	TTTGAAGAAG	ATAAAGAAAA	CAGTTCTAAA	GAAATCTTAA	AGTTCTTGA	2880
	GGCTGTACGT	CAGGAGAAAC	AGAAAGAGAC	GGCCAAAGTG	GAGCAGCAGA	TGGCAAAAGT	2940
60	ACAGAAACTA	GAAGAGAGCT	TGCTTGCTAC	TGAAAAGTGT	ATCAGTTCCC	TGAAAAGTGC	3000
	TAGAGATTCT	GATAAGAAAG	TTGTAGCTGA	CCTCATGAAC	CAGATCCAGG	AGCTAAGAAC	3060
	ATCGGTCTGT	GAGAAAACAG	AACTATAGA	CACCCTGAAA	CAAGAACTGA	AGGACATAAA	3120
	TTGCAAAATC	AACTCTGCTT	TGGTTGACAG	AGAAGAGAGC	AGAGTGTGGA	TCAAGAAGCA	3180
	GGAAAGTGAT	ATTCTGGATC	TGAAAGAAAC	CCTTAGGCTG	AGAATACTTT	CTGAGGACAT	3240
65	AGAGAGGGAT	ATGCTCTGTG	AGGACCTGGC	TCATGCCACT	GAGCAGCTGA	ACATGCTCAC	3300
	AGAGGCTCTA	AAAAAACACT	CGGGCTGCT	GCAGTCTGCC	CAGGAAGAAC	TGACCAAGAA	3360
	GGAAGCCCTG	ATTACGGAAC	TTACGCACAA	GCTAAACCAA	AAGAAAGAGG	AAGTAGAACA	3420
	GAAGAAGAAT	GAATATAACT	TCAAAATGAG	GCAACTAGAA	CATGTGATGG	ATTCTGCTGC	3480
	TGAGGATCCC	CAGAGTCTTA	AGACACCACC	TCACTTTCAA	ACACATTTGG	CAAACTCTCT	3540
70	GAAGAACATA	GAACAAAGAG	TAGAAGATGG	AAGAGCCTCT	AAGACTTCTT	TGGAACACCT	3600
	TGTAAACAA	CTAAATGAAG	ACAGAGAAGT	CAAAAATGCT	GAAATCTTCA	GAATGAAGGA	3660
	GCAGTTGCGT	GAAATGGA	ACCTACGCT	GGAAAGTCAG	CAGTTAATAG	AGAAAACTG	3720
	GCTCCTGCAA	GGTCAGCTGG	ATGATATTAA	AAGACAAAAG	GAAAACAGTG	ATCAGAATCA	3780
	TCCAGATAAT	CAACAGCTGA	AGAAAGAAC	AGAAGAAAGT	ATCAAGAGAA	GACTTGCAAA	3840
75	AAGTAAATA	GTGTGAAGAA	TGCTGAAAT	GAAAGCAGAC	CTAGAAGAG	TCCAAAGTGC	3900
	CCTTTACAAC	AAAGAGATGG	AATGCCTTAG	AATGACTGAT	GAAGTCGAAC	GAACCCAAAC	3960
	TTTGGAGTCT	AAAGCATTCC	AGGAAAAGAA	ACAACCTGGA	TCAAAGCTGG	AAGAAATGTA	4020
	TGAAGAAAGA	GAGAGAACAT	CCCAGGAGAT	GGAAATGTTA	AGGAAGCAGG	TGGAGTGTCT	4080

5 TGCTGAGGAA AATGGAAAGT TGGTAGGTCA CCAAAATTG CATCAGAAGA TTCAGTACGT 4140
 AGTGCAGCTA AAGAAAGGAAA ATGTCAGGCT TGCTGAGGAG ACAGAAAAGT TGGTGGCCGA 4200
 AAATGTATTT TTAAGAGAAA AGAAAAGAG TGAATCTTGA GGATTCGGGT CAGCTACCTA 4260
 GGCATCACCT TGTTTGAAGA TGTTCTTCT CTTTACAAG TAAGACCTAC TCCTGGCCAC 4320
 TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAATAGTT TATAAGGTGG TGGTAACCAC 4380
 CTCAGTTTTC TGATGAACAT TCTGCATCCA TATACACCTC GTGACAGTCA GCAGTCTGCT 4440
 ATTAAGTGGC CTACTTCAAG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA 4500
 AAATAAAGC CTGTAGCTAA GGTTTACAGT GGACATTAGC CAGATCATTT TCTTCTTAGA 4560
 10 TTATGCCATA ATCTCTTTG ATTCTTATGG AAGTTCTAAC AATATATGGT GGTTCACACA 4620
 CCTGCAGTGA GTTTAATGAC TGACTTAGTA GCAGGTACAA GAAGCAAAC TGTTAATATA 4680
 GATTATTTT GTATTCTTAC TTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAATAA 4740
 AAGCATTTT TTAAGATAAA AAAAAAAAAA AAAAA

15 Seq ID NO: 164 Protein Sequence
 Protein Accession #: NP_064627

1 11 21 31 41 51
 20 MAPGCKTELK SVTNGQSNQP SNEGDAIKVF VRIRPPAERS GSADGEQNL LSVLSSTSLR 60
 LHSNPEKTP TFDHVDVDT TQESVFATVA KSIVESCMSG YNGTIFAYGQ TGGSKTFTMM 120
 GPSESDNFH NLRGVIFRSF EYLFSLIDRE KEKAGAGKSF LCKCSFIEIY NEQIYDLDS 180
 ASAGLYLREH IKKGVFVVG AVEQVTSAAE AYQVLSGGWR NRRVASTSMN RESSRSHAVP 240
 TTIESMEKS NEIVNIRTS LNLVDLAGSE RQKDTAHBGM RLKEAGNINR SLSCLGQVIT 300
 25 ALVDVGNGKQ RHVCYRDSKL TFLRDSLGG NAKTAIANV HPGSRFCGET LSTLNPAQRA 360
 KLINAKAVVN EDTQGNVSQL QAEVKRLKEQ LAELASGQTP PSSFLTRDKK KTNMYEYFQE 420
 AMLFFKSEQ EKKSLEIKVT QLEDLTKEE KFIQSNKMIV KFREDQIIRL EKLHKESESG 480
 FLPEEQDRLL SELRNEIQTL REQIEHPRV AKYAMENHSL REENRRLRL EPVKRAQEMD 540
 AQTIKLEKA FSEISGMEKS DKNQGGFSK AQKEPCLFAN TEKLKAQLLQ IQTELNNKQ 600
 30 EYEEPKELTR KRQLESESL QSLQKANLNL ENLEATKAC KRQEVSQLNK IHAETLKIIT 660
 TPTKAYQLHS RVPVKLSPEM SPFGSLYTQN SSILDNDILN EPVPEPMNEQ AFEAISEELR 720
 TVQEQMSALQ AKLDEEHNH LKLLQHVHKL EHRSTQMQL FSSERIDWTK QQEELLSQLN 780
 VLEKQLQETQ TKNDPLKSEV HDLRVVLHSA DKELSSVKLE YSSFKNQLEK EFNKLSERHM 840
 HVQLQDNLRL LENEKLLSEK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSIDL 900
 35 NLMELLEAEK ERNKLKSLQF EEDKENSKE ILKVLEAVRQ EKQKETAKCE QOMAKVQKLE 960
 ESSLATEKVI SLEKSRSDS KKVVDLMNQ IQELRTSVCE KTETIDTLKQ ELKDINCKYN 1020
 SALVDREESR VLIKQEVQDI LDLEKTLRL ILSEDIERDM LCEDLAHATE QLNMLTEASK 1080
 KHSGLQSAQ BELTKKEALI QELQKLNQK KEEVEQKQNE YNFKMRQLEH VMSAAEDPQ 1140
 SPKTPPHFQT HLAKLELQEQ QEIEDGRASK TSLEHLVTKL NEDREVKNAE ILRMKEQLRE 1200
 40 MENLRLESQ LIEKNWLLQG QLDLIRKQKE NSDQNHDPNQ QLKNEQEBSI KERLAESKIV 1260
 EEMLKAKADL EEVQSALYNK EMECLRMTE VERTQTLESK APQSEKQLRS KLEEMYEERE 1320
 RTSQEMEMLR KQVECLAEN GKLVGHQNLH QKIQYVVRK KENVRLAET EKLRAENVFL 1380
 KEKKRSES

45 Seq ID NO: 165 DNA Sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 50 TTTTTTTTTT TTTTTTCACA TGCTGATGTT GCTGCCGATG ATTTCAACGC CTGGCTTTGA 60
 GATTCCGCTGA GTAGTCTTGA ATAATTAAAT ATTCGAAAT CAAATCTAC TTTATTTCTC 120
 TTAATGCTAT TGTATTTCTT AATCTCAGC TTTAATCATG AAGAAAGTAC TTTGCTAGG 180
 GGTCTTAATT GAATGGTGGG GTCGAGATGA CTGCGTCAGA ATTAATCTC TGGAAAGCCT 240
 CTGAGCTCCT TTTAAATCA TCAACAAGCG AAAATCCCTA TCAATAGCGA TGTGGGAATG 300
 55 CATTAGGTAC AGTATTTTAA ACATACAAAA CCTAGGCATA TTAAGAAACA CTCCTCTGGT 360
 AATTAAATTA GGAATAATGA TGTCTTAAAG TTTATTTTAA TCAGCAAGTA TGACTCAATT 420
 TGAATATATG AGAACAATA GATTTAAATA GGAACACCCA GTAACTATG GTATGCAAT 480
 AAACCTCAGAG GTAACTTGT GAATACATA ATCTAAATA GTCACTTACC ATCAAAATAT 540
 TACGTGATCC TATATTTTTC TGTCACGTC TTAAGATAT TTTTACCTT GGGGCTTTAT 600
 60 TTTCTTTCCC TCTTCCCAAG ATTATCCAAG GCAGTTCCAA TACCGGTTT CAATAATGGT 660
 AATTAAACTT TTGGAGGGTA ATGCCAGCT GTTCCAGAA AAATACTTTT AATAGGTGGT 720
 AGTCCTCCCT GTAACCTGGT TTTCCCGGGA ATCCGGGGG GGCATGTTGT TTTTATGTG 780
 GCCATTTTGT TTTGCTCTTT TTTGTTTGT TGGTGGTCAG GTTTCTTTT CATAGCGGG 840
 GAGAAGATTT TGGTCGACT AGCGCCATCC AGCGGGTTA GAGAAGGAGC ACACCTTTTC 900
 65 CCGAATAGTG GCTTTTGGAT GAACAATGAA

70 Seq ID NO: 166 DNA Sequence
 Nucleic Acid Accession #: NM_006953.1
 Coding sequence: 33..896

1 11 21 31 41 51
 75 CGGTTCGCGC CTCTGGCGGC TCCTCCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC 60
 TCGGCTGCTCT GCGGTTTCGGC TCGGCTGTGA ACCTGCAGCC CCAACTGGCC AGTGTGACTT 120
 TCGCCACCAA CAACCCACCA CTTACCACCTG TGGCCTTGGA AAAGCCTCTC TGCATGTTTG 180
 ACAGCAAGA GGCCTCACT GGCACCCACG AGGTCTACCT GTATGCTCTG GTCGACTCAG 240
 CCATTTCAG GAATGCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTCC 300
 TACAACAGA GGGTGGGAGG ACAGTCCCT ACAAGCTGT GSCCTTTGAC CTGATCCCT 360
 GCAGTGACCT GCCCAGCCTG GATGCCATTG GGGATGTGTC CAAGGCCTCA CAGATCTCTGA 420

5 ATGCTACCT GGTGAGGTG GGTGCCAAG GGACCTGCCT GTGGGATCCC AACTTCCAGG 480
 GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCTGGTCA 540
 ATATGTCCAC GGGCTTGTA GAGGACCAGA CCCTGTGGTC GGACCCATC CGCACCAACC 600
 AGCTCACCCC ATACTCGAGC ATCGACACGT GGCCAGGCCG GCGGAGCGGA GGCATGATCG 660
 TCATCACTTC CATCTGGGC TCCCTGCCCT TCTTCTACT TGTGGGTTT GCTGGCGCCA 720
 TTGCCCTCAG CCTCGTGGAC ATGGGGAGTT CTGATGGGGA AACGACTCAC GACTCCCAA 780
 TCACTCAGGA GGCTGTTCCC AAGTCGCTGG GGGCCTCGGA GTCTTCTAC ACGTCCGTGA 840
 ACCGGGGGCC GCCACTGAGC AGGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC 900
 10 AGCACCACCC CTGGGACAGA GCATCCTCCT CTCTGGCCTT GCCCCAGGCC CTGCAGCGGT 960
 GGTGTGCACA CCCTGACTTC AGGGAAAGTG AAACAGGGCT TGTCCCTCCA ACTGCAGGAA 1020
 AACCTTAAT AAAATCTTCT GATGAGTTCT AAAAAAAA

Seq ID NO: 167 Protein Sequence
Protein Accession #: NP_008884.1

15 1 11 21 31 41 51
 | | | | | |
 MPPLWALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLITV ALEKPLCMFD SKEALTGTHE 60
 20 VYLVLVDSA ISRNASVQDS TNTPLGSTFL QTGGRTGPY KAVAFDLIPC SLDPLDAIG 120
 DVSKASQILN AYLVRVGANG TCLMDPNFQG LCNAPLSAAT EYRPKYVLVN MSTGLVEDQT 180
 LWSDPIRTNQ LTPYSTIDTW PGRRSQGMIV ITSILGSLPF FLLVGFAGAI ALSLVDHGSS 240
 DGETTHDSQI TQEAVPKSLG ASESSTSVN RGPPLDRAEV YSSKLQD

Seq ID NO: 168 DNA Sequence
Nucleic Acid Accession #: NM_005672.1
Coding sequence: 18..389

30 1 11 21 31 41 51
 | | | | | |
 AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC 60
 TGCAGCCAGG CACTGCOCTG CTGTGCTACT CCTGCAAGC CCAGGTGAGC AACGAGGACT 120
 GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG 180
 35 CAGTTGCGCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACCTGGGTG GATGACTCAC 240
 AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGCCTGTA CACCGACTTG TGCAACGCCA 300
 GCGGGGCCCA TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCATCCGGCC 360
 TGCTGCTCTG GGGACCCGCG CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCACACTG 420
 GGTGTGGTGC CCCAGGCCTT TGTGCCACTC CTCACAGAAC CTGGCCCACT GGGAGCCTGT 480
 CCTGGTTCCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGA CCCCTTTTCC 540
 40 CCNAACCCCTG ACCTTCCCAT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTITAG 600
 TGANACANAT CCGNTGCAG ATGGCCCTTC CAACCTTTN TGTGNTGTT TCCATGGCCC 660
 AGCATTITTC ACCCTTAACG GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 780
 CCACCCCAT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 840
 45 ACAGGCATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG 900
 ACAAGAGTTG ACGTAGTTTC CTGGGAGTTT CCAGAGATGG GGCCTGGAGG CCTGGAGGAA 960
 GGGGCCAGGC CTCACATTTG TGGGGNTCCC GAATGGCAGC CTGAGCAGAG CGTAGGCCCT

Seq ID NO: 169 Protein Sequence
Protein Accession #: NP_005663.1

50 1 11 21 31 41 51
 | | | | | |
 MKAVLLALLM AGLALQPSTA LLCYSCKAQV SNEDCLQVEN CTQLGEQCWT ARIRAVGLLT 60
 55 VISKGCSLNC VDDSDQYYVG KKNITCCDTD LCNASGAHAL QPAAAILALL PALGLLLWGP 120
 GQL

Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

60 1 11 21 31 41 51
 | | | | | |
 AATCCCGACA ATGGCGAAG ACAACTCAAC TGTGCTTGC TTCCAGGGCC TGCTGATTTT 60
 65 TGGAATGTG ATTATTGGTT GTTGGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCTGGG ATCGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTTCATC TGATGTTTAT 300
 70 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCACAAACA 420
 TGATGACCCG TGGAAAAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CTTCCGGAGC 540
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 75 AGAACCTCTC AACCTGGAGG CTGTGAACT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTGT CTTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 171 Protein Sequence
Protein Accession #: NP_008883.1

```

5  1      11      21      31      41      51
   |      |      |      |      |      |
  MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAN 60
  IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDPFPTNL 120
  PLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180
  DADYPWPQRQ CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAVWGPPI 240
10 LCWTFWVLLG TMFYNSRIEY

```

Seq ID NO: 172 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

```

15  1      11      21      31      41      51
   |      |      |      |      |      |
  ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGCGG GGCGCGCGCC CCGGGGCGGG 60
  CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
20  AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCTGGG CACCGCTGGG GACGATGGCG 180
  CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
  GCGAGACAAC GAGATCCAGA GGAATCCAGC CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
  TGTGATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAATGG 360
  ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTT CACGTTTTTT CATGGTTGCG 420
25  AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
  CTCCTGGAAG AGCCCATGCC CTCTCTTTAC CTCAGGTGTT GTAAAATTGG CTACTGCAAT 540
  TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
  AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC 660
30  AGCCTGCTTT GA

```

Seq ID NO: 173 Protein Sequence
Protein Accession #: Eos sequence

```

35  1      11      21      31      41      51
   |      |      |      |      |      |
  MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA 60
  LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF EQCNPRRCKW 120
  TEPYCVIAAV KIFPRPFMVA KQCSAGCAAM BRPKPEBKRP LLEPMPPFFY LKCKKIRYCN 180
40  LEGPPINSSV FKEYAGSMGB SCGGLWLAIL LLLASIAAGL SLS

```

Seq ID NO: 174 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

```

45  1      11      21      31      41      51
   |      |      |      |      |      |
  GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
  CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCTCCGCC TCCAGCTCGG 120
50  CGCTGCCCGG CAGCCGCGGAG CCATGCGACC CCAGGGCCCC GCGCGCTCCC CGCAGCGGCT 180
  CCGCGGCCCT CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCCGAGCG CCTCTGAGAT 240
  CCCCAAGGGC AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGACC TGTATAATGG 300
  AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
  CATTCCGGGT ACACCTGGGA TCCCAGGTGC GGATGGATTG AAAGGAGAAA AGGGGGAATG 420
55  TCTGAGGAAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
  ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
  AAATAGTGCT CTAAGAGTTT TGTTCAAGTG CTCACCTCGG CTAAATGCA GAAATGCATG 600
  CTGTACGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
  AGCTATAAAT TATTGGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
60  CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
  CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
  TTCTGCGATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
  TTTTTTTTAT ATGCTTGGGA ATGCTTCACT TAAATGACAT TTTAATAAAG TTTATGTATA 960
  CATCTGAATG AAAAGCAAGG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
65  TTTAAATCTA GCATTATTCA TTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT 1080
  TGGTTAGAAT ACTTCTTCCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
  GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
  TGTACAATTT GTAAATGTGA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
70  CAACCTTAAA AAAAAAAAAA AAAA

```

Seq ID NO: 175 Protein Sequence
Protein Accession #: XP_057014

```

75  1      11      21      31      41      51
   |      |      |      |      |      |
  MRPGQPAASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
  GVPRDGSPPG ANGIPGTGPI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNNGIDL 120
  GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT PNGAECSSGPL PIEAIIYLDQ 180

```


GSPEMNSTIN IHRSSSVEDGL CBGIGAGLVD VAIWVGTCSD YPKGDASTGN NSVSRRIIEE 240
LPK

Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 1..2268

1 11 21 31 41 51
10 ATGGCGAGGA AGTTATCTGT AATCTTGATC CTGACCTTTG CCTCTCTGT CACAAATCCC 60
CTTCATGAAC TAAAGCAGC TGCTTTCCCC CAGACCACTG AGAAAATTAG TCCGAATTGG 120
GAATCTGGCA TTAATGTTGA CTGGCAATT TCCACACGGC AATATCATCT ACAACAGCTT 180
TTCTACCGCT ATGGAGAAAA TAATTCTTTG TCAGTTGAAG GGTTCAGAAA ATTACTTCAA 240
AATATAGGCA TAGATAAGAT TAAAAGAATC CATATACACC ATGACCACGA CCATCACTCA 300
15 GACCACGAGC ATCACTCAGA CCATGAGCGT CACTCAGACC ATGAGCATCA CTCAGACCAC 360
GAGCATCACT CTGACCATGA TCATCACTCC CACCATAATC ATGCTGCTTC TGGTAAAAAT 420
AAGCGAAAAA CTCTTTGCCC AGACCATGAC TCAGATAGTT CAGGTAAAGA TCCTAGAAAC 480
AGCCAGGGGA AAGGAGCTCA CCGACCAGAA CATGCCAGTG GTAGAAGGAA TGTCAAGGAC 540
AGTGTAGTG CTAGTGAAGT GACCTCAACT GTGTACAACA CTGTCTCTGA AGGAACTCAC 600
20 TTTCTAGAGA CAATAGAGAC TCCAAGACCT GGAAACTCT TCCCAAAGA TGTAAAGCAGC 660
TCCACTCCAC CCAAGTGCAC ATCAAAGAGC CGGGTGAGCC GGCTGGCTGG TAGGAAAAA 720
AATGAATCTG TGAGTGAGCC CCGAAAAGGC TTTATGTATT CCAGAAACAC AAATGAAAT 780
CCTCAGGAGT GTTTCATGTC ATCAAAGCTA CTGACATCTC ATGGCATGGG CATCCAGGTT 840
CGCTGAATG CAACAGAGTT CAATATCTC TGTCCAGCCA TCATCAACCA AATTGATGCT 900
25 AGATCTTGTC TGATTCATAC AAGTGAAAAG AAGGCTGAAA TCCCTCCAAA GACCTATTCA 960
TTACAAATAG CCTGGGTGGG TGGTTTTATA GCCATTTCCA TCATCAGTTT CTGTCTCTG 1020
CTGGGGTTTA TCTTAGTGCC TCTCATGAAT CGGGTGTGTT TCAAAATTTCT CCTGAGTTTC 1080
CTGTGGCAC TGGCGGTGG GACTTTGAGT GGTGATGCTT TTTACACCT TCTCCACAT 1140
TCTCATGCA GTACACCACT TAGTCATAGC CATGAAGAAC CAGCAATGGA AATGAAAAGA 1200
30 GGACCACTTT TCAGTCATCT GTCTTCTCAA AACATAGAAG AAAGTGCCCTA TTTGATTCC 1260
ACGTGAAGG GTCTAACAGC TCTAGGAGGC CTGTATTCCA TGTTCCTGT TGAACATGTC 1320
CTCACATTGA TCAACCAATT TAAAGATAAG AAGAAAAAGA ATCAGAAGAA ACCTGAAAT 1380
GATGATGATG TGGAGATTAA GAAGCAGTTG TCCAAGTATG AATCTCAACT TTCACAAAT 1440
GAGGAGAAAG TAGATACAGA TGATCGAACT GAAGGCTATT TAGAGCAGA CTCACAAGAG 1500
35 CCTCCCACT TTGATTCTCA GCAGCCTGCA GTCTTGGAAG AAGAAGAGGT CATGATAGCT 1560
CATGCTCATC CACAGGAAGT CTACAATGAA TATGTACCCA GAGGGTGCAA GAATAAATGC 1620
CATTCACTAT TCCACGATAC ACTCGGCCAG TCAGACGATC TCATTCACCA CCATCATGAC 1680
TACCATCTAT TTCTCCATCA TCACCACCAC CAAACCACCT ATCCTCACAG TCACAGCCAG 1740
CGCTACTCTC GGGAGGAGCT GAAAGATGCC GCGCTGCCA CTTTGGCCTG GATGGTGATA 1800
40 ATGGGTGATG GCCTGCACAA TTTCAGCGAT GGCCTAGCAA TTGGTGCTGC TTTTACTGAA 1860
GGCTTATCAA GTGGTTTAAG TACTTCTGTT GCTGTGTCT GTCATGAGTT GCCTCATGAA 1920
TTAGGTGATC TTGCTGTCT ACTAAAGGCT GGCATGACCG TTAAGCAGCG TGTCTTTAT 1980
AATGCATTGT CAGCCATGCT GCGTATCTT GGAATGGCAA CAGGAATTTT CATTTGGTCAT 2040
TATGCTGATA ATGTTTCTAT GTGGATATTT GCACITACTG CTGGCTTATT CATGTATGTT 2100
45 GCTCTGGTTG ATATGGTACC TGAATGCTG CACAATGATG CTAGTGACCA TGGATGTAGC 2160
CGCTGGGGGT ATTTCTTTT ACAGAATGCT GGGATGCTTT TGGGTTTTGG AATTATGTTA 2220
CTTATTTCCA TATTGAACA TAAATCGTG TTTCTGATAA ATTTCTAG

Seq ID NO: 177 Protein Sequence
Protein Accession #: XP_084007

1 11 21 31 41 51
55 MARKLSVILI LTFALSVTNP LHELKAAAPP QTTEKISPNW ESGINVDLAI STROYHLQOL 60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHHS DHEHSDHER HSDHEHSDH 120
EHSDHSDHHS HHNHAASGKN KRKALCPDHD SDSSGKDPN SQKGARPE HASGRRNVKD 180
SVSASEVTST VYNTVSEGT FLETIETPRP GLFPKDVSS STPPSVTSKS RVSLLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGNGIQV PLNATEFNYL CPAIINQIDA 300
60 RSLIHTSEK KAEIPPKTYS LQIANVGGFI AISIISFLSL LGVILVPLMN RVFFKFLSF 360
LVALAVGTLS GDAFLHLLPH SHASHHSHS HEPEMEMKR GPLFSLSSQ NIESAYFDS 420
TWKGLTALGG LYFMPLEHV LTLIKQPKDX KKNQKPKEN DDDVEIKKQL SKYESQLSTN 480
BEKVDTDRT EGYLRADSQE PSHFDSQPPA VLEEEVMIHA HAPQEVYNE YVPRGCKNKC 540
HSHFDTLQ SDDLHHHHH YHHILHHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600
MGDLHNFSD GLAIGAAETE GLSSGLSTSV AVFCHLPHE LGDFAVLKKA GMTVKQAVLY 660
65 NALSAMLAYL GMATGIPGH YAEVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RMGYFFLQNA GMLLFGGIML LISIFEHKIV FRINF

Seq ID NO: 178 DNA Sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

1 11 21 31 41 51
75 CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCAGGCT TCTTGGGGGT 60
AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGGTCCTCT AGTGAGAGCC 120
CAAGTGGGAG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGGTCAGTTC CTTATTCAAG 180
TCTGCAGCCG GCTCCAGGG AGATCTCGGT GGAACCTCAG AAACGCTGGG CAGTCTGCCT 240
TTCAACCATG CCCCCTGCC TGGGAGCCGA GATGTGGGGC CTTGAGGCT GGCTGCTGCT 300

5 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGCG GGTGAGCTGG AGACCTCAGA 360
 CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC 420
 CGGGAGCAAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GGGGGCGAAG GGGCCAGGA 480
 ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC COGGCTTACG AGGGCCGCGT 540
 GGAGCAGCCG CCGCCCCCAC GCAACCCCTT GGACGGCTCA GTGCTCCTGC GCAACGCAGT 600
 GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTGAGCACC TTCCCCCGCG GCAGCTTCCA 660
 GGCGCGGCTG CGGCTCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC 720
 ACTAGAAGAG GGCCAGGGCC TGACCTGTGC AGCTCTCTGC ACAGCTGAGG GCAGCCAGC 780
 10 CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAAAG TCCAGCCGTT CCTTCAAGCA 840
 CTCGCGCTCT GCTGCCCTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG 900
 GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCTGTCTC CAGGACCAAA GGATCACCCTA 960
 CATCTCTCAC GTGTCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
 GTGGCACAAT GGCAGAGAAG GAGCTATGCT CAAGTGCCCTG AGTGAAGGGC AGCCCCCTCC 1080
 CTCATACAA C TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAG TGGATGGGGA 1140
 15 CACTTTGGGC TTTCCCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTCAG 1200
 CAATGAGTTT TCCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
 CTCTGGGAAG CAGGTGGAGG TAGTGTGAGC CTCGGTGGTG GTGGTGGGTG TGATCGCCGC 1320
 ACTCTGTTC TGCCTTCTGG TGGTGGTGGT GGTGCTCATG TCCCATAACC ATCGCGCAA 1380
 GGCCAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCGGG AGAACTCCAT 1440
 20 CCGGAGCTCG CATTCCCATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500
 GAGAGCCGAG GGCCACCCTG ATAGTCTCAA GGACAAACAGT AGCTGCTCTG TGATGAGTGA 1560
 AGAGCCGAG TTCTTGCGGA AGATCCAGCT GACCAAGGTG AGGGAGATAG AAACACAGAC 1620
 TGAAGTCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT 1680
 CAAACAGGCC ATGAACCAT TTTTTCAGGA GAATGGGACC CTACGGGCCA AGCCACGGG 1740
 25 CAATGGCATC TACATCAATG GCGGGGACA CCTGTCTGA CCCAGGCTG CTCTCTTCC 1800
 CTAGGCTCTG CTCTCTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCTCTCTTAA 1860
 ACACCCGAG TTCTTGCGGA AGATGCTCCC CATCCCACTG ACTGCTTGAC CTTTACCTCC 1920
 AACCTTCTG TTTCTCGGA GGGCTCCACC AATTGAGTCT CTCCACCAT GCATGCAGST 1980
 CACTGTGTGT GTGCTGTGT GCCTGTGTGA GTGTGACTG ACTGTGTGTG TGTGGAGGGG 2040
 30 TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC 2100
 AAGTGAAGTG TGGTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTGAGG 2160
 GTTGGCGGTG TGTGTGTGT GGCCTGTGTG GACCTGCTCC TGAAAAAGCA GGTATTTTCT 2220
 CAGACCCAG AGCAGTATTA ATGATGCAGA GGTTCAGGA GAGAGGTGGA GACTGTGGCT 2280
 CAGACCCAGG TGTGCGGGCA TAGCTGGAGC TGGAACTGCG CTCGGTGTG AGGGAACCTG 2340
 35 TCTCTTACCA CTTGCGAGCC ATGCGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400
 GAGGCTTGAA CTGTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT 2460
 ACATATTTTC TGTAAATATA CATGCGCGG GAGCTTCTG CAGGAATACT GCTCGAATC 2520
 ACTTTTAATT TTTTCTTTT TTTTCTTTG CCCTTTCCAT TAGTTGTATT TTTTATTAT 2580
 40 TTTTATTTT ATTTTCTTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCTGT 2640
 CTGTAAAAA ACCAAAAACC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 179 Protein Sequence
Protein Accession #: AAH10423

45 1 11 21 31 41 51
 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE 60
 QVQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPRNPLDG SVLLRNAVQA 120
 50 DEGEYECRV TFPAGSPQAR LRLRLVPLP FSLNPGPALE EQGLTLAAS CTAEGSPAPS 180
 VTWTEVKGT TSSRSFKHSR SAAVTSEPHL VPSRSMNQRP LTCVSHPLG LQDQRITHL 240
 HVSFLAEASV RGLDQNLWH IREGAMLK LSEGGPPPSY NWTRLGDLPL SGVRVDGDTL 300
 GFPLPTTEHS GIYVCHVSN FSRDSQVTV DVLDPEQDSG QQVLDVSAV VVGVIAALL 360
 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEL TLTRENSIRR LSHHTDPRS QPEESVGLRA 420
 55 EGHFDSLKDN SSCSVMSSEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIQ 480
 AMNHFVQENG TLRAPKPTNG IYINGRGHLV

Seq ID NO: 180 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 482..3007

60 1 11 21 31 41 51
 AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGTCTG AGCTTGGATC 60
 TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC 120
 65 TGCAATCAGC AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180
 ATGCGGTGAA TTTTAAATGA GGGAAAAAGG GACAAATGCT TCAGGATGCT CTAGATATGA 240
 CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTAA 300
 CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTGA GAAGAAAGTA CGCAGTGGTT 360
 70 GGTGTTTCT TTTTCTTAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC 420
 ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAA CCGATTTCAT CACATGACAA 480
 CATGAAGCTG TGGATTATC TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540
 CCAACTCCA GTGCTCTCAT CCAGAGGCTC TTGTGATTCT CTTTGAATT GTGAGGAAAA 600
 AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660
 75 TGTGCCACCA TCAGGACCTT TCCAATAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA 720
 CACAAATGAC TTTTCTGGGC TTACCAATGC TATTTCAATA CACCTTGGAT TTAACAATAT 780
 TGCAGATATT GAGATAGGTG CATTAAATGG CCTTGGCCCT CTGAAACAAC TTCAATACAA 840
 TCACAAATCT TAGAAATCT TTAAGAGGGA TACTTTCCAT GGACTGGAAA ACCTGGAATT 900
 CCTGCAAGCA GATAACAATT TTATCACAGT GATTGAACCA AGTGCCTTTA GCAAGCTCAA 960

CAGACTCAAA GTGTTAATTT TAAATGACAA TGCTATTGAG AGTCTTCTC CAAACATCTT 1020
 CCGATTGTGT CCTTAAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA 1080
 TGTGTGTTTT CTGGAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAAATG 1140
 5 GGCTGCAAT TGTGACTTAT TGCAGTTAAA AACTTGGTTG GAGAACATGC CTCCACAGTC 1200
 TATAATGGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG 1260
 ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCCTC 1320
 AGGATCATT CATCTGGCAG CAACATCTTC AATAAATGAT AGTCGCATGT CAACTAAGAC 1380
 CACGTCCATT CTAAACATAC CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC 1440
 10 ATCCACTCAA CTTCCAGGAC CTTACTGCCC TATTCTTGT AACTGCAAG TCCTATCCCC 1500
 ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC 1560
 TCCTCCGCAA AATCCTAGAA AGCTCATTCT AGCGGGAAT ATTATTCACA GTTTAATGAA 1620
 GTCTGATCTA GTGGAATATT TCACCTTGGG AATGCTTAC TTGGGAAACA ATCGTATTGA 1680
 AGTTCGTGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAACTCT ATCTAAATGG 1740
 TAACCACCTG ACCAAATTA GTAAAGGCAT GTTCTTGGT CTCCATAATC TTGAATACTT 1800
 15 ATATCTTGAA TACATGCGCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCCTAA 1860
 ACTTAAAGTC CTGTATTATA ATAACAACCT CCTCCAAGTT TTACCACCACT ATATTTTTTC 1920
 AGGGGTTCCT CTAATCAGG TAAATCTTAA AACAAACCCAG TTTACCCATC TACCTGTAAG 1980
 TAATATTTTG GATGATCTTG ATTTACTAAC CCAGATTGAC CTTGAGGATA ACCCTGGGA 2040
 20 CTGCTCCTGT GACCTGGTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100
 GACAGATGAC ATCCTCTGCA CTTCCCGCG GCATCTCGAC AAAAAGGAAT TGAAAGCCCT 2160
 AAATAGTGAA ATCTCTGTCT CAGGTTTGTG AAATAACCCA TCCATGCCAA CACAGACTAG 2220
 TTACTTTATG GTACCACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280
 TCTTACGGAC GCTGTGCCAC TGTCTGTCT AATATTGGGA CTTCTGATTA TGTTCATCAC 2340
 25 TATTGTTTTT TGTGCTGCGG GGATAGTGGT TCTTGTCTT CACCGCAGGA GAAGATACAA 2400
 AAAGAAACAA GTAGATGAGC AAATGAGAGA CAACAGTCTT GTGCATCTTC AGTACAGCAT 2460
 GTATGGCCAT AAAACCACTC ATCACAACAT TGAAAGACCC TCTGCCTCAC TCTATGAACA 2520
 GCACATGTTG AGCCCAATGG TTTCTGTCTA TAGAAGTCCA TCTTTGGTC CAAAGCATCT 2580
 GGAAGAGGAA GAAAGAGGGA ATGAGAAAGA AGGAAGTGAT GCAAAACATC TCCAAAGAAG 2640
 30 TCTTTGGAA CAGGAAATC ATTCACCACT CACAGGGTCA AATATGAAAT ACAAACACAC 2700
 GAACCAATCA ACAGAAATTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT 2760
 AGAAAAAGAA AGGGAACCTC AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC 2820
 TCAGCTCGAG CCGTATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880
 GGAACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940
 35 TTTTGAACCT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA 3000
 AACATAGATG GAGAGTTTGA GGGCTTTCGC AGAAATGCTG TGATTCTGTT TTAAGTCCAT 3060
 ACCTGTGAAA TAAAGTGCTT ACGTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120
 AACTATGGGG AAAAAAAGG AAGAGAAAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180
 GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCTTGCA TGTAATC 3238

Seq ID NO: 181 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MKLWIHLFYS SLLACISLHS QTFVLSSRGS CDSLNCCEER DGTMLINCEA KGIKRVSEIS 60
 VPPSRPFQLS LLNNGLTMLH TNDPSSGLTNA ISIHLEFPNI ADIEIGAFNG LGLLKQLHIN 120
 HNSLEILKED TFGLENLFP LQADNNFITV IEPFAPSKLN RLKVLILNDN AIESLPPNIF 180
 RFVPLTHLDL RGNQLQTLFY VGFLEHIGRI LDLQLEDNKN ACNCDLIQLK TWLENMPPQS 240
 50 IIGDVVCSNP PFFKGSILSR LKESICPTP PVYEHEDPS GSHLAATSS INDSRMSTKT 300
 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSL SGLLIHQER NIESLSDLRP 360
 PPQNPRLIL AGNIHSLMK SDLVEYPTLE MLHLGNRIE VLEBGSFPMNL TRLQLKLYNG 420
 NHLTKLSKGM FLGLWNLLEV LVEYNAIKEI LPGTFNPMKP LKVLVNNNL LQVLPPHIFS 480
 GVPLTKVNLK TNQPTHLFVS NILDDL DLT QIDLEDNPDW CSCDLVLQLO WIKLSKNTV 540
 55 TDDILCTSPG HLDKELKAL NSEILCPGLV NNPSMPTQTS YLMVTPATT TNTADTILRS 600
 LTDAVPLSVL ILGLLIMPIT IVFCAAGIVV LVLHRRRRYK RKQVDEQMRD NSPVHLQYSM 660
 YGHKTHHTT ERPSASLYEQ HMVSPMVHVY RSPSFPGKHL EEEEEERNEKE GSDAKHLQRS 720
 LLEQENHSPL TGSNMKYKTT NQSTEFSLFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA 780
 60 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEBQQ 840
 T

Seq ID NO: 182 DNA Sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 1..1524

1 11 21 31 41 51
 ATGGCGGGTG CGGCGCCGAA GCGCGCGCGG CTAGCGGCGC CGGCGGCGGA GGAGAAGGAA 60
 GAGGCGCGGG AGAAGATGCT GGCGGCCAAG AGCGCGGACG GCTCGGCGCC GGCAGGCGAG 120
 70 GCGAGGGGCG TGACCTCTGCA GCGGAACATC ACGCTGCTCA ACGGCGTGGC CATCATCGTG 180
 GGGACCATTA TCGGCTCGGG CATCTTCTGT ACGCCACGCG GGTGCTCAA GGAGGACAGC 240
 TCGCGGGGCG TGGCGCTGGT GGTGTGGGCC GCGTGGCGCG TCTTCTCCAT CGTGGGCGCG 300
 CTCTGCTACG CGGAGCTCGG CACCACCATC TCCAAATCGG GCGGCGACTA CGCTCATATG 360
 CTGGAGGTCT ACGGCTCGCT GCCCGCCTTC CTCAAGCTCT GGATCGAGCT GCTCATCATC 420
 75 CGGCTTCTAT CGCAGTACAT CGTGGCCCTG GTCTTCGCCA CCTACCTGCT CAAGCGCTC 480
 TTTCCCACTC GCCCGGTGCC CGAGGAGGCA GCCAAGCTCG TGGCTGCTCT CTGCTGCTG 540
 CTGCTCAACG CCGTGAACGT CTACAGCGTG AAGGCCGCCA CCGGCTGCCA GGATGCCTTT 600
 GCCCGGCCCA AGCTCCTGGC CTTGCGCTG ATCATCTGCG TGGCTTCTGT CCAGATCGGA 660

5 AAGGGTGATG TGTCCAATCT AGATCCCAAC TTCTCATTG AAGGCACCAA ACTGGATGTG 720
 GGAACATTG TGCTGGCATT ATACAGCGGC CTCTTTGCCT ATGGAGGATG GAATTACTTG 780
 AATTTCTGCA CAGAGGAAAT GATCAACCCC TACAGAAACC TGCCCTGGC CATCATCATC 840
 TCCCTGCCCA TCGTGACGCT GGTGTACGTG CTGACCAACC TGGCTACTT CACCACCTG 900
 TCCACCGAGC AGATGCTGTC GTCCGAGGCC GTGGCGTGG ACTTCGGGAA CTATCACCTG 960
 GGCCTCATGT CTTGGATCAT CCCCCTCTTC GTGGGCTGT CTTGCTTCGG CTCGTCAT 1020
 GGGTCCCTGT TCACATCTCT CAGGCTCTTC TTCTGGGGT CCGGGGAAG CCACCTGCC 1080
 TCCATCTCTT CCATGATCCA CCCACAGCTC CTCACCCCG TCGCTCCCT CGTGTTCAG 1140
 TGTGTGATGA CGCTGCTCTA CGCCTTCTCC AAGGACATCT TCTCGTCTCAT CAATCTCTTC 1200
 10 AGCTTCTTCA ACTGGCTCTG CGTGGCCCTG GCCATCATCG GCATGATCTG GCTGCGCCAC 1260
 AGAAAGCCTG AGCTTGAGCG GCCATCAAG GTGAACCTGG CCTGCTCTGT GTTCTTCATC 1320
 CTGGCTGCCC TCTTCTGAT CGCCGTCTCC TTCTGGAAGA CACCCGTGGA GTGTGGCATC 1380
 GGCTTCAACA TCATCTCTAG CGGGCTGCC GTCTACTTCT TCGGGTCTG GTGAAAAAC 1440
 15 AAGCCCAAGT GGCTCTCTCA GGGCATCTTC TCCACGACCG TCCTGTGTCA GAAGCTCATG 1500
 CAGGTGGTCC CCGAGGAGAC ATAG

Seq ID NO: 183 Protein Sequence
 Protein Accession #: XP_035292.2

20 1 11 21 31 41 51
 | | | | | |
 MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGVLEKAG SPGLALVVWA ACVPSIVGA LCYABLTITI SKSGGDYAYM 120
 25 LEVYGSIPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLVL 180
 LITAVNYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
 GNIVLALYSY LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPITVLVYV LTNLAYFTTL 300
 STEQMLSSSE VAVDFGNVHL GVMSWIIIPV VGLSCFSGVN GSLFTSSRLP FVGSREGHLP 360
 SILSMIHPQL LTPVPSLVFT CVMTLIYAFS KDIFSVINFP SFNMLCVAL AIIGMIWLRH 420
 30 RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GPTIILSGLP VYFVGWNNKN 480
 KPKMLLQGI FSTVLQCKLM QVVPQET

Seq ID NO: 184 DNA Sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 1..822

35 1 11 21 31 41 51
 | | | | | |
 ATGAAGTGA GTATCTTTGA GGGACTCCTG AGTGGGGTCA ACAAGTACTC CACAGCCTTT 60
 GGGCGCATCT GGCTGTCTCT GGTCTTCATC TTCCGCGTGC TGGTGTACCT GGTGACGGCC 120
 40 GAGCGTGTGT GGAGTGATGA CCACAAGGAC TTGCACTGCA ATACTCGCCA GCCCGCTGTC 180
 TCCAACGTCT GCTTTGATGA GTTCTTCCCT GTGTCCCATG TGCGCCTCTG GGCCTGCGAG 240
 CTTATCCTGG TGACATGCC CTCACTGCTC GTGGTCAATG ACGTGGCCTA CCGGAGGTT 300
 CAGGAGAAGA GGCACCGAGA AGCCCATGGG GAGAACAGTG GCGCCTCTA CCTGAACCCC 360
 45 GGCAAGAAGC GGGGTGGGCT CTGGTGGACA TATGTCTGCA GCCTAGTGTT CAAGGCGAGC 420
 GTGGACATCG CCTTTCTCTA TGTGTTCCAC TCATTCTACC CCAATATAT CCTCCCTCTC 480
 GTGGTCAAGT GCCACGACAG TCCATGTCCC AATATAGTGG ACTGCTTCAT CTCCAAGCCC 540
 TCAGAGAAGA ACATTTTAC CCTCTCATG GTGGCCACAG CTGCCATCTG CATCCTGCTC 600
 AACCTCTGAG AGCTCATCTA CCTGGTGAAG AAGAGATGCC ACGAGTGCCT GGCAGCAGAG 660
 50 AAAGCTCAAG CCATGTGCAC AGGTCTATCACC CCCACGGTA CCACCTCTTC CTGCAACCAA 720
 GACGACCTCC TTTCCGGTGA CCTCATCTTT CTGGGCTCAG ACAGTCAATC TCCTCTCTTA 780
 CCAGACGCC CCCGAGACCA TGTGAAGAAA ACCATCTTGT GA

Seq ID NO: 185 Protein Sequence
 Protein Accession #: NP_005259.1

55 1 11 21 31 41 51
 | | | | | |
 MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVT ERMVSDDHKO FDCNTRQPGC 60
 60 SNVCPDEFPP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKHREAHG ENSGRLYLNP 120
 GKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLPV VATAAICILL NLVELIYLVS KRCHCELAAR KAQAMCTGRH PHGTTSSCKQ 240
 DLLSGDLIF LGSDSHPLLL PDRPRDHVKK TIL

Seq ID NO: 186 DNA Sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 25..457

65 1 11 21 31 41 51
 | | | | | |
 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCCTCCT 60
 CGCCCTGCTG GCGCTCACTT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGAGC GAGTGGCTG AGTGGGCTG GGGGCGCTGC ACCCCAGCA GCAAGGATTG 180
 CGCGTGGGT TTCCCGAGG GCACCTGCGG GCGCCAGACC CAGCGCATCC GGTGACGGGT 240
 70 GCCTGCAAC TGAAGAAGG AGTTTGAGC CGACTGCAAG TACAAGTTTG AGAAGTGGG 300
 TGGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGGCTA 360
 CAATGCTCAG TGCCAGGAGA CCATCCGCTT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
 75 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCGCCGTGTC TCATATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540

5 CACCAGTGCC TTCTGTCTGC TCGTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCCAGC CCACACCCTA AGTGCCCAAA GTGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCCGTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 187 Protein Sequence
 Protein Accession #: NP_002382.1

10 1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLAL TSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DGVGFREGT 60
 CGAQTQIRIC RVPKNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
 RVTKPCTPKT KAKAKAKGKG GKD

15 Seq ID NO: 188 DNA Sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902

20 1 11 21 31 41 51
 | | | | |
 CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGCCCCCA GCGCTCCCC AGGCCGOGAG 60
 GCGCCCTGCC GCGGTGCTTG GCCTCCCTCT CCAGACTGCA GGGACAGCAC CCGGTAAGT 120
 CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 25 GGGTCCGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCTCTGCG CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
 GGGAAAGCGG CCAGTGCAGG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCGAAAC TGGATGTAAG TTTGGTGAAT GGTGGGAC AAACAAATGC 480
 30 AGATGCTTTC CAGGATACAC CGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
 CTCAATGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAACTGTCT AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCTCGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
 35 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
 AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
 GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
 40 ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTGC TTGCTCACA AAACAGCATG AAAAAGAAAG CAAAATTA AAATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
 45 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
 CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GCGCTTGCCA 1560
 GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
 50 AACTCTGTTT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
 TGGGAAGCAG GGAATAATCA GTTGATATCA GGAACCTGAT CTACCAAAG CATCATTTTT 1800
 GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 55 TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
 TCTTGATATA GATATGCCAA TATTGTCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
 TTTCTGAATT TTTCCACATT ATATTATAAA ATATGGAAT GTCACTTTAT CTCCCCTCCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
 TAGAAAAAAA AGCACAGAGA AATGTTTAAAC TGTPTGACTC TTATGATAC TCTTGGAAAC 2280
 60 TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGCTTTTCA TAGCCAAACT 2340
 TGTATATTTA AATCTTTTGT AATAATAATA TCCAAATCAT CAAAAA AAAA

Seq ID NO: 189 Protein Sequence
 Protein Accession #: NP_056322.2

65 1 11 21 31 41 51
 | | | | |
 MPLPWSLALP LLLSWVAGGF GNAASARHKG LLASARQPGV CHYGTKLACC YGWRNSKGV 60
 CEATCEPGCK FGECVGFENK RCPFGVTGKT CSQDVNEQGM KPRPOHRCV NTHGSYKFCF 120
 70 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EGGPQCLCPG SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNTQ 240
 GSPKCKCQGG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLALHKNMS KKKAKIKNVT 300
 PEPTRTPTFK VNLQPFNYEE IVSRGGNSHG GKKGNEEMKM EGLEDEKREE KALKQNDIEER 360
 SLRGDVPFPPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFMHGI CD WKQDREDDFD 420
 75 WNPADRDNAI GPFYMAVPALA GHKKDIGRLK LLLPDLPQPS NPLLLFDYRL AGDKVGKLRV 480
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF BAERGKGTG EIAVDGVLLV 540
 SGLCPDLSLLS VDD

Seq ID NO: 190 DNA Sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 12..2522

5	1	11	21	31	41	51	
	AGAGACTCAA	GATGATTCCC	TTTTTACCCA	TGTTTTCTCT	ACTATTGCTG	CTTATTGTTA	60
	ACCCATATAA	CGCCAAACAAT	CATTATGACA	AGATCTTGCC	TCATAGTCGT	ATCAGGGGTC	120
10	GGGACCAAGG	CCCAAAATGTC	TGTGCCCTTC	AACAGATTTT	GGGCACCAAA	AAGAAATACT	180
	TCAGCACTTG	TAAGAACTGG	TATAAAAAGT	CCATCTGTGG	ACAGAAAAACG	ACTGTTTTAT	240
	ATGAATGTTG	CCCTGGTTAT	ATGAGAAATG	AAGGAATGAA	AGGCTGCCCA	GCAGTTTTGC	300
	CCATTGACCA	TGTTTATGGC	ACTCTGGGCA	TCGTGGGAGC	CACCACAACG	CAGCGCTATT	360
	CTGACGCTTC	AAAACCTGAGG	GAGGAGATCG	AGGGAAGGGG	ATCCTTCACT	TACTTTGCAC	420
	CGAGTAAATG	GGCTTGGGAC	AACCTGGATT	CTGATATCCG	TAGAGGTTTG	GAGAGCAACG	480
15	TGAATGTTGA	ATTACTGAAT	GCTTTACATA	GTCACATGAT	TAATAAGAGA	ATGTTGACCA	540
	AGGACTTAA	AAATGGCATG	ATTATTCTCT	CAATGTATAA	CAATTGGGGG	CTTTTCATTA	600
	ACCATTAACC	TAATGGGGTT	GTCACTGTTA	ATTGTGCTCG	AATCATCCAT	GGGAACCAGA	660
	TTGCAACAAA	TGGTGTGTCT	CATGTCAATTG	ACCGTGTGCT	TACACAAATT	GGTACCTCAA	720
	TTCAAGACTT	CATTGAAGCA	GAAGATGACC	TTTCATCTTT	TAGAGCAGCT	GCCATCACAT	780
20	CGGACATATT	GGAGGCCCTT	GGAAGAGACG	GTCACCTTAC	ACTCTTTGCT	CCCACCAATG	840
	AGGCTTTTGA	GAAACTTCCA	CGAGGTGTCC	TAGAAAGGTT	CATGGGAGAC	AAAGTGGCTT	900
	CCGAAGCTCT	TATGAAGTAT	CACATCTTAA	ATACTCTCCA	GIGTTCTGAG	TCTATTATGG	960
	GAGGAGCAGT	CTTTGAGACG	CTGGAAGGAA	ATACAAATGA	GATAGGATGT	GACGGTGACA	1020
25	GTATAACAGT	AAATGGGAAT	AAAAATGGTG	ACAAAAAGGA	TATTGTGACA	AATAATGGTG	1080
	TGATCCATTG	GATTGATCAG	GTCCTAATTC	CTGATTCTGC	CAAAACAAGTT	ATTGAGCTGG	1140
	CTGGAAACCA	GCAAAACCAC	TTCAAGGATC	TTGTGGGCCA	ATTAGGCTTG	GCATCTGCTC	1200
	TCAGGCGAGA	TGGAGAATCA	ACTTTGCTGG	CACCTGTGAA	TAATGCATTT	TCGTATGATA	1260
	CTCTCAGCAT	GTTTCAGCGC	CTCCTTAAAT	TAATTCTGCA	GAATCACATA	TTGAAAGTAA	1320
	AAGTTGGCCT	TAATGAGCTT	TACAACGGGC	AAATACTGGA	AACCATCGGA	GGCAAAACGC	1380
30	TCAGAGTCTT	CGTATATCGT	ACAGCTGTCT	GCATTGAAAA	TTATGCATG	GAGAAAGGGA	1440
	GTAAGCAAGG	GAGAAACGGT	GCGATTACCA	TATTCGCGGA	GATCATCAAG	CCAGCAGAGA	1500
	AATCCCTCCA	TGAAAAGTTA	AAACAAGATA	AGCGCTTTAG	CACCTTCCTC	AGCCTACTTG	1560
	AAGCTGCAGA	CTTGAAAGAG	CTCCTGACAC	AACCTGGAGA	CTGSACATTA	TTTGTGCCAA	1620
35	CCAATGATGC	TTTAAAGGGA	ATGACTAGTG	AAGAAAAAGA	AATTCTGATA	CGGGACAAAA	1680
	ATGCTCTTCA	AAACATCATT	CTTTATCACC	TGACACCAGG	AGTTTTTCAT	GGAAAAGGAT	1740
	TTGAACCTGG	TGTTACTAAC	ATTTTAAAGA	CCACACCAAG	AAGCAAAATC	TTTCTGAAAG	1800
	AAGTAATGA	TACACTCTCG	GTGAATGAAT	TGAAATCAAA	AGAATCTGAC	ATCATGACAA	1860
	CAAAATGGTG	AATTCATGTT	GTAGATAAAC	TCCTCTATCC	AGCAGACACA	CCTGTTGGAA	1920
40	ATGATCAACT	GCTGGAAATA	CTTAATAAAT	TAATCAAATA	CATCCAAATT	AAGTTTGTTC	1980
	GTGGTAGCAG	CTTCAAGGAA	ATCCCCGTGA	CTGTCTATAC	AATCAAAATT	ATAACCAAG	2040
	TTGTGGAAAC	AAAAATTAAT	GTGATTGAAG	GCAGTCTTCA	GCCTATTATC	AAAACTGAAG	2100
	GACCCACACT	AACAAAAGTG	AAAATTGAAG	GTGAACCTGA	ATTCAGACTG	ATTAAAGAAG	2160
	GTGAACAAT	ACTGAAAGTG	ATCCATGGAG	AGCCAATTAT	TAAAAAATAC	ACCAAAATCA	2220
45	TTGATGGAGT	GCCTGTGGAA	ATAACTGAAA	AAGAGACACG	AGAAGAACGA	ATCATTACAG	2280
	GTCTCTGAAAT	AAAAACACT	AGGATTCTTA	CTGGAGGTGG	AGAAACAGAA	GAAACTCTGA	2340
	AGAAATGTTT	ACAAGAAGAG	GTACCAAGG	TCACCAAAAT	CATTGAAGGT	GGTGATGGTC	2400
	ATTTATTGTA	AGATGAAGAA	ATTAAAAGAC	TGCTTCAGG	AGACACACCC	GTGAGGAAGT	2460
	TGCAAGCCAA	CAAAAAAGTT	CRAAGTTCTA	GAAGACGATT	AAGGGAAGGT	CGTCTCTCAGT	2520
50	GAAAAATCAA	AAACAGAGAA	AAAAATGTTA	TACAACCCCTA	AGTCAATAAC	CTGACCTTAG	2580
	AAAAATTTGTA	GAGCCAAAGT	GACCTCAGGA	ACTGAAACAT	CAGCACAAAG	AAGCAATCAT	2640
	CAAAATATTC	TGAACACAAA	TTTAATATTT	TTTTTTCTGA	ATGAGAAACA	TGAGGGAAAT	2700
	TGTGGAGTTA	GCCTCCTGTG	GTAAGGAAT	TGAAGAAAT	ATAACACCTT	ACACCTTTT	2760
	TCATCTTGAC	ATTAAAAGTT	CTGGCTAACT	TTGGAATCCA	TTAGAGAAAA	ATCCTTGTCA	2820
55	CCAGATTGAT	TACAATTCAA	ATCGAAGAGT	TGTGAACGTG	TATCCCATTG	AAAAGACCGA	2880
	GCCTTGATG	TATGTTATGG	ATACATAAAA	TGCACGCAAG	CCATTATCTC	TCCATGGGAA	2940
	GCTAAGTTAT	AAAAATAGGT	GCTTGGTGTA	CAAAACTTTT	TATATCAAAA	GGCTTTGCAC	3000
	ATTTCTATAT	GAGTGGGTTT	ACTGGTAAAT	TATGTTATTT	TTTACAACCTA	ATTTTGTACT	3060
	CTCAGAAATG	TTGTCATATG	CTTCTTGCAA	TGCATATTTT	TTAATCTCAA	ACGTTTCAAT	3120
60	AAAACCATTT	TTGAGATATA	AAGAGAATTA	CTTCAAAATG	AGTAATTCAG	AAAAACTCAA	3180
	GATTTAAGTT	AAAAAGTGGT	TTGGACTTGG	GAA			

Seq ID NO: 191 Protein Sequence
Protein Accession #: BAA02836.1

65	1	11	21	31	41	51	
	MIPFLPMFSL	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQG	PNVCAQQIL	GTKKKYFSTC	60
	KNWYKKSICG	QKTTVLYECC	PGYMRMEGMK	GCPAVLPIDH	VYGTGLGIVGA	TTTQRYSDAS	120
70	KLREEIEGKG	SFTYFAPNSE	AWDNLDSDIR	RGLESNNVVE	LLNALHSHMI	NKRMLTKDLK	180
	NGMIIPSMYN	NIGLFINHYF	NGVVTVNCAR	IIHGNQIATN	GVVHVIVDRVL	TQIGTSIQDF	240
	IEAEDDLSSP	AAAAITSDIL	EALGRDGHFT	LFAPTNEAFE	KLPRGVLERF	MGDKVASEAL	300
	MKYHILNTLQ	CSESIMGGAV	FETLEGNTIE	IGCDGDSITV	NGIKMWNKKD	IVTNNGVIHL	360
75	IQQVLIPDSA	KQVIELAGKQ	QTFTDLVAQ	LGLASALRFD	GEYTLAPVN	NAPSDDTLSM	420
	VQRLKLILQ	NHILKVKVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGATHIFRE	IKPAEKSLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTQPGD	WTLFVPTNDA	540
	FKGMTSEEKE	ILIRDKNALQ	NIILYHLTPG	VFIGKGFEPG	VTNLIKTTQG	SKIPLKEVND	600
	TLVLVNELKSK	ESDIMTTNGV	IHVVDKLLYP	ADTPVGNLQ	LEILNKLIKY	IQIKFVRGST	660

PKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTBGPTL TKVKIEGEPE FRLIKEGETI 720
TEVIHGEPPII KKYTKIIDGV PVEITEKETR EERIITGPPI KYTRISTGGG ETEETLKKLL 780
QSEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

5

Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

10 1 11 21 31 41 51
| | | | | |
CCGGCTCGCG CCCTCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC 60
AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCGGG 120
GACGGGCGTC TGCGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT 180
TCTCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGGTG 240
15 TCCGCCAGC CCGCGCTGCC GGACCAAGTC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACGAGGTGCG CCACGGACCT GCCCGCTTAC 360
GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCGGTGC TCCCTGCGGG CGCCTTCGCC 420
CGCGGGCGCG CGCTGGCGGA GCTGGCGCGC CTCACCTCA GCGGCGAGCG CCTGGACGAG 480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
20 CCACTGGCCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTGCGCCCCC 600
AGTCCCTCTG TGGAACTCAT CTTGAACCAAC ATCGTCCCCC CTGAAGATGA GCGGCGAAGC 660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCAT GCAGGGGCTC 720
CGCGCTTCGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGGGGATGT GCTGGCCCAA 780
CTGCCCGACC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
25 TCTTCCGCA ACCTGACACA TCTAGAAAGC CTCACCTGG AGGACAATGC CCTCAAGTTC 900
CTTCAATATG GCACCTGGCG TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960
AACAACTCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAGGAAACA 1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
30 CAAACCTCTT ATGCTTCTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCCTG 1200
GTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCTTGC 1260
AGGATACACA TGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
35 TAGATACAAAC GACTTTGAC TAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG 1500
TTTCTCGGTG TGTCTGTGTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCTTC 1560
TCTTTTCT TGGAACCTCT CAACAGTAT GGAGGGATT TTCAGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAATACTT TATTATAAAA 1740
40 TATCAGTTTT ATTCTCATGT ACCTAAGTGT TGGAGAAAT AATGTCATCC TATAAAGTGC 1800
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCATGGTGC CACAGGAGCA CCTGCATCCA 1860
AGAGATGACT TACATTTTAT TGTCTGCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAATGT ACTGATTTTT 1980
45 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAATAAAG 2040
ATTCTAAAAA GAA

Seq ID NO: 193 Protein Sequence
Protein Accession #: CAA82324.1

50 1 11 21 31 41 51
| | | | | |
MPOGCSRGA AGDGRLLRL LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPPLD 60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLAVLPAGA FARRPPLAEL 120
55 AALNLSSSRL DEVRAFAEH LPSLRQLDLS HNPLADLSPF AFGSNGASVS APSPLVELIL 180
NHIVPPFEDER QNRSFEGMVV AALLAGRALQ GLRRLLEASN HPLYLPRDVL AQLPSLRHLD 240
LSNNSLVSLT YVSFRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVP LDNNPWVDCD 300
HMADHVTNKK ETEVVQGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILEP SLQTSYVFLG 360
IVLALIGAIF LVLVLYLRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

60

Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

65 1 11 21 31 41 51
| | | | | |
GGTTACTCAT CTGGGCTCA GGTAAAGAGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG OCCAGGCCAT 120
70 GATCTGGACT CGAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TCGGTGCAGA AAGCAGATGA CGATGCTCC CGGAACAAGA TGAAGACAGT 240
GAAGTGCCTG CCGGCGCTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCAATCA 300
CGGACAATTC TCGCTGGCAG TCGSGGTTG CGGTTCGGGA CTCCCGGCA AGAATGACCG 360
CGGCTGGAT CTTCACGGCG TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
75 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCC AACCGCGTGG AGTGCTACAG CTGTGTGGCG CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CCGCGGCTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTGACCGGC AACGTCACTT TGACGCGAGC TAATGTGACT GTGTCTTGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720

5 TGGCTCCTGT TGGCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
 CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCAT 900
 GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCTT CCGGGGATGA 960
 GGAGCCGAGG TTGACTGGAG GCGCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGC AAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTCTGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCCACCTGG 1140
 AAATTTCCTT CTCACTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 10 CCACACCATG GACTGGGCTG GCCAGGCCCC TGTTTTCCCA ACATTCCCA GTATCCCCAG 1260
 CTCTGTCTGC GCTGTGTTGC GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320
 GGGTGTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCTTGTCT TCTCCGCTTG 1380
 TCCTCTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
 AGGATGTCTA GCTTCTACT CACTTCTTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 15 GGTGGGACAA TGGCTCCCA CTCTAAGCAC TGCCTCCCTT ACTCCCGCA TCTTTGGGGA 1560
 ATCGGTTCCT CATATGTCTT CTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
 CTTATGTCTG TGTGTGATCA GTTCTGCGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
 TTGTATAGTG AAAAAAAA

Seq ID NO: 195 Protein Sequence
 Protein Accession #: NP_055215

20 1 11 21 31 41 51
 25 MDPAKAGAG AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSNPKMK TVKCAPGVDDV 60
 CTEAVGAVET IHGQSLAVX GCGSLPGKN DRGLDLHGLL AFILQLQCAQ DRCAKLNLT 120
 SRALDPAGNE SAYPPNGVEC YSCVLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVLT 180
 AANVTVSLPV RGCVDDEFCT RDGVTGPFT LSGSCQGSR CNSDLRNKTY FSPRIPLVR 240
 LPPPEPTTVA STTSVTTSTS APVRPTSTK PMPAPTSQTP RQGVHEBASR DEEPRLTGGA 300
 AGHQDRNSG QYPARGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 196 DNA Sequence
 Nucleic Acid Accession #: NM_006536
 Coding sequence: 109..2940

35 1 11 21 31 41 51
 40 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCAATTGCAG GTCTTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300
 ATAACTGAAG CTTCATTTTA CTTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAAGAA 360
 ATAAAGATTT TAATACCTGC CACATGGAAG GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCATAATGT CATAGTGACT GACTGGTATG GGGCAGATGG AGATGATCCA 480
 45 TACACCTTAC AATACAGAGG GTGTGAAAA GAGGAAAAAT ACATTCATT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TAGGGATCAC GAGGCGAGT GTTTGTCCAT 600
 GAATGGGCC ACCCTCCGTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGCTCTTG CCCCAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 50 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTTGTAA GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAAC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCAGACA CTCTGCTGAC 960
 TTTCAACACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCACAT ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 55 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
 ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAG GAGAGATCAG AGCCACAGCTA 1200
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGTTT CATATCTGCC CACCCTGTA 1260
 TCAGTAAAA CAGACATCAG CATTGTTC TGGCTTAAAG AAGGATTGGA GGTGGTTGAA 1320
 60 AAACGTGAATG GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCG AGATGATAAG 1380
 CTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGT CAACAATTCA CTCCATTGCC 1440
 CTGGGTTTCT CTGAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 TTCTTTGTT CAGATATATC AAACCTCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
 TCTGGAACCT GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAATAATGTC 1620
 65 AAACCTCAC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTATT TGATCCTGAT 1740
 GGACGAAAA ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
 TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCTGAAACAA TACCCATCAT 1860
 TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTCGGCTT CCAACTCAGC TGTGCCCCCA 1920
 GCACTGTGG AAGCCTTTGT GGAAGAGAG AGCCTCAAT TTCTCATCC TGTGATGATT 1980
 70 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTGAC TGCCACAGTT 2040
 GAGCCAGAGA CTGAGATCC TGTATAGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTACTGAGG TATTTTTTCT CTTTGTGCTG AAATGGTAGA 2160
 TATAGCTTGA AAGTGCAATG CAATCACTCT CCCAGCATAA GCACCCAGC CCACTCTATT 2220
 75 CCAGGAGTC AAGCCTTTGT TGTACCAAGT TACACAGCAA ACGGTAAAT TCGATGAAT 2280
 GCTCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGCTT TAGCCAGTCT 2340
 AGCTCAGGAG GCTCCTTTTC AGTGTGGGA GTTCCAGCTG GCCCCACCCC TGATGTGTTT 2400
 CCACCATGCA AAATTATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460
 TGGACAGCAC CTGAGAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAAATG 2520

5 AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTC 2640
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATATGT 2700
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCACGGCG 2760
 CCTCTGTTTA TTCCCCCCTT TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT 2880
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAAACAA ATTATTATAA 2940
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTGG ACTACAAAAA 3000
 10 CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
 ATACAGATAA GATTTTATCA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAAC 3120
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTTATCT TTAAGTAAT GTCTTTAAAG 3180
 GCAAAGGGAA GGGTAAAGTC GGACCAAGTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA 3240
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACGTCTCT TGTGAAGCAA 3300
 TCAITTAGIT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360
 15 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAGG CTCTTTACCT 3420
 CTGCTATTT TGTATATAT ATTTTCTGAT ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAAAC TTTAAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
 TTTATGACAA AGGTCTATTG AATTTATTGT TMTGTAAAGT TCTACTCCCA TCAAAGCAGC 3600
 20 TTTCTAAGTT TATTCGCTTG GGTATTATAG GAATGATAGT TATAGCCCCN TATAATGCCT 3660
 TACCTAGGAA A

Seq ID NO: 197 Protein Sequence
 Protein Accession #: NP_006527

25 1 11 21 31 41 51
 | | | | |
 MTQRSIAGPI CNLKFVTLV ALSSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLIIN 60
 IKEMITAEAF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAAH 120
 30 GDDPYTLQYR GCGKEGKYIH FTFNLLNDN LTAGYGRSRG VFVHEWAHLR WGVDFEYNND 180
 KPFIYINGNQ IKVTRCSSDI TGIFVCEKGP CPQENCIIISK LFKEGCTFIY NSTQNATASI 240
 MFMQSLSSVY EFCNASTHNQ EAPNLQNMCM SLRSANDVIT DSADFHSFPP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAAEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDKRLVSVYL PTTVSAKTDI SICSLKKKGF EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSLRT GGLKPFVVDI SNSNSMIDAF 480
 35 SRISSGTGDI PQQHIIQEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPPEIIL 540
 FDPDGRKYIT NNPIITNLTPR TASLWIPGTA KPGHWTYTLN NTHSLQALK VTVTSRASNS 600
 AVPPATVEAF VERDSLHFPF PVMYANVKQ GFYFPLNATV TATVEPETGD PVTLLRLDDG 660
 AGADVINKDG IYSRYFFSFA ANGRYSLKVH VNHSFISISTP AHSIPGSHAM VYPGYTANGN 720
 IQMNAPRKSV GRNEERKMG FSRVSSGGSF SVLGVVPAGPH PDVPPCKII DLEAVKVEEE 780
 40 LTLSWTAPGE DFDQGGATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPOQ AGIREIFTFS 840
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
 LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGIT KLL

45 Seq ID NO: 198 DNA Sequence
 Nucleic Acid Accession #: NM_001944
 Coding sequence: 84..3083

50 1 11 21 31 41 51
 | | | | |
 TTTTCTTAGA CATTAAGTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGACTT 60
 TTTCAACAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT 180
 55 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAGAAGAG GCAAAAACGT GAATGGGTGA 240
 AATTGGCCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAAA AAGAAACCCA ATTGCCAAGA 300
 TTACTCTAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCGGCC TTTTGGAAAT TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCCC 480
 AAGGACTAGA TGTAGAGAAA CCACCTTATC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 60 ATCCTCCAAT ATTTTCACAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCCTCA 600
 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCCAC TTGAATTCTA 660
 AAATTGCTTT CAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCTTAAGCA 720
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTTCTTGA CCGAGAGCAA GCTAGCAGCT 780
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
 65 GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCACGTAT TGAAGAAAAT ATTTTAAGTT CTGAATTAAT TCGATTTCAA GTAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAAATGAAG 1020
 GAAATTGGTT TGAATATCAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080
 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAAACAAAG 1140
 70 CTGAATTTCA CCAATCAGTT ATCTCTGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200
 AGGTAATAAA TGTAAAGAAA GGAATTGCAT TCCGCTCTGC TTCCAAGACA TTTACTGTGC 1260
 AAAAAGGCAT AAGTAGCAAA AAATTGGTGG ATTTATATCT GGGAAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAATATGT CATGGGACGT AACGATGGTG 1380
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAATT TGTCAAAAAT ATGAACCGAG 1440
 75 ATCTACTTTT CATGATTAA CAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CGGGTAAAC TTCTCAGGC ACGGTATATG TTAGAGTACC CGATTTCAT GACAATTGTC 1560
 CAACAGCTGT CCTCGAAAAA GATGCAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCTG 1620
 CTAGAACACT GAATAATAGA TACTAGGCC CCTATACATT TGCCTGGAA GATCAACCTG 1680

5 TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG 1740
CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800
ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAAGT CTGTCTAGTG GACAAACAGG 1860
GCATCTGTGG AACTTCTTAC CCAACCACAA GCCCTGGGAC CAGGTATGGC AGGCCGCACT 1920
CAGGGAGGCT GGGGCTGCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980
TGGCCCCCTT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040
GTGGTTTAT CCAGTTCCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100
GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTGTGT GCCTCCTGTA ACAGCCAATG 2160
GAGCCGATT CATGGAAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220
10 TGGAAGGCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280
GTGCTGCAGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340
CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACCAAGG CATTCCACTG 2400
GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTCTG GACTCCTACT 2460
TTTCTCAGAA AGCATTGCCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520
15 TGTGATCTA TGATAATGAA GGCAGAGATG CCACTGGTTC TCCTGTGGGC TCGGTGGGTT 2580
GTTGCAGTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640
TTAAAAAATC TCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700
CCTCTAAGAA CAGCGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760
CAGGATTGT TAAGTGGCAG ACTTGTCTAG GAAGTCAAGG AGCTTCTGCT TTGTCGCGCT 2820
20 CTGGGTCTGT CCAGCCAGCT GTTTCATCC CTGACCTCT GCAGCATGGT AACTATTAG 2880
TAAGGAGAC TTACTGGCT TCTGGTTCCC TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940
CACTTCTCAC ACAAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCATT TCCAGTGTTC 3000
CTGGCAACT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060
ATCCTGCTC CCGTCTAATA TGACCAGAA GAGCTGGAAT ACCACACTGA CCAATCTGG 3120
25 ATCTTTGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180
TGGCACTTAT TAGCTTCTCT CATAAACTGA TCAGGATTAT AAATTAATG TTTGGGTTCA 3240
TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCCTCAAGT ACTATTCAAA TTGTAGTAAA 3300
TCTTAAAGT TTTCAAAACC CTAATATCAT ATTCGC

30 Seq ID NO: 199 Protein Sequence
Protein Accession #: NP_001935

35 1 11 21 31 41 51
MMGLFPRTTG ALAIFVVVIL VHGELEIETK QQYDEEEMTM QQAKRRQKRE WVKFAKPCRE 60
GEDNSKRNP AKITSDYQAT QKITYRISGV GIDQPPFGIF VVDKNTGDIN ITAIVDREET 120
PSFLITCRAL NAQLDVEKP LILTVKILDI NDNPPVFSQQ IFMGEIBENS ASNSLVMLN 180
ATDADEPNHL NSKIAFKIVS QEPAGTFMFL LSRNTGEVRT LTNSLDREQA SSYRLVVSQA 240
DKDGEGLSTQ CECNIVKDV NDNFPMFRDS QYSARIEENI LSSELLRFQV TDLDEEYTDN 300
40 WLAVVFFTSQ NEGNWFEIQT DPRTNBQILK VVKALDYEQL QSVKLSTAVK NKAEFHQSVI 360
SRYRVQSTPV TIQVINVRG IAPRPASKTF TVQKGISSEK LVDYILGTQY AIDEDTNKAA 420
SNVYVVMGRN DGGYLMIDSK TABIKPVKNM NRDSTFIVNK TITAEVLAI DYTGTSTGT 480
VYVRVPDFND NCPATVLEKD AVCSSESFSV VSARTLNNRY TGPYTFALD QPVKLPVWS 540
45 ITTLNATSL LRAQEQIPPG VYHISLVLD SQNNRCMPR SLTLEVQCQD NRGICGTSYP 600
TTPGTRYGR PHSGRLGPA IGLLLGLLL LLLAPLLLT CDCGAGSTGG VTGGFIPVPD 660
GSEGTIHQNG IEGAHPEDEK ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSME 720
MTTLGAATE SGGAAAGFATG TVSGAASGPG AATGVGICSS QGSQTMTRH STGGTNKDYA 780
DGAISMNFD SYFSQKAFAC AEEDDQGEAN DCLLIYDNEG ADATGSPVGS VGCCSPIADD 840
LDDSFLLSLG PKFKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPLEV QQTGFVKCQT 900
50 LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVETETYSAS GSLVQPSLAG FDPILLQNV 960
VTERVICPIS SVPGNLGAPT QLRSHTMLC TEDPCSRLI

55 Seq ID NO: 200 DNA Sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86..526

60 1 11 21 31 41 51
GGACCTGGGA AGGAGCATAG GACAGGGCAA GGCGGGATAA GGAGGGGCAC CACAGCCCTT 60
AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTGGTGCC CACCTCAGT GCGCATGTC 120
ACTGGGCGTC TTCCATCGG CCCCTTCGCC AGTGTGGGGA ACGGGGCGGA GCTGTGAGCC 180
GGCGACTCGG GTCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
65 ACAAACACAG AACCAACAG CAGTCCCAG GAGCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACACGAG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCAGTGC GACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAA 420
ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAGAGGA 480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
70 AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
CAGCTTTCAC CAAAAA AAAAAA

75 Seq ID NO: 201 Protein Sequence
Protein Accession #: NP_065144.1

75 1 11 21 31 41 51
MLLWCPQCA CSLGVFPSP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHSTAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120

SGVKVKIIPK EEHCKMPEAG EEQPQV

Seq ID NO: 202 DNA Sequence

Nucleic Acid Accession #: AA172056

Coding sequence: 121..339

5
10
15
20
25

1	11	21	31	41	51	
TTTAGCCACC	AGAGGANTTC	TCTTGAAATA	CCCAAAATCC	ATCAGTATCT	TGAATCATGC	60
TGGATTTTGA	AGAATTCCTA	AGAAGCCATG	TAAAGGGGGC	TCTCTGGCCT	TGAAATAGTG	120
ATGTTTTTTA	TACAGAAAGG	AGAATGCAGA	ATGGTCAGAC	TATCATGCAC	TGTTAAATTT	180
GATTTCAGA	AATTACAGGA	AAACTTTTCA	AAGTTCATC	TCACAGANN	TTATTTTNC	240
AAGAATTC	AGATAAGTTT	AGTTTATGG	AAGACTTTA	TGTGGTTTT	ACTCACTCT	300
CATCTCAGAC	ATCGACAGAT	GATTACATCA	CTTATAGTTC	TAGTAAATTT	ATTAATATA	360
AACTCAGAGA	CATTCCAATA	TCCACATTGC	TTACACCAAT	AGGCATAGAT	TCAGTGTGAG	420
CTATGCAAT	TGAAATGAG	CTGTTTGTG	ATTTAAAGGT	TTAAATTTCT	CTAACCAAC	480
TGCTTGATCC	AGATGCAGGA	CTGCAATGT	TAATATTTGT	TCTGGAAGAA	CAATCAATA	540
AGACTTAAGA	GGAAAGGGAA	TGGCCCAAT	CCACCTGAAA	TTTTTCTTA	AAAAGTGTG	600
AGCCTACTAA	ATCAGATGA	AAATAGAAAT	ACAAGATTAT	AAACAAATG	CAATCAAACT	660
TTTCTTAAG	TTACCTAAG	TTATTTTATC	TGAAATTTTC	AAGCAACTTT	GTTCAACATT	720
AAATTGACAA	TCTAACTAA	CAAGTCTTTT	GAATTTATGC	ATGGTAGTAA	ACATTCTCTC	780
TATTAACTTT	ATTACCTAAG	GCTAAACCTA	AAATTTTAA	GCAAAATTAG	AAAAATAGTC	840
TTCACTCATC	AAAAAATAAA	GTITGTATCA	TTTAGTATTT	TCCCAATAAA	ATTGGTGTG	900
CTTGGTTTTT	TATTTGGAGA	GTCTGTGCAA	AATGTCACTA	AAAATAAATT	AGCACTAGAA	960
ATTATTTCTA	AATACCAAA					

Seq ID NO: 203 DNA Sequence

Nucleic Acid Accession #: NM_005656.1

Coding sequence: 57..1535

30
35
40
45
50
55
60
65
70
75

1	11	21	31	41	51	
GTCATATTGA	ACATTCCAGA	TACCTATCAT	TACTCGATGC	TGTTGATAAC	AGCAAGATGG	60
CTTTGAACCT	AGGGTCAACA	CCAGCTATTG	GACCTTACTA	TGAAAACCAT	GGATACCAAC	120
CGGAAAACCC	CTATCCCGCA	CAGCCCACTG	TGGTCCCCAC	TGCTACGAG	GTGCATCCGG	180
CTCAGTACTA	CCCGTCCCC	GTGCCCCAGT	ACGCCCCGAG	GGTCTGACG	CAGGCTTCCA	240
ACCCCGTGT	CTGCACGAG	CCCAATTC	CATCCGGGAC	AGTGTGCACC	TCAAAGACTA	300
AGAAAGCACT	GTGCATCACC	TTGACCTGG	GGACCTTCCT	CGTGGGAGCT	CGCGTGGCG	360
CTGGCTACT	CTGGAAGTTC	ATGGGAGCA	AGTGCTCCAA	CTCTGGGATA	GAGTGGGACT	420
CCTCAGGTAC	CTGCATCAAC	CCCTCTAAT	GGTGTGATGG	CGTGTACAC	TGCCCCGGCG	480
GGGAGGACGA	GAATCGGTGT	GTTCGCTCT	ACGAGACAAA	CTTCATCCTT	CAGATGTACT	540
CATCTCAGAG	GAACTCCTGG	CACCTGTGT	GCCAAGACGA	CTGGAACGAG	AACTACGGCG	600
GGGCGGCTG	CAGGACATG	GGCTATAAGA	ATAATTTTAA	CTCTAGCCAA	GGAAATAGTG	660
ATGACAGCG	ATCCACCAGC	TTTATGAAAC	TGAACACAAG	TGCGGGCAAT	GTGCATATCT	720
ATAAAAACT	GTACCACAGT	GATGCCGTGT	CTTCAAAAGC	AGTGGTTTCT	TTACGCTGTG	780
TAGCCTGGGG	GGTCAACTTG	AACTCAAGCC	GCCAGAGCAG	GATCGTGGG	GGTGAGAGCG	840
CGCTCCCGGG	GGCTCGGCC	TGGCAGGTCA	GCCTGCACGT	CCAGAACGTC	CACGTGTGCG	900
GAGGCTCCAT	CATCACCCCC	GAGTGGATCG	TGACAGCCCG	CCACTGCGTG	GAAAAACCTC	960
TTAACAACT	ATGGCATTGG	ACGGCATTTG	CGGGGATTTT	GAGACAACT	TTTATGTTCT	1020
ATGGAGCCGG	ATACCAAGTA	CAAAAAGTGA	TTTCTCATCC	AAATTATGAC	TCCAAGACCA	1080
AGAACAATGA	CATTGCGCTG	ATGAAGCTGC	AGAAGCCTCT	GACTTTCAAC	GACCTAGTGA	1140
AACCACTGTG	TCTGCCCAAC	CCAGGCATGA	TGCTGCAGCC	AGAACAGCTC	TGCTGGATTT	1200
CCGGGTGGGG	GGCCACCGAG	GAGAAAGGGA	AGACCTCAGA	AGTGTGAAC	GCTGCCAAGG	1260
TGCTTCTCAT	TGAGACACAG	AGATGCAACA	GCAGATATGT	CTATGCAAC	CTGATCACAC	1320
CAGCCATGAT	CTGTGCCGCG	TTCTGTCAGG	GGAACTGCGA	TTCTTGCCAG	GGTGACAGTG	1380
GAGGCGCTCT	GGTCACTTCG	AACAACAATA	TCTGGTGGCT	GATAGGGGAT	ACAAGCTGGG	1440
GTCTGCTG	TGCCAAAGCT	TACAGACCA	GAGTGTACGG	GAATGTGATG	GTATTACCGG	1500
ACTGATTTA	TGCAGAAATG	AAGGCAACG	GCTAATCCAC	ATGGTCTTCG	TCCTTGACGT	1560
GGTTTACAA	GAATAACAATG	GGGCTGGTTT	TGCTTCCCGG	TGCATGATTT	ACTCTTAGAG	1620
ATGATTCAGA	GGTCACTTCA	TTTTTATTAA	ACAGTGAAT	TGTCTGGCTT	TGGCACTCTC	1680
TGCCATACTG	TGCAGGCTGC	AGTGGCTCCC	CTGCCAGACC	TGCTCTCCCT	AACCCCTTGT	1740
CCGCAAGGGG	TGATGGCCGG	CTGTTGTGG	GCACTGGCGG	TCAATTGTGG	AAGGAAGAGG	1800
GTGTGAGGCT	GCCCCATTG	AGATCTTCCT	GCTGAGTCCT	TTCCAGGGGC	CAATTTTGGG	1860
TGAGCATGGA	GCTGTCACTT	CTCAGCTGCT	GGATGACTTG	AGATGAAAAA	GGAGAGACAT	1920
GGAAAGGGAG	ACAGCCAGGT	GGCACCTGCA	GCGGCTGCCC	TCTGGGGCCA	CTTGGTAGTG	1980
TCCCCAGCCT	ACTTCAACAAG	GGGATTTTGC	TGATGGGTTT	TTAGAGCCTT	AGCAGCCCTG	2040
GATGGTGGCC	AGAAATAAAG	GGACCAAGCC	TTTATGGGTT	GTGACGTGGT	AGTCACTTGT	2100
AAGGGGAACA	GAACATTTT	TGTTCTTATG	GGGTGAGAA	ATAGACAGTG	CCCTTGGTGC	2160
GAGGGGAACA	ATTGAAAGG	AACTTGCCCT	GAGCACTCCT	GGTGCAGGTC	TCCACCTGCA	2220
CATTGGGTGG	GCTCTCTGGG	AGGGAGACTC	AGCCTTCCCT	CTCATCTCTC	CTGACCCCTGC	2280
TCCTAGCACC	CTGGAGAGTG	AATGCCCTT	GGTCCCTGGC	AGGGCGCCAA	GTTTGGCACC	2340
ATGTCCGGCT	CTTCAGGCT	GATAGTCATT	GGAAATTGAG	GTCCATGGGG	GAAATCAAGG	2400
ATGCTCAGTT	TAAGGTACAC	TGTTTCCATG	TTATGTTTCT	ACACATTGAT	GGTGGTGACC	2460
CTGAGTTCAA	AGCCATCTT					

Seq ID NO: 204 Protein Sequence

Protein Accession #: NP_005647.1

	1	11	21	31	41	51	
5	MALNSGSPPA	IGPYENHGY	OPENPYPAQP	TVVPTVYEVH	PAQYYPSPVP	QYAPRVLTQA	60
	SNFVVCTQPK	SPSGTVCTSK	TKKALCITLT	LGTFLVGAAL	AAGLLWKFMG	SKCSNSGIEC	120
	DSSGTCINPS	NWCDGVSHCP	GGEDENRCVR	LYGPNFILQM	YSSQRKSWHP	VQDDWNENY	180
	GRAACRDMGY	KNNFYSSQGI	VDDSGSTFSM	KLNTSAGNVD	IYKKLYHSDA	CSSKAVVSLR	240
	CLACGVNLNS	SRQSRIVGGE	SALPGAWPWQ	VSLHVQNVHV	CGSSIITPEW	IVTAAHCVKE	300
	PLNNPMHHTA	FAGILRQSFM	PYGAGYQVQK	VISHPNYDSK	TQNDIALMK	LQKPLTFNDL	360
10	VKPVCLPNPG	MMQLPDEQLCW	ISGWGATEEK	GKTSEVLNAA	KVLLIETQRC	NSRYVYDNLI	420
	TPAMICAGFL	QGNVDSQCGD	SGGPLVTSNN	NIWNLIGDTS	WGSCKAKAYR	PGVYGNVMVF	480
	TDWIYRQMK	NG					

Seq ID NO: 205 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

	1	11	21	31	41	51	
20	GCTCTGCCCA	AGCCGAGGCT	GCGGGGCCGG	CGCCGGCGGG	AGGACTGCGG	TGCCCCGCGG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CCTGTTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGGCGGG	GCCCCCGGG	CGACTCGGGG	GCGGACCGCG	GCGCGGAGCT	GCCGCCCGTG	180
	AGTCCGCGCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCGT	GAGGAGCTGG	CTCGCCGCCC	CATGGGGCGC	GCTGCCCGCT	300
25	CGGCCACCGG	TGCTGCTGCT	CCTGCTGCTG	CTGCTCCTGC	TGCAGCCGCG	GCCTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCTCTAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACGTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	CGATGCGAGC	600
30	TTCAAGGCGA	AGGACCCACA	GCGCGACTGT	CAAAACTACA	TCAAGATCCT	CTTGCCGCTC	660
	AGCGGCAGTC	ACCTGTTTAC	CTGTGGCACA	GCAGCCCTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTCAACCT	GGCAAGGGAC	GAGAAGGGGA	ATGTCTCTCT	GGAAGATGGC	780
	AAGGGCGGTT	GTCCCTTCTG	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
35	AGCCTTCGCG	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTCTG	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTCTA	AGGCCAGCTG	GCTGTGCTCA	CGGCCGACG	ATGGCTTCCC	CTTCAAGCTG	1200
40	CTGCAGGATG	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GCGGTGACAC	CCTTTCTTAT	1260
	GGGGTCTTCA	CTTCCAGTGG	GCACAGGGGA	ACTACAGAA	GCTCTGCCGT	CTGTGCTCTC	1320
	ACAAATGAAG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CGGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTGCCC	GGGAAGAGAA	GATCAACTCA	TCCCTGCAGC	TCCAGACCG	CGTGCTGAAC	1500
45	TTCTCAAGG	ACCACTTCTC	GATGGACGGG	CAGGTTCGAA	GCGCATGTCT	GCTGCTCGAG	1560
	CCCCAGGCTC	GCTACACAGG	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCTC	TCTGTGCGAC	TGGTGAACGG	CGGCTTCCAC	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAACTCT	1740
	CTCTGGGACA	CCCCAGGGGG	GCTGCTGTAT	GCGGCCCTAC	ACTCGGGCGT	AGTCCAGGTG	1800
50	CCCATGGCCA	CTCTCAGCCT	GTACAGGAGC	TGTGGGGACT	GCCTCTCTCG	CGGGGACCCC	1860
	TACTGTGCTT	GGAGCGGCTC	CAGCTGCAAG	CACGTACAGC	TCTACAGGCC	TCAGCTGGCC	1920
	ACCAGGCCGT	GGATCCAGGA	CATCGAGGGA	GCCAGCGCCA	AGGACCTTTG	CAGCGCGTCT	1980
	TCGGTTGTGT	CCCCGTCTTT	TGTACCAACA	GGGGAGAAGC	CATGTGAGCA	AGTCCAGTTC	2040
	CAGCCCAACA	CAGTGAACAC	TTTGGCCTGC	CCGCTCTCTT	CCAACCTGGC	GACCCGACTC	2100
55	TGGCTACGCA	ACGGGGGCCC	CGTCAATGCC	TGCGCCTCCT	GCCACGTGCT	ACCCACTGGG	2160
	GACCTGTGTC	TGGTGGGCAC	CCAACAGCTG	GGGGAGTTCC	AGTGCTGGTC	ACTAGAGGAG	2220
	GGCTTCCAGC	AGCTGGTAGC	CAGCTACTGC	CCAGAGGTGG	TGGAGGACGG	GSTGGCAGAC	2280
	CAACAGATG	AGGGTGGCAG	TGTACCCGTC	ATTATCAGCA	CATCCGCTGT	GAGTGCACCA	2340
	GCTGGTGCCA	AGGCCAGCTG	GGGTGCAGAC	AGGTCCCTACT	GGAAGGAGTT	CCTGGTGATG	2400
60	TGCACGCTCT	TTGTGCTGGC	CGTGTGCTC	CCAGTTTAT	TCTTGTCTTA	CCGGCACCGG	2460
	AACAGCATGA	AAGTCTTCTC	GAAGCAGGGG	GAATGTGCCA	GCGTGACCCC	CAAGACCTGC	2520
	CCTGTGTGTC	TGCCCCCTGA	GACCCGCCCA	CTCAAACGCC	TAGGGCCCCC	TAGCAACCCG	2580
	CTCGATCACC	GAGGATACCA	GTCCCTGTCA	GACAGCCCCC	CGGGTCCCCG	AGTCTTCACT	2640
	GAGTCAGAGA	AGAGGCCACT	CAGCATCCAA	GACAGCTTCG	TGGAGGTATC	CCAGTGTGTC	2700
65	CCCCGGCCCC	GGGTCCGCTT	TGGCTCGGAG	ATCCGTGACT	CTGTGGTGTG	AGAGCTGACT	2760
	TCCAGAGGAC	GCTGCCCTGG	CTTCAGGGGC	TGTGAATGCT	CGGAGAGGGT	CAACTGGACC	2820
	TCCCTTCCCG	TCTGCTCTTC	GTGGAAACAG	ACCGTGGTGC	CGGGCCCTTG	GGAGCCTTGG	2880
	GGCCAGCTGG	CCTGCTGCTC	TCCAGTCAAG	TAGCGAAGCT	CCTACCACCC	AGACACCCAA	2940
	ACAGCCGTGG	CCCCAGAGGT	CCTGGCCAAA	TATGGGGGCC	TGCTTAGGTT	GGTGGAAACG	3000
70	TGCTTCTTAT	GTAACCTGAG	CCCTTTGTTT	AAAAAACAA	TCCAAATGTG	AAACTAGAAT	3060
	GAGAGGGAAG	AGATAGCATG	GCATGCAGCA	CACACGGCTG	CTCCAGTTCA	TGGCCTCCCA	3120
	GGGTGCTCTG	GGATGCATCC	AAAGTGGTTG	TCTGAGACAG	AGTTGGAAC	CCTCACCAAC	3180
	TGGCCTCTTC	ACCTTCCACA	TTATCCCGCT	GCCACCGGCT	GCCCTGTCTC	ACTGCAGATT	3240
	CAGGACCGAC	TTGGGCTGGG	TGCGTTCTGC	CTTGCCAGTC	AGCCGAGGAT	GTAGTTGTTG	3300
75	CTGCGTCTGT	CCACCACTCT	CAGGACCCAG	AGGGCTAGGT	TGGCACTGCG	GCCCTCACCA	3360
	GGTCTTGGGC	TGGGACCCAA	CTCTGGGACC	TTTCCAGCCT	GTATCAGGCT	GTGGCCACAC	3420
	GAGAGGACAG	GCGAGCTCTA	GGAGAGATT	CGTGACAATG	TACGCTTTTC	CCTCAGAAAT	3480
	CAGGGAAGAG	ACTGTGCGCT	GCCTTCTCTC	GTGTTTGTGT	GAGAACCCGT	GTGCCCCCTT	3540

CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCCTG 3600
 GTCCTCTCCC CAGTCCCCAG TTCACCCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
 ATGCACTTTA TGTCAITTTT TAATAAAGTC TGAAGAATTA CTGTTT

5 Seq ID NO: 206 Protein Sequence
 Protein Accession #: XP_044533.6

10 1 11 21 31 41 51
 | | | | | |
 MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
 SFGKGDPORD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180
 15 GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDFPAISRS QSLRPPTKTES SLNWLQDPAP 240
 VASAYIPESL GSLQDDDDXI YFFPSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGPPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
 FTMKDVRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 NFLKDHFLMD GQVRSRMLLL QPQARYQRVA VHRVPGLHHT YDVLFLGTGD GRLHKAVSVG 480
 20 PRVHIEELQ IFSSSQPVQN LLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSGSSC KHVSLYQPQL ATRPWIQDIE GASAKDLCSA SSVVSPSPVP TGEKPCEQVQ 600
 FQPNVTNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGFQCWSLE 660
 EGFQQLVASV CPEVVEDGVA DQTDGGGSVP VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
 25 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 PLDHRGYQSL SDSPPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSV

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a bladder cancer-associated transcript in a cell from a patient,
5 the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.
2. The method of Claim 1, wherein the biological sample comprises isolated nucleic
10 acids.
3. The method of Claim 2:
 - a) wherein the nucleic acids are mRNA; or
 - b) further comprising the step of amplifying nucleic acids before the step of contacting
15 the biological sample with the polynucleotide.
4. The method of Claim 1, wherein the polynucleotide:
 - a) comprises a sequence as shown in Tables 1A-13; or
 - b) is immobilized on a solid surface.
20
5. The method of Claim 1, wherein the patient is:
 - a) undergoing a therapeutic regimen to treat bladder cancer; or
 - b) suspected of having bladder cancer.
- 25 6. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.
7. The nucleic acid molecule of Claim 6, which is labeled.
- 30 8. An expression vector comprising the nucleic acid of Claim 7.

9. A host cell comprising the expression vector of Claim 8.
10. An isolated polypeptide which is encoded by a nucleic acid molecule having
5 polynucleotide sequence as shown in Tables 1A-13.
11. An antibody that specifically binds a polypeptide of Claim 10.
12. The antibody of Claim 11, further conjugated to an effector component.
- 10 13. The antibody of Claim 12, wherein the effector component is a fluorescent label.
14. The antibody of Claim 12, wherein the effector component is a radioisotope or a
cytotoxic chemical.
- 15 15. The antibody of Claim 11, which is
a) an antibody fragment; or
b) a humanized antibody
- 20 16. A method of detecting a bladder cancer cell in a biological sample from a patient, the
method comprising contacting the biological sample with an antibody of Claim 11.
17. The method of Claim 16, wherein the antibody is further conjugated to an effector
component.
- 25 18. The method of Claim 17, wherein the effector component is a fluorescent label.
19. A method for identifying a compound that modulates a bladder cancer-associated
polypeptide, the method comprising the steps of:

- a) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and
- b) determining the functional effect of the compound upon the polypeptide.

5

20. A drug screening assay comprising the steps of

- a) administering a test compound to a mammal having bladder cancer or a cell isolated therefrom;
 - b) comparing the level of gene expression of a polynucleotide that selectively hybridizes
- 10 to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
16 January 2003 (16.01.2003)

PCT

(10) International Publication Number
WO 03/003906 A3

(51) International Patent Classification⁷: **C12Q 1/68**,
C07H 21/04, C07K 14/00

(21) International Application Number: PCT/US02/21338

(22) International Filing Date: 3 July 2002 (03.07.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/302,814 3 July 2001 (03.07.2001) US
60/310,099 3 August 2001 (03.08.2001) US
60/343,705 8 November 2001 (08.11.2001) US
60/350,666 13 November 2001 (13.11.2001) US
60/372,246 12 April 2002 (12.04.2002) US

(71) Applicant: **EOS BIOTECHNOLOGY, INC.** [US/US];
225A Gateway Boulevard, South San Francisco, CA 94080
(US).

(72) Inventors: **MACK, David, H.**; 2076 Monterey Avenue,
Menlo Park, CA 94025 (US). **AZIZ, Natasha**; 411 Cali-
fornia Avenue, Palo Alto, CA 94306 (US).

(74) Agents: **PARENT, Annette, S.** et al.; Townsend and
Townsend and Crew LLP, Two Embarcadero Center,
Eighth Floor, San Francisco, CA 94111 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN,
YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK,
TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, ML, MR, NE, SN, TD, TG).

Published:
— with international search report

(88) Date of publication of the international search report:
6 November 2003

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.



WO 03/003906 A3

(54) Title: **DIAGNOSTIC AND SCREENING METHODS FOR BLADDER CANCER**

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/21338

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/04; C07K 14/00

US CL : 536/24.3; 435/6; 514/2; 530/350, 300

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/24.3; 435/6; 514/2; 530/350, 300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y, B	US 2003/0050470 A1 (AN et al) 13 March 2003 (13.03.03), column page 6, par. 57-62; page page 13, par. 135-141; page 15, par. 158-163; page 30, par. 349-351.	1-20
Y	US 5,866,535 A (GBTZENBERG et al) 02 February 1999 (02.02.1999), column col. 5, lines 43-55; col. 10, lines 31-60; col. 11, lines 30-67.	1-5, 7-20
A	SRINIVAS, P.R. Proteomics in Early Detection of Cancer. Clinical Chemistry. 22 June 2001, Vol. 47, No. 10, pages 1901 -1911, especially pages 1906-1908.	1-20

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

07 April 2003 (07.04.2003)

Date of mailing of the international search report

23 MAY 2003

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Gary Benzion

Telephone No. 703-308-1235